

94 183

From: Parkin, Jeffrey  
Sent: Thursday, May 15, 2003 6:41 PM  
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MAY 16 2003

Please search **SEQ ID NOS.: 1, 3, 4, 5, 117, 118, 119, 534, 535, 536, 537, 538, 540, and 541** from the aforementioned application (09/623,533) v. all relevant databases including interference. Please note that these sequences are all close variations of the same parent peptide.

Place results on both paper and disk.

Thanks!

JSP  
AU 1648  
CM01-8E15  
308-2227

ck

Point of Contact:  
Toby Port  
Technical Info. Specialist  
CM1 6A04  
703-308-3534

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 5/16  
Date Completed: 5/19  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

## TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

## VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 25.512 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-117

Perfect score: 188

Sequence: 1 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mmc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	645	15	0993A6 human immun
2	188	100.0	747	15	070607 human immun
3	188	100.0	748	15	070606 human immun
4	188	100.0	752	15	070604 human immun
5	188	100.0	752	15	070605 human immun
6	188	100.0	752	15	070608 human immun
7	188	100.0	851	15	078243 human immun
8	188	100.0	852	15	089797 human immun
9	188	100.0	854	15	085582 human immun
10	188	100.0	854	15	072502 human immun
11	188	100.0	856	15	092877 human immun
12	188	100.0	856	15	074599 human immun
13	188	100.0	856	15	074090 human immun
14	184	97.9	854	15	090178 human immun
15	184	97.9	854	15	078705 human immun
16	183	97.3	856	15	0905M7 human immun

17	182	96.8	616	15	0993B0 human immun
18	182	96.8	618	15	0993B2 human immun
19	182	96.8	757	15	090732 human immun
20	182	96.8	848	15	069990 human immun
21	180	95.7	838	15	003806 human immun
22	180	95.7	854	15	078225 human immun
23	180	95.7	855	15	003805 human immun
24	179	95.2	42	15	069910 human immun
25	179	95.2	443	15	080023 human immun
26	179	95.2	841	15	041556 human immun
27	179	95.2	849	15	077368 human immun
28	179	95.2	849	15	080851 human immun
29	179	95.2	851	15	056110 human immun
30	179	95.2	851	15	080852 human immun
31	179	95.2	856	15	072993 human immun
32	179	95.2	856	15	041539 human immun
33	179	95.2	857	15	080170 human immun
34	179	95.2	858	15	080190 human immun
35	179	95.2	858	15	080188 human immun
36	179	95.2	859	15	080185 human immun
37	179	95.2	859	15	080180 human immun
38	179	95.2	859	15	080179 human immun
39	179	95.2	859	15	080177 human immun
40	179	95.2	859	15	080173 human immun
41	179	95.2	859	15	080850 human immun
42	179	95.2	862	15	080184 human immun
43	179	95.2	862	15	080183 human immun
44	179	95.2	862	15	080182 human immun
45	179	95.2	862	15	080178 human immun

## ALIGNMENTS

RESULT 1  
ID 0993A6 PRELIMINARY: PRT; 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 100.0%; Score 188; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 8.8e-15;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 35  
DB 608 TSLIHSLIEESQNOQEKNEOELLELDKWSLWNMF 642

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 FT NON\_TER 747 747  
 SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245P14 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 747;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 35  
 DB 634 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1;

DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 FT NON\_TER 748 748  
 SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67994B CRC64;

Query Match 100.0%; Score 188; DB 15; Length 748;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 35  
 DB 635 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 FT NON\_TER 752 752  
 SQ SEQUENCE 752 AA: 84894 MW: 8B30AEB894013B45A CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 35  
 DB 639 TSLIHSLEESQNOQKNEQELLELDKWSLWMMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||  
 DB 639 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT; 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84780 MW; 708672A2DC0E8F8 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||

DB 639 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borselli A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: 211530; CAA77628.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 851  
 SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 851;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 35  
 |||||  
 DB 634 TSLHSLIESONQOEKNEOELLELDKMSLWNMF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 RA AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 852  
 SEQUENCE 852 AA; 96630 MW; 1A3767B987E98027 CRC64;

RT Infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [12]  
RC SEQUENCE FROM N.A.  
RC STRAIN-LW90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12053; AAA76685.1; -  
DR EMBL: U12036; AAA76671.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4E33CF CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 35  
635 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 669  
  
RESULT 9  
ID 085582 PRELIMINARY; PRT: 854 AA.  
AC 085582;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope polypeptide.  
CN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
"Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E.;  
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92219406; PubMed=1373204;  
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
"Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes."  
RT J. Virol. 66:3151-3154(1992).  
DR EMBL: M19921; AAA44992.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 35  
637 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 671  
  
RESULT 10  
ID 072502 PRELIMINARY; PRT: 854 AA.  
AC 072502;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ENV polypeptide.  
CN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
"Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction."  
RT Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-NL4-3;  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
"Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
DR EMBL: U26942; AAB60578.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT CONFLICT 214 214 H -> L (IN REF. 2).  
FT CONFLICT 530 530 A -> S (IN REF. 2).  
FT CONFLICT 739 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
  
Query Match 100.0%; Score 188; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 35  
637 TSLIHSLEESONQOEKNEOELLELDKASLWNMF 671  
  
RESULT 11  
ID 092877 PRELIMINARY; PRT: 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
CN ENV.  
OS Simian-human immunodeficiency virus.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99098984; PubMed=9882298;

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1; -  
 DR InterPro: IPR000328; Env-GP41.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 673

## RESULT 12.

Q74599 PRELIMINARY; PRT; 856 AA.  
 AC Q74599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1; -  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 673

## RESULT 13

Q74090

ID Q74090 PRELIMINARY; PRT; 856 AA.  
 AC Q74090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 188; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 35  
 DB 639 TSLIHSIESQNOQEKNEOELLELDKWSLWNMF 673

## RESULT 14

O90178 PRELIMINARY; PRT; 854 AA.  
 AC O90178;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95074930; PubMed-7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 RT selected with immunotoxins from human immunodeficiency virus type 1-  
 RT infected T cells.";  
 RT J. Virol. 69:75-81(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 RT immunotoxin-resistant variant T cell line.";  
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF070521; AAC28452.1; -  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120.1.  
 DR Pfam: PF00517; GP41.1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.9%; Score 184; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-14;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONQOEKNEELLELDKWSLWNWF 35  
 ||||||||||||||||||||||||||||||||  
 DB 637 TSLIHSLESONQOEKNEELLELDKWSLWNWF 671

## RESULT 15

O78705 PRELIMINARY; PRT; 854 AA.  
 AC O78705;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 GN Human immunodeficiency virus type 1.  
 Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 resistant cell lines chronically infected with human immunodeficiency  
 virus type 1";  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AAA86326.1;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 97.9%; Score 184; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 3.6e-14;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONQOEKNEELLELDKWSLWNWF 35.  
 ||||||||||||||||||||||||||||||||  
 DB 637 TSLIHSLESONQOEKNEELLELDKWSLWNWF 671

Search completed: May 16, 2003, 11:19:45  
 time : 26.5835 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.90964 Seconds  
(Without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-117  
Perfect score: 188  
Sequence: 1 TSLIHSLEESONQOEKNEDELDDKWSLWNF 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents-AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCBUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	35	1 US-08-073-028-74	Sequence 74, App1
2	188	100.0	35	3 US-08-484-223B-234	Sequence 234, App
3	188	100.0	35	4 US-08-554-616-74	Sequence 74, App1
4	188	100.0	35	4 US-09-082-279B-638	Sequence 638, App
5	188	100.0	35	4 US-09-082-279B-799	Sequence 799, App
6	188	100.0	35	4 US-08-474-349A-416	Sequence 416, App
7	188	100.0	35	4 US-09-315-304B-638	Sequence 638, App
8	188	100.0	35	4 US-09-315-304B-799	Sequence 799, App
9	188	100.0	36	1 US-08-073-028-1	Sequence 1, App1
10	188	100.0	36	3 US-08-486-099-1	Sequence 1, App1
11	188	100.0	36	3 US-09-071-877-1	Sequence 1, App1
12	188	100.0	36	3 US-08-360-107A-1	Sequence 1, App1
13	188	100.0	36	3 US-08-484-223B-1	Sequence 1, App1
14	188	100.0	36	3 US-08-484-223B-231	Sequence 231, App
15	188	100.0	36	3 US-08-919-597-1	Sequence 1, App1
16	188	100.0	36	3 US-08-475-668A-1	Sequence 1, App1
17	188	100.0	36	3 US-08-485-551A-1	Sequence 1, App1
18	188	100.0	36	3 US-08-471-913A-1	Sequence 1, App1
19	188	100.0	36	4 US-08-554-616-1	Sequence 1, App1
20	188	100.0	36	4 US-08-485-264A-1	Sequence 1, App1
21	188	100.0	36	4 US-09-082-279B-15	Sequence 15, App1
22	188	100.0	36	4 US-08-082-279B-497	Sequence 497, App
23	188	100.0	36	4 US-09-082-279B-498	Sequence 498, App
24	188	100.0	36	4 US-09-082-279B-561	Sequence 561, App
25	188	100.0	36	4 US-09-082-279B-603	Sequence 603, App
26	188	100.0	36	4 US-09-082-279B-630	Sequence 630, App
27	188	100.0	36	4 US-09-082-279B-631	Sequence 631, App

28	188	100.0	36	4 US-09-082-279B-705	Sequence 705, App
29	188	100.0	36	4 US-09-082-279B-834	Sequence 834, App
30	188	100.0	36	4 US-09-082-279B-1076	Sequence 1076, App
31	188	100.0	36	4 US-09-082-279B-1121	Sequence 1121, App
32	188	100.0	36	4 US-09-082-279B-1161	Sequence 1161, App
33	188	100.0	36	4 US-08-965-056-1	Sequence 1, App1
34	188	100.0	36	4 US-08-965-056-108	Sequence 108, App
35	188	100.0	36	4 US-09-045-920-1	Sequence 1, App1
36	188	100.0	36	4 US-08-474-349A-1	Sequence 1, App1
37	188	100.0	36	4 US-08-474-349A-399	Sequence 399, App
38	188	100.0	36	4 US-08-474-349A-400	Sequence 400, App
39	188	100.0	36	4 US-08-474-349A-413	Sequence 413, App
40	188	100.0	36	4 US-09-315-304B-15	Sequence 15, App1
41	188	100.0	36	4 US-09-315-304B-497	Sequence 497, App
42	188	100.0	36	4 US-09-315-304B-498	Sequence 498, App
43	188	100.0	36	4 US-09-315-304B-561	Sequence 561, App
44	188	100.0	36	4 US-09-315-304B-603	Sequence 603, App
45	188	100.0	36	4 US-09-315-304B-630	Sequence 630, App

ALIGNMENTS

RESULT 1  
US-08-073-028-74  
Sequence 74, Application US/08073028  
Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-74  
Query Match 100.0%; Score 188; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLIHSLEESONQOEKNEDELDDKWSLWNF 35  
DB 1 TSLIHSLEESONQOEKNEDELDDKWSLWNF 35

RESULT 2  
US-08-484-223B-234  
Sequence 234, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-484-223B-234

Query Match 100.0%; Score 188; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35  
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DB 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

RESULT 3  
US-08-554-616-74  
Sequence 74, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-74

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35  
|||||  
DB 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35

RESULT 4  
US-09-082-279B-638  
Sequence 638, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 638  
LENGTH: 35  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-638

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKNASLWNWF 35  
|||||

Db 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

RESULT 5

US-09-082-279B-799

Sequence 799, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 799

LENGTH: 35

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-799

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35-

RESULT 6

US-08-474-349A-416

Sequence 416, Application US/08474349A

Patent No. 6333395

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-024

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 416:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-474-349A-416

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

RESULT 7

US-09-315-304B-638

Sequence 638, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 638

LENGTH: 35

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-638

Query Match

Best Local Similarity 100.0%; Score 188; DB 4; Length 35;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

Db 1 TSLHSLIEESONQOEKNEQELLELDKKNASLWNWF 35

RESULT 8

US-09-315-304B-799

Sequence 799, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: PASTSEQ for Windows Version 3.0  
SEQ ID NO 799  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-799

Query Match 100.0%; Score 188; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.3e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 35  
DB 1 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 35

US-08-073-028-1  
Sequence 1, Application US/08073028

Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, DANI P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1

Query Match 100.0%; Score 188; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 35  
DB 2 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 36

RESULT 10  
US-08-486-099-1  
Sequence 1, Application US/08486099  
Patent No. 6013263

GENERAL INFORMATION:  
APPLICANT: Bolognesi, DANI P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Retaway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 35  
DB 2 TSLIHSLEESONQOEKNEQLLELDKMSLWNMF 36

RESULT 11  
US-09-071-877-1

Sequence 1, Application US/09071877  
Patent No. 6015881  
GENERAL INFORMATION:  
APPLICANT: Kang, Myung-Chol  
APPLICANT: Bray, Brian  
APPLICANT: Lichty, Maynard  
APPLICANT: Wader, Catherine  
APPLICANT: Merutka, Gene  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
FILE REFERENCE: 7872-050  
CURRENT APPLICATION NUMBER: US/09/071,877  
CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 1  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Human immunodeficiency virus  
 US-09-071-877-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 ||||||||||||||||||||||||||||||||  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 12

US-08-360-107A-1  
 Sequence 1, Application US/08360107A  
 Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
 OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 149  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Pennie & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/360,107A  
 FILING DATE: 20-DEC-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-013  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-360-107A-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 ||||||||||||||||||||||||||||||||  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 13

US-08-484-223B-1  
 Sequence 1, Application US/08484223B  
 Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 TITLE OF INVENTION: TRANSMISSION  
 NUMBER OF SEQUENCES: 245  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/484,223B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-029  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-484-223B-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 35  
 ||||||||||||||||||||||||||||||||  
 Db 2 TSLHSLIEESONOEKNEQELLELDKWSLWNWF 36

RESULT 14

US-08-484-223B-231  
 Sequence 231, Application US/08484223B  
 Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Petteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 231:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-231

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLIHLIEESQNOEKNEQELLELDKWSLWNMF 35  
|||||  
Db 1 TSLIHLIEESQNOEKNEQELLELDKWSLWNMF 35

RESULT 15  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dant P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 100.0%; Score 188; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLIHLIEESQNOEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLIHLIEESQNOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:11  
Job time : 9.90964 secs

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15:3213 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-117  
Perfect score: 188  
Sequence: 1 TSLIHSLEESQNOEKNEQLELDKWSLWNF 35

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues  
1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCF\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep:\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/PCF\_US\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	188	100.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	188	100.0	36	9 US-09-493-346-1	Sequence 1, Appl
4	188	100.0	36	10 US-09-796-202-10	Sequence 10, Appl
5	188	100.0	36	10 US-09-779-451-5	Sequence 5, Appl
6	188	100.0	36	10 US-09-834-628-1	Sequence 1, Appl
7	188	100.0	36	10 US-09-854-816-1	Sequence 1, Appl
8	188	100.0	36	10 US-09-854-816-108	Sequence 108, App
9	188	100.0	37	9 US-09-848-616-176	Sequence 176, App
10	188	100.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	188	100.0	56	10 US-09-779-451-4	Sequence 4, Appl
12	188	100.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	188	100.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	188	100.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	188	100.0	254	9 US-10-059-271-82	Sequence 82, Appl
16	188	100.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	188	100.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	188	100.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	188	100.0	268	10 US-09-854-816-18	Sequence 18, Appl

20	188	100.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	188	100.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	188	100.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	188	100.0	392	9 US-10-059-271-93	Sequence 93, Appl
24	188	100.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	188	100.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	188	100.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	188	100.0	861	9 US-10-026-741-103	Sequence 103, Appl
28	188	100.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	188	100.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	185	98.4	36	10 US-09-912-824-1	Sequence 1, Appl
31	185	98.4	268	10 US-09-854-816-19	Sequence 19, Appl
32	182	96.8	1231	9 US-10-059-271-94	Sequence 94, Appl
33	180	95.7	268	10 US-09-854-816-13	Sequence 13, Appl
34	179	95.2	233	10 US-09-854-816-50	Sequence 50, Appl
35	179	95.2	268	10 US-09-854-816-9	Sequence 9, Appl
36	179	95.2	269	10 US-09-854-816-12	Sequence 12, Appl
37	178	94.7	269	10 US-09-854-816-46	Sequence 46, Appl
38	177	94.1	269	10 US-09-854-816-28	Sequence 28, Appl
39	176	93.6	268	10 US-09-854-816-26	Sequence 26, Appl
40	176	93.6	619	10 US-09-891-609-4	Sequence 4, Appl
41	176	93.6	646	10 US-09-891-609-2	Sequence 2, Appl
42	176	93.6	847	10 US-09-476-242-2	Sequence 2, Appl
43	175	93.1	46	10 US-09-854-816-109	Sequence 109, App
44	175	93.1	267	10 US-09-854-816-38	Sequence 38, Appl
45	175	93.1	268	10 US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication NO. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
FILE REFERENCE: 2793/65166  
CURRENT APPLICATION NUMBER: US/09/874,475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 188; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6; 2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TSLIHSLEESQNOEKNEQLELDKWSLWNF 35  
Db 2 TSLIHSLEESQNOEKNEQLELDKWSLWNF 36  
RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US2003004411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116,797  
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 100.0%; Score 188; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Madison, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 100.0%; Score 188; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

HT 4  
US-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 100.0%; Score 188; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 100.0%; Score 188; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DPL78  
US-09-834-628-1

Query Match 100.0%; Score 188; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 35  
|||||  
Db 2 TSLHSLIEESONOQEKNEQELLELDKWSLWNMF 36

Query Match	Best Local Similarity	Score	DB ID	Length
Matches 35: Conservative	100.0%	188	DB 10:	36
	0			Indels 0; Gaps 0
<p>1 TSLIHSLEESQNOEKNEQELLEDKVASLWNWF 35</p> <p>2 TSLIHSLEESQNOEKNEQELLEDKVASLWNWF 36</p>				
<p>RESULT 9</p> <p>US-09-848-616-176</p> <p>Sequence 176, Application US/09848616</p> <p>Publication No. US20030054010A1</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Seibel, Peter</p> <p>APPLICANT: Dunant, Nicolas</p> <p>APPLICANT: Bachmann, Martin</p> <p>APPLICANT: Tissot, Alain</p> <p>APPLICANT: Lechner, Franziska</p> <p>TITLE OF INVENTION: Molecular Antigen Array</p> <p>FILE REFERENCE: 1700.0180002</p> <p>CURRENT APPLICATION NUMBER: US/09/848.616</p> <p>CURRENT FILING DATE: 2001-05-05</p> <p>NUMBER OF SEQ ID NOS: 186</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 176</p> <p>LENGTH: 37</p> <p>TYPE: PRT</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: DP178c peptide</p> <p>US-09-848-616-176</p>				
Query Match	100.0%	Score 188;	DB 9:	Length 37;
Best Local Similarity	100.0%	Pred. NO. 6.4e-16;		
Matches 35: Conservative	0	Mismatches 0;	Indels 0;	Gaps 0;
<p>1 TSLIHSLEESQNOEKNEQELLEDKVASLWNWF 35</p>				

```
Db      3  TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 37
RESULT 10
US-09-779-451-41
; Sequence 41, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-41
Query Match      100.0%; Score 188; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 8e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 35
Db      12 TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 46
RESULT 11
US-09-779-451-4
; Sequence 4, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4
Query Match      100.0%; Score 188; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 35
Db      17 TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 51
RESULT 12
US-10-040-349B-2
; Sequence 2, Application US/10040349B
; Publication No. US20030082521A1
; GENERAL INFORMATION:
; APPLICANT: Brasseur, Robert
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; APPLICANT: Charloleaux, Benoit
; APPLICANT: Chevallier, Michel
; APPLICANT: El Habib, Raphaelle
; APPLICANT: Krell, Tino
; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
; FILE REFERENCE: 01-078-A
; CURRENT APPLICATION NUMBER: US/10/040,349B
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(177)
; OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2
Query Match      100.0%; Score 188; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 35
Db      105 TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 139
RESULT 13
US-10-059-271-84
; Sequence 84, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; SOFTWARE: PatentIn Ver. 2.1
; NUMBER OF SEQ ID NOS: 97
; SEQ ID NO 84
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84
Query Match      100.0%; Score 188; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 35
Db      132 TSLIHSLEESONQOEKNEOELLELDKWSLWNMF 166
RESULT 14
US-10-059-271-81
; Sequence 81, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
```

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; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

```

```

Query Match          100.0%; Score 188; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

1 TSLIHSLSIESQNOQEKNEQELLELDKWSLWME 35
|||||
DB 145 TSLIHSLSIESQNOQEKNEQELLELDKWSLWME 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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```

Query Match          100.0%; Score 188; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TSLIHSLSIESQNOQEKNEQELLELDKWSLWME 35
|||||
DB 167 TSLIHSLSIESQNOQEKNEQELLELDKWSLWME 201

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Search completed: May 16, 2003, 12:10:23  
Job time : 15.3213 secs

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07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petteway SR, Wild CT;  
 DR WPI: 1995-036105/05.  
 XX  
 XX  
 PT Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11: Page 133; 182pp; English.  
 CC AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
 CC truncated at the amino terminus. DP-178 corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. The peptide derivs. were identified by a computer assisted  
 CC peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype  
 CC specific diagnostic tools.  
 XX  
 SQ Sequence 34 AA:

Query Match 100.0%; Score 183; DB 16; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 ||||||||||||||||||||||||||||  
 DB 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34

RESULT 2  
 AAB52686  
 ID AAB52686 standard; Peptide: 34 AA.  
 XX  
 AC AAB52686;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #64.  
 XX  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.  
 XX  
 KW Human immunodeficiency virus type 1.  
 XX  
 PN WO200066622-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 05-MAY-2000; 2000WO-US12371.  
 XX  
 PR 05-MAY-1999; 99US-0132686.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX  
 DR WPI: 2000-656493/63.  
 XX  
 PT Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation -  
 XX  
 PS Claim 12; Page 25; 148pp; English.  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is

CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemottractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 XX  
 SQ Sequence 34 AA:

Query Match 100.0%; Score 183; DB 21; Length 34;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34  
 ||||||||||||||||||||||||||||  
 DB 1 SLIHSLIESONQOEKNEQELLELDKWSLWMWF 34

RESULT 3  
 AAB14669  
 ID AAB14669 standard; peptide: 34 AA.  
 XX  
 AC AAB14669;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #63.  
 XX  
 KW HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 KW isolate LAI.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200040616-A1.  
 XX  
 PD 13-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000WO-US00456.  
 XX  
 PR 08-JAN-1999; 99US-0115404.  
 XX  
 PR 07-JAN-2000; 2000US-0480336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX  
 PI Wild CT, Weiss CD;  
 XX  
 DR WPI: 2000-465959/40.  
 XX  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled coil solution structure -  
 XX  
 PS Disclosure; Page 33; 97pp; English.  
 XX  
 XX Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralizing antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides

CC can be administered either singly or as a combination (particularly  
CC a combination of N-helical and C-helical peptides), and can be  
CC multimerised. For example, N- and C-helical domain peptides can be  
CC alternately linked together to form a peptide which mimics the core  
CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
CC response, with the production of antibodies against gp41 structures  
CC involved in viral entry. As these portions of gp41 are well conserved,  
CC such antibodies may be effective against a broad range of HIV strains  
CC and isolates. The peptide compositions may be administered as a  
CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
CC or inhibit the ability of HIV to infect uninfected cells. A composition  
CC comprising polyclonal or monoclonal antibodies can be administered to  
CC reduce HIV infection of uninfected cells. Antibodies raised against  
CC entry-relevant gp41 structures may also be used therapeutically and as  
CC tools to further elucidate the mechanism of HIV cell entry.

XX Sequence 34 AA:

Query Match 100.0%; Score 183; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34  
|||||  
DB 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34

RESULT 4

AAV89389

ID AAV89389 standard; peptide; 34 AA.

AC AAV89389;

DT 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 924.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX anti-fusogenic; differentiation factor; interleukin; interferon;  
XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS WO959615-A1.

XX WO959615-A1.

XX 25-NOV-1999.

PD 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1999; 99WO-US11219.

PR 20-MAY-1998; 98US-0082279.

PA (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -

PT Disclosure; Page 35; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAV8651-190055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

XX Sequence 34 AA:

Query Match 100.0%; Score 183; DB 21; Length 34;  
Best Local Similarity 100.0%; Pred. No. 1.1e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY -1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34  
|||||  
DB 1 SLIHSLEESQNOQEKNEQELLELDKWSLWNMF 34

RESULT 5

ABW00797

ID ABW00797 standard; peptide; 34 AA.

AC ABW00797;

DT 03-JAN-2002 (first entry)

XX Viral DP178/107-like region peptide T924.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
XX virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
XX infection.

XX Virididae.

OS

XX Key Modified-site 34 Location/Qualifiers

FT Modified-site 34 /note="C-terminal amide"

XX MO200164013-A2.

XX 07-SEP-2001.

PD 07-FEB-2001; 2001WO-US03988.

XX 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

PR (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
XX fusion, useful for treating HIV and Respiratory syncytial virus  
XX infection -

PT Disclosure; Page 49; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
XX 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
XX HR1) respectively, of HIV-1/IIA1 transmembrane protein gp41. The HRI  
XX and HR2 regions of proteins interact non-covalently with each other  
XX and/or with peptides derived from them. This interaction is required for  
XX normal infectivity of viruses such as RSV and HIV. The heptad  
XX repeat region peptide analogues may be used to inhibit respiratory  
XX syncytial virus (RSV) infection in a cell. They may also be used to  
XX inhibit HIV infection. The present sequence is a peptide provided in  
XX the specification.

XX Sequence 34 AA:

```

Query Match          100.0%; Score 183; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34
    |||||||
DB 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34

RESULT 6
ABB02273
ID ABB02273 standard; Peptide; 34 AA.
XX
AC ABB02273;
XX
DT 03-JAN-2002 (first entry)
XX
DE Viral core polypeptide, SEQ ID NO: 800.
XX
DE Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX infection; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX infection.
XX
OS Virididae.
XX
PN WO200164013-A2.
XX
PD 07-SEP-2001.
XX
PF 07-FEB-2001; 2001WO-US03988.
XX
PR 29-FEB-2000; 2000US-0515965.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX WPI; 2001-514829/56.
XX
DR WPI; 2001-514829/56.
XX
PT Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX infection.
XX
PS Disclosure; Page 380; 587pp; English.
XX
XX The invention relates to isolated analogues of the heptad repeat region
XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
XX 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
XX HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1
XX and HR2 regions of proteins interact non-covalently with each other
XX and/or with peptides derived from them. This interaction is required for
XX normal infectivity of viruses such as RSV and HIV. The heptad
XX repeat region peptide analogues may be used to inhibit respiratory
XX syncytial virus (RSV) infection in a cell. They may also be used to
XX inhibit HIV infection. The present sequence is a peptide provided in
XX the specification.
XX
SQ Sequence 34 AA;

Query Match          100.0%; Score 183; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34
    |||||||
DB 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34

RESULT 7
AAU13343
ID AAU13343 standard; Peptide; 34 AA.
XX
AC AAU13343;

```

```

XX
DT 21-NOV-2001 (first entry)
XX
XX DPl78-1like/DPl07-1like peptide T-924.
DE DPl78-1like/DPl07-1like peptide T-924.
XX
XX Anti-retroviral; DPl78-1like; DPl07-1like; transmembrane protein gp41;
KW antifusogenic; antiviral; HIV transmission; mutant; mutain.
XX
XX Human immunodeficiency virus 1 isolate LAI.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 34
FT /note= "C-terminal amide"
XX
XX WO200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US35727.
XX
XX 09-JUL-1999; 99US-0350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX DR WPI; 2001-442157/47.
XX
XX PT Identifying a compound that inhibits the formation of or disrupts a
XX DPl07/DPl78 complex, especially compounds with antifusogenic, antiviral
XX or intracellular modulatory activity, by detecting the formation of a
XX DPl07/DPl78 complex.
XX
XX PS Disclosure; Page 68; 259pp; English.
XX
XX CC The present invention relates to peptides which exhibit anti-retroviral
XX activity. The peptides of the invention (AAU12559-AAU14009) comprise
XX DPl78-1like and DPl07-1like peptides. The DPl78 peptide corresponds
XX to amino acids 639-673 of the transmembrane protein gp41 from human
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DPl07 peptide
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
XX also relates to a method of identifying compounds that inhibit the
XX formation of or disrupts a DPl07/DPl78 complex. The method comprises
XX detecting the formation of a DPl07/DPl78 complex, both in the presence
XX or absence of a test compound, in a reaction mixture containing DPl07
XX and DPl78 peptides. The method is useful for identifying compounds,
XX including small molecule compounds, which may themselves exhibit
XX antifusogenic, antiviral or intracellular modulatory activity. The
XX DPl78-1like/DPl07-1like peptides are useful to inhibit human and non-human
XX retroviral, particularly HIV, transmission to uninfected cells. The
XX present sequence represents one of the DPl78-1like/DPl07-1like peptides
XX of the invention.
XX
SQ Sequence 34 AA;

Query Match          100.0%; Score 183; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34
    |||||||
DB 1 SLIHSLSIESQNOQEKNEDELLELDKWSLWNNF 34

RESULT 8
AAB77790
ID AAB77790 standard; Peptide; 34 AA.
XX
AC AAB77790;
XX
DT 19-APR-2001 (first entry)
XX

```



OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 1 /note= "optionally has an amino- acetyl,  
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or  
FT macromolecular carrier gp. attached"  
FT Modified-site 35 /note= "optionally has a carboxyl, amido, hydrophobic  
FT or macromolecular carrier gp. attached"  
XX  
XX WO9428920-A.  
XX  
XX 22-DEC-1994.  
XX  
XX 07-JUN-1994; 94WO-US05739.  
XX  
XX 07-JUN-1993; 93US-0073028.  
XX  
XX (UYDU-) UNIV DUKE.  
XX  
XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
PI Petterwey SR, Wild CT;  
XX WPI; 1995-036105/05.  
XX  
XX Computer search generated synthetic peptides - are inhibitors of  
PT HIV transmission  
XX  
XX Claim 11; Page 133; 182pp; English.  
XX  
XX AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
CC truncated at the amino terminus. DP-178 corresponds to amino acids  
CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
CC forms a putative alpha helix at the C-terminal end of the gp41  
CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
CC 558-595) which contains a leucine zipper motif. The peptides complex  
CC via non-covalent protein-protein interactions, and possess anti-viral  
CC activity. The peptide derivs. were identified by a computer assisted  
CC peptide sequence search. The peptides inhibit transmission to  
CC uninfected cells, and can also be used as type and/or subtype  
CC specific diagnostic tools.  
XX  
XX Sequence 35 AA:  
SQ  
Query Match 100.0%; Score 183; DB 16; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 34  
|||||  
2 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 35  
DB  
RESULT 11  
AAB52687  
ID AAB52687 standard; Peptide; 35 AA.  
XX  
XX AAB52687;  
XX  
XX 23-FEB-2001 (first entry)  
XX  
XX T20/DP178 peptide fragment #65.  
DE  
XX  
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KW chemottractant.  
XX  
XX Human immunodeficiency virus type 1.  
OS  
XX  
XX WO20006622-A1.  
XX  
XX 09-NOV-2000.

XX  
XX 05-MAY-2000; 2000WO-US12371.  
XX  
XX 05-MAY-1999; 99US-0132686.  
XX  
XX (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
PI WPI; 2000-656493/63.  
XX  
XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 25; 148pp; English.  
XX  
XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemottractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX Sequence 35 AA:  
SQ  
Query Match 100.0%; Score 183; DB 21; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 34  
|||||  
2 SLIHSLSIESQNOQEKNEDELLELDKWSLWMNF 35  
DB  
RESULT 12  
AAB14670  
ID AAB14670 standard; peptide; 35 AA.  
XX  
XX AAB14670;  
XX  
XX 24-NOV-2000 (first entry)  
XX  
XX HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #64.  
DE  
XX  
XX HIV-1; gp41 C-helical domain;  
KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
KW core 6-helix bundle; viral entry inhibition; immunogenic;  
KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
KW isolate LAI.  
XX  
XX Human immunodeficiency virus type 1.  
OS  
XX  
XX WO200040616-A1.  
XX  
XX 13-JUL-2000.  
XX  
XX 10-JAN-2000; 2000WO-US00456.  
XX  
XX 08-JAN-1999; 99US-0115404.  
XX  
XX 07-JAN-2000; 2000US-0480336.  
XX  
XX (WIID/) WIID C T.  
XX (WEISS/) WEISS C D.  
XX  
XX Wild CT, Weiss CD;  
PI WPI; 2000-465959/40.  
XX  
XX

PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

PS Disclosure; Page 34; 97pp; English.

CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralising antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane/proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can be  
 CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures,  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC tools to further elucidate the mechanism of HIV cell entry.

SO Sequence 35 AA:

Query Match 100.0%; Score 183; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSIIESNQOEKNEDELLEDKWASLWMPF 34  
 ||||||||||||||||||||||||||||||||  
 DB 2 SLIHSIIESNQOEKNEDELLEDKWASLWMPF 35

RESULT 13  
 AAY89388

AAY89388 standard; peptide; 35 AA.

AC AAY89388;

DT 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 923.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US11219.

PR 20-MAY-1998; 98US-0082279.

PA (TRIM-) TRIMERIS INC.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 35; 124pp; English.

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SO Sequence 35 AA:

Query Match 100.0%; Score 183; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-15;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSIIESNQOEKNEDELLEDKWASLWMPF 34  
 ||||||||||||||||||||||||||||||||  
 DB 2 SLIHSIIESNQOEKNEDELLEDKWASLWMPF 35

RESULT 14  
 ABB00634

ID ABB00634 standard; peptide; 35 AA.

AC ABB00634;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T715.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRL; HR2;  
 KW infection.

XX Viridiae.

OS Viridiae.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal is substituted by Ac"

FT Modified-site 35 /note= "C-terminal amide"

PN WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.



GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.4699 Seconds

(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-118

Perfect score: 183  
Sequence: 1 SLIHSLEESQNOQEKNEQELLELDKWSLWVNF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

al number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	851	2	S33985 env polypotein - huma
2	183	100.0	854	2	S13288 env polypotein pr
3	183	100.0	856	1	VCLJH3 env polypotein pr
4	183	100.0	861	1	VCLJLV env polypotein pr
5	174	95.1	856	1	C41621 env polypotein pr
6	174	95.1	856	1	VCLJVL env polypotein pr
7	174	95.1	856	1	VCLJW env polypotein pr
8	174	95.1	861	1	VCLJSC env polypotein pr
9	171	93.4	357	2	S21994 env polypotein pr
10	171	93.4	358	2	S21998 env polypotein g
11	170	92.9	347	2	S21996 env polypotein g
12	167	91.3	847	2	T09448 env polypotein g
13	167	91.3	847	2	S13289 env polypotein g
14	166	90.7	445	2	A41621 env polypotein M
15	165	90.2	358	2	S22002 env polypotein g
16	165	90.2	358	2	S22000 env polypotein g
17	165	90.2	358	2	S70417 env polypotein g
18	165	90.2	852	2	T12016 env polypotein g
19	165	90.2	859	2	VCLJMN env polypotein pr
20	164	89.6	357	2	S22004 env polypotein g
21	164	89.6	855	1	VCLJAJ2 env polypotein pr
22	162	88.5	843	1	H44001 env polypotein pr
23	162	88.5	853	1	S54384 env polypotein pr
24	162	88.5	855	1	VCLJZR env polypotein pr
25	161	88.0	357	2	S22006 env polypotein pr
26	160	87.4	846	1	VCLJND env polypotein pr
27	158	86.3	357	2	S21992 env polypotein pr
28	158	86.3	852	1	VCLJBR env polypotein pr
29	156	85.2	729	1	VCLJXK env polypotein pr

30	156	85.2	861	1	VCLJKB env polypotein pr
31	155	84.7	859	2	T01672 env polypotein pr
32	154	84.2	454	2	B41621 env polypotein D
33	152	83.1	868	1	VCLJH4 env polypotein -
34	148	80.9	136	2	J00266 env polypotein -
35	148	80.9	136	2	J00266 env polypotein -
36	141	77.0	854	1	VCLJST env polypotein pr
37	137	74.9	856	1	A44963 env polypotein pr
38	135	73.8	357	2	S21990 env polypotein g
39	135	73.8	877	2	S49197 env polypotein g
40	118	64.5	863	2	A53034 env polypotein -
41	86	47.0	881	1	VCLJG3 env polypotein -
42	86	47.0	881	2	S03068 env polypotein -
43	86	47.0	889	1	VCLJG5 env polypotein -
44	85	46.4	151	2	S30448 env polypotein -
45	85	46.4	151	2	S30452 env polypotein -

#### ALIGNMENTS

RESULT 1  
S33985  
env polypotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-References: EMBL:211530; NID:960192; PIDN:CAA7628.1; PID:960199  
C:Superfamily: type E retrovirus env polypotein

Query Match  
Best Local Similarity 100.0%; Score 183; DB 2; Length 851;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLIHSLEESQNOQEKNEQELLELDKWSLWVNF 34  
Db 635 SLIHSLEESQNOQEKNEQELLELDKWSLWVNF 668

RESULT 2  
S13288  
env polypotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match  
Best Local Similarity 100.0%; Score 183; DB 2; Length 854;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLIHSLEESQNOQEKNEQELLELDKWSLWVNF 34  
Db 638 SLIHSLEESQNOQEKNEQELLELDKWSLWVNF 671

RESULT 3  
VCLJH3

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora  
nberger, J.A.; Papas, T.S.; Chareb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAAA442  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
E:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:31-316/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predi  
cated  
Query Match 100.0%; Score 183; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,1e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEOELLELDKASLWNF 34  
DB 640 SLIHSLEESQNOEKNEOELLELDKASLWNF 673

RESULT 4  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allison, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85093333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAI>  
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
E:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:31-316/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predi  
cated  
Query Match 100.0%; Score 183; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 4,1e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEOELLELDKASLWNF 34  
DB 645 SLIHSLEESQNOEKNEOELLELDKASLWNF 678

RESULT 5  
env polypeptide precursor - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity.  
A:Reference number: A41621; MUID:92107924; PMID:1765038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
E:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
predicted  
Query Match 95.1%; Score 174; DB 2; Length 443;  
Best Local Similarity 94.1%; Pred. No. 2.4e-13;  
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEOELLELDKASLWNF 34  
DB 380 SLIHSLEESQNOEKNEOELLELDKASLWNF 413

RESULT 6  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Muesling, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr  
ovirus.  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:9328559  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
E:1-30/Domain: signal sequence #status predicted <Sig>  
F:1-30/Domain: signal sequence #status predicted <Sig>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre  
dicted  
Query Match 95.1%; Score 174; DB 1; Length 856;  
Best Local Similarity 97.0%; Pred. No. 4.9e-13;  
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEOELLELDKASLWNF 33  
DB 640 SLIHSLEESQNOEKNEOELLELDKASLWNF 672

RESULT 7  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774  
 R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 95.1%; Score 174; DB 1; Length 856;  
 Best Local Similarity 94.1%; Pred. No. 4.9e-13;  
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSILIESQNOEKNEQELLELDKWSLWNMF 34  
 DB 640 SLIYTLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #ext\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:7,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.1%; Score 174; DB 1; Length 861;  
 Best Local Similarity 94.1%; Pred. No. 5e-13;  
 Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSILIESQNOEKNEQELLELDKWSLWNMF 34  
 DB 645 SLIYTLIESQNOEKNEQELLELDKWSLWNMF 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.4%; Score 171; DB 2; Length 357;  
 Best Local Similarity 91.2%; Pred. No. 4.3e-13;  
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSILIESQNOEKNEQELLELDKWSLWNMF 34  
 DB 141 TLIVTLIESQNOEKNEQELLELDKWSLWNMF 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE1>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222, 'X', 224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.4%; Score 171; DB 2; Length 358;  
 Best Local Similarity 91.2%; Pred. No. 4.3e-13;  
 Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSILIESQNOEKNEQELLELDKWSLWNMF 34  
 DB 142 SLIYTLIESQNOEKNEQELLELDKWSLWNMF 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #ext\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypotein

Query Match 92.9%; Score 170; DB 2; Length 357;  
Best Local Similarity 93.9%; Pred. No. 5,6e-13;  
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLHSLIESQNOQEKNEQLELDKWSLWNF 34  
DB 142 LLYTLIESQNOQEKNEQLELDKWSLWNF 174

# RESULT 12

env polypotein - human immunodeficiency virus type 1 (strain JRP1)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Panig, S.; Vinters, H.V.; Akashl, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
Reference number: Z1673  
Accession: T09448  
Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.3%; Score 167; DB 2; Length 847;  
Best Local Similarity 91.2%; Pred. No. 3,4e-12;  
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEQLELDKWSLWNF 34  
DB 631 SEIYTLIESQNOQEKNEQLELDKWSLWNF 664

# RESULT 13

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
Accession: S13289  
Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.3%; Score 167; DB 2; Length 847;  
Best Local Similarity 91.2%; Pred. No. 3,4e-12;  
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEQLELDKWSLWNF 34  
DB 631 SEIYTLIESQNOQEKNEQLELDKWSLWNF 664

# RESULT 14

env polypotein M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypotein  
M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: A41621  
R:Burger, H.; Weisner, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621  
A:Molecule type: DNA  
A:Residues: 1-445 <BUR>  
A:Cross-references: GB:M77228; NID:9328627; PID:NAB03790.1; PID:9555013  
A:Note: this virus was isolated from the mother  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:426-445/Domain: transmembrane #status predicted <TM>  
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 90.7%; Score 165; DB 2; Length 445;  
Best Local Similarity 88.2%; Pred. No. 2,2e-12;  
Matches 30; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEQLELDKWSLWNF 34  
DB 382 SLIYTLIESQNOQEKNEQLELDKWSLWNF 415

# RESULT 15

env polypotein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 3L  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S22002; S70418  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by regions of gp120  
A:Reference number: S21990  
Accession: S22002  
A:Molecule type: DNA  
A:Residues: 1-358 <STEL>  
A:Cross-references: EMBL:X61352; NID:960186; PID:CA43616.1; PID:960187  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by regions of gp120  
A:Reference number: S70417; MUID:92144209; PMID:1736540  
Accession: S70418  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-333, 'X', 335-358 <STEL>  
A:Cross-references: EMBL:X61352; NID:960186  
C:Superfamily: type E retrovirus env polypotein

Query Match 90.2%; Score 165; DB 2; Length 358;  
Best Local Similarity 88.2%; Pred. No. 2,2e-12;  
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 SLHSLIESQNOQEKNEQLELDKWSLWNF 34  
DB 142 SLIYTLIESQNOQEKNEQLELDKWSLWNF 175

Search completed: May 16, 2003, 11:25:08  
Job time: 12.4699 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 5.73494 Seconds  
(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-118  
Perfect score: 183  
Sequence: 1 SLIHSLIESSQNOEKNEELLEIDKMASLWNNF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues  
al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	100.0	851	1 ENV_HV1B8	P04582 human immun
2	183	100.0	856	1 ENV_HV1B1	P03375 human immun
3	183	100.0	856	1 ENV_HV1H2	P04578 human immun
4	183	100.0	856	1 ENV_HV1H3	P04624 human immun
5	183	100.0	856	1 ENV_HV1LW	O70626 human immun
6	183	100.0	861	1 ENV_HV1LW	P03377 human immun
7	180	98.4	853	1 ENV_HV1M6	P19551 human immun
8	174	95.1	856	1 ENV_HV1P6	P03376 human immun
9	174	95.1	856	1 ENV_HV1SC	P03878 human immun
10	174	95.1	856	1 ENV_HV1S3	P19549 human immun
11	172	94.0	852	1 ENV_HV1S3	P19550 human immun
12	171	93.4	847	1 ENV_HV1S1	P19550 human immun
13	168	91.8	847	1 ENV_HV1M2	P05880 human immun
14	167	91.3	867	1 ENV_HV1J3	P12489 human immun
15	165	90.2	856	1 ENV_HV1M2	P05877 human immun
16	164	89.6	855	1 ENV_HV1A2	P03378 human immun
17	163	89.1	853	1 ENV_HV1E2	P04581 human immun
18	163	89.1	865	1 ENV_HV1RH	P04579 human immun
19	162	88.5	843	1 ENV_HV1Y2	P33961 human immun
20	162	88.5	853	1 ENV_HV1Y2	P12487 human immun
21	162	88.5	855	1 ENV_HV1Z6	P04580 human immun
22	161	88.0	855	1 ENV_HV1Y6	P12487 human immun
23	160	87.4	846	1 ENV_HV1ND	P18799 human immun
24	158	86.3	852	1 ENV_HV1BN	P12488 human immun
25	157	85.8	848	1 ENV_HV1JR	P20871 human immun
26	156	85.2	861	1 ENV_HV1KB	P31819 human immun
27	155	84.7	859	1 ENV_HV1MA	P04583 human immun
28	152	83.1	868	1 ENV_HV1C4	P05879 human immun
29	150	82.0	863	1 ENV_HV1Z8	P05882 human immun
30	141	77.0	854	1 ENV_HV1C2	P17281 chimpanzee
31	137	74.9	856	1 ENV_HV1ZH	P05881 human immun
32	90	49.2	854	1 ENV_HV1AI	O02837 simian immu
33	86	47.0	881	1 ENV_STVMK	P05884 simian immu

34	86	47.0	882	1 ENV_STVM1	P05885 simian immu
35	85	46.4	885	1 ENV_STVS4	P12492 simian immu
36	84	45.9	859	1 ENV_HV2D2	P15831 human immu
37	84	45.9	860	1 ENV_HV2BE	P18094 human immu
38	82	44.8	880	1 ENV_STVMK	P11267 human immu
39	80	43.7	859	1 ENV_HV2CA	P24105 human immu
40	80	43.7	889	1 ENV_STVSP	P19503 simian immu
41	77	42.1	846	1 ENV_HV2SB	P12449 human immu
42	77	42.1	851	1 ENV_HV2D1	P17755 human immu
43	77	42.1	851	1 ENV_HV2G1	P18040 human immu
44	77	42.1	858	1 ENV_HV2RO	P04577 human immu
45	77	42.1	859	1 ENV_HV2ST	P20872 human immu

ALIGNMENTS

RESULT 1	ENV_HV1B8	STANDARD;	PRT;	851 AA.
ID	ENV_HV1B8			
AC	P04582;			
DT	13-AUG-1987 (rel. 05, Last sequence update)			
DT	13-AUG-1987 (rel. 05, Last sequence update)			
DT	15-JUL-1999 (rel. 38, Last annotation update)			
DE	Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11684;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patara R., Lyack K.J., Starich B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.D., Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RA	Nature 313:277-284(1985).			
RL				
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CC	EMBL, K02011; AAA44661.1; -			
CC	HTV, K02011; ENVS8H8.			
DR	GlycosultedB: P04582; -			
DR	InterPro: IPR000328; ENV_Gp41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS: Coat protein; Polypeptide; Polypeptide; Transmembrane; Signal.			
KW	SIGNAL.			
FT	CHAIN	1	30	
FT	CHAIN	507	506	
FT	CHAIN	507	851	
FT	DISULFID	54	74	
FT	DISULFID	119	205	
FT	DISULFID	126	196	
FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	440	
FT	DISULFID	385	413	
FT	CARBOHYD	8	88	
FT	CARBOHYD	136	136	
FT	CARBOHYD	141	141	
FT	CARBOHYD	141	141	

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA: 96644 MW: D16A3C90857785F1 CRC64:

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Query Match 100.0%; Score 183; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SLIHSLEESQNOEKNEDELLELDKWSLWNF 34
DB 635 SLIHSLEESQNOEKNEDELLELDKWSLWNF 668

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RESULT 2
ENV_HV1B1 STANDARD: PRT; 856 AA.
ID ENV_HV1B1
AC P03375;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
RA Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
RA Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RA NCBI_TaxID=11678;
RN SEQUENCE FROM N.A.
RP MEDLINE=8511123; PubMed=2578615;
RX Ratter L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumelster K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Ghayab J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RA Nature 313:277-284(1985).
RL Nature 313:277-284(1985).
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RP MEDLINE=90285159; PubMed=2355006;
RX Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382(1990).
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```

CC EMBL: M15654; AAA44205.1;
CC PIR: A03973; VCLJH3.
CC HIV: M15654; ENVSBH102.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA: 97224 MW: 0BF6B1A18931BB27 CRC64:

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Query Match 100.0%; Score 183; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6.5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SLIHSLEESQNOEKNEDELLELDKWSLWNF 34
DB 640 SLIHSLEESQNOEKNEDELLELDKWSLWNF 673

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```

RESULT 3
ENV_HV1B2 STANDARD: PRT; 856 AA.
ID ENV_HV1B2
AC P04578; 009779;

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DT	13-AUG-1987	(Rel. 05, Created)	
DT	15-JUL-1999	(Rel. 38, Last sequence update)	
DT	30-MAY-2000	(Rel. 39, Last annotation update)	
DE	Envelope polyprotein	GPI60 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].	
GN	ENV.		
OS	Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11706;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=87299196; PubMed=3040055;		
RA	Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,		
RA	Gallo R.C., Wong-Staal F.;		
RT	"Complete nucleotide sequences of functional clones of the AIDS virus."		
RL	AIDS Res. Hum. Retroviruses 3:57-69(1987).		
RN	[2]		
RP	REVIEWS.		
RA	Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,		
RA	Gallo R.C., Wong-Staal F.;		
CC	Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.		
CC	-----		
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL, AF0455; AAB50262.1; -		
DR	EMBL, AF038399; AAB99976.1; -		
DR	EMBL, AF033819; AAC82596.1; -		
DR	HIV, K03455; ENVSXB2.		
DR	InterPro: IPR000328; E0V, GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam: PF00516; GP120; 1.		
DR	Pfam: PF00517; GP41; 1.		
KW	AIDS; Coat protein; Glycoprotein; Glycoprotein; Transmembrane;		
KW	Signal.		
FT	SIGNAL.	30	
FT	CHAIN	1	511
FT	CHAIN	512	856
FT	DISULFID	54	74
FT	DISULFID	119	205
FT	DISULFID	126	196
FT	DISULFID	131	157
FT	DISULFID	218	247
FT	DISULFID	228	239
FT	DISULFID	296	331
FT	DISULFID	378	445
FT	DISULFID	385	418
FT	CARBOHYD	88	
FT	CARBOHYD	136	136
FT	CARBOHYD	141	141
FT	CARBOHYD	156	156
FT	CARBOHYD	160	160
FT	CARBOHYD	186	186
FT	CARBOHYD	197	197
FT	CARBOHYD	230	230
FT	CARBOHYD	234	234
FT	CARBOHYD	241	241
FT	CARBOHYD	262	262
FT	CARBOHYD	276	276
FT	CARBOHYD	289	289
FT	CARBOHYD	295	295
FT	CARBOHYD	301	301
FT	CARBOHYD	332	332
FT	CARBOHYD	339	339
FT	CARBOHYD	356	356
FT	CARBOHYD	386	386
FT	CARBOHYD	392	392
FT	CHAIN	392	511
FT	DISULFID	54	74
FT	DISULFID	119	205
FT	DISULFID	126	196
FT	DISULFID	131	157
FT	DISULFID	218	247
FT	DISULFID	228	239
FT	DISULFID	296	331
FT	DISULFID	378	445
FT	DISULFID	385	418
FT	CARBOHYD	88	
FT	CARBOHYD	136	136
FT	CARBOHYD	141	141
FT	CARBOHYD	156	156
FT	CARBOHYD	160	160
FT	CARBOHYD	186	186
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FT	CARBOHYD	332	332
FT	CARBOHYD	339	339
FT	CARBOHYD	356	356
FT	CARBOHYD	386	386
FT	CARBOHYD	392	392
FT	CHAIN	392	511
FT	DISULFID	54	74
FT	DISULFID	119	205
FT	DISULFID	126	196
FT	DISULFID	131	157
FT	DISULFID	218	247
FT	DISULFID	228	239
FT	DISULFID	296	3

Query Match	Best Local Similarity	Matches	Score	DB 1	Pred.	NO. 6.5e-15	Length	856
34	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	SLIHSLSIESQNOQEKNEQELTDLKMASLSLNMWF	34					
Db	640	SLIHSLSIESQNOQEKNEQELTDLKMASLSLNMWF	673					
RESULT 4								
ID	ENV_HV1H3	STANDARD:	PRT:	856	AA.			
AC	P04624.							
DT	13-AUG-1987	(Rel. 05, Created)						
DT	01-FEB-1996	(Rel. 33, Last sequence update)						
DT	15-JUL-1999	(Rel. 38, Last annotation update)						
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].							
GN	ENV.							
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).							
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.							
OX	NCBI_TaxID=11707;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEDLINE=85228248; PubMed=2988795;							
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Krmer R., Shaw G.M., Wong-Staal F., Reddy E.P.;							
RT	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";							
RL	Cell 41:979-986(1985).							
CC	-----							
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CC	-----							
DR	EMBL, M14100; AAA4679.1; -							
DR	HIV, M14100; ENVSHX3.							
DR	InterPro: IPR000328; Env GP41.							
DR	InterPro: IPR000777; GP120.							
DR	Pfam: PF00516; GP120; 1.							
DR	Pfam: PF00517; GP41; 1.							
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.							
FT	SIGNAL.	1	30					
FT	CHAIN	511	511					
FT	CHAIN	512	856					
FT	DISULFID	119	205					
FT	DISULFID	126	196					
FT	DISULFID	131	157					
FT	DISULFID	218	247					
FT	DISULFID	228	239					
FT	DISULFID	296	331					
FT	DISULFID	378	445					
FT	DISULFID	385	418					
FT	CAROHYD	88	88					
FT	CAROHYD	136	136					

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97188 MW; 3373688884C1AFC CRC64;

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Query Match 100.0%; Score 183; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6,5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 SLIHSLEESONOEKNEOLLELDKASLWNMF 34
Db 640 SLIHSLEESONOEKNEOLLELDKASLWNMF 673

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RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
P Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

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OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=95127297; Pubmed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC GlycosultedB: Q70626; -
CC InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 511 511
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
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FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
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FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
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FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match 100.0%; Score 183; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 6,5e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 SLIHSLEESONOEKNEOLLELDKASLWNMF 34
Db 640 SLIHSLEESONOEKNEOLLELDKASLWNMF 673

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```

RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
EN.
OS Human immunodeficiency virus type 1 (BR1 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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Query Match	Best Local Similarity	100.0%	Score 183	DB 1	Length 861
Matches 34	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-65099333; PubMed-2981635;				
RA	Wain-Hobson S., Sonigo P., Danos O., Cole S., Allison M.;				
RT	"Nucleotide sequence of the AIDS virus, LAV.";				
RL	Cell 40:9-17(1985).				
CC	-----				
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).				
DR	EMBL; K02013; AAB59751.1; -				
DR	EMBL; A04321; CAA00352.1; -				
DR	PIR; A03975; VCLJLV.				
DR	HIV; K02013; ENV5BRU.				
DR	InterPro; IPR000328; Env_Gp41.				
DR	InterPro; IPR000777; GP120.				
PF	Pfam; PF00516; GP120; 1.				
PF	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;				
FT	Signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	516		
FT	CHAIN	517	861		
FT	DISULFID	54	74		
FT	DISULFID	119	210		
FT	DISULFID	126	201		
FT	DISULFID	131	162		
FT	DISULFID	223	252		
FT	DISULFID	233	244		
FT	DISULFID	301	336		
FT	DISULFID	383	450		
FT	DISULFID	390	423		
FT	DISULFID	88			
FT	CARBOHYD	136	136		
FT	CARBOHYD	141	141		
FT	CARBOHYD	146	146		
FT	CARBOHYD	161	161		
FT	CARBOHYD	165	165		
FT	CARBOHYD	191	191		
FT	CARBOHYD	202	202		
FT	CARBOHYD	235	235		
FT	CARBOHYD	239	239		
FT	CARBOHYD	246	246		
FT	CARBOHYD	267	267		
FT	CARBOHYD	281	281		
FT	CARBOHYD	294	294		
FT	CARBOHYD	300	300		
FT	CARBOHYD	306	306		
FT	CARBOHYD	337	337		
FT	CARBOHYD	344	344		
FT	CARBOHYD	361	361		
FT	CARBOHYD	391	391		
FT	CARBOHYD	397	397		
FT	CARBOHYD	402	402		
FT	CARBOHYD	411	411		
FT	CARBOHYD	453	453		
FT	CARBOHYD	468	468		
FT	CARBOHYD	616	616		
FT	CARBOHYD	621	621		
FT	CARBOHYD	630	630		
FT	CARBOHYD	642	642		
FT	CARBOHYD	679	679		
FT	CARBOHYD	755	755		
FT	CARBOHYD	821	821		
SO	SEQUENCE	861 AA;	97487 MM;	04DE2B4D4E4FD63A	CRC64;

[illegible]

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match
Best Local Similarity 98.4%; Score 180; DB 1; Length 853;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 SLHSLIEESQNOQEKNEQELLELDKWSLWMNF 34
|||||:|||||:|||||:|||||:|||||:
638 SLHSLIEESQNOQEKNEQELLELDKWSLWMNF 671

RESULT 8
ENV_HV1PV STANDARD; PRT; 856 AA.
ID ENV_HV1PV
AC P03376;
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/Lymphadenopathy retrovirus.";
RC Nature 313:450-458(1985).
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: K02083; AAB59873.1;
DR EMBL: X01762; CA235903.1; ALT_SEQ.
DR PIR: A03974; VCLJVL.
DR HIV: K02083; ENVSPV22.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
KW SIGNAL.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.

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FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C1209B3 CRC64;

Query Match
Best Local Similarity 95.1%; Score 174; DB 1; Length 856;
Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 SLHSLIEESQNOQEKNEQELLELDKWSLWMNF 33
|||||:|||||:|||||:|||||:|||||:
640 SLHSLIEESQNOQEKNEQELLELDKWSLWMNF 672

RESULT 9
ENV_HV1SC STANDARD; PRT; 856 AA.
ID ENV_HV1SC
AC P05878;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
CC -----
CC MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN AHC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----

DR EMBL: M17450; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJSC.

DR HTV: M17450; ENV5SC.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 129

FT CARBOHYD 129 129

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 95.1%; Score 174; DB 1; Length 856;  
Best Local Similarity 94.1%; Pred. No. 8.3e-14;  
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESONOQEKNEOLELIDKWSLWNMF 34  
||||:|||||

DB 640 SLIYTLIEESONOQEKNEOLELIDKWSLWNMF 673

RESULT 10  
ENV\_HV1M1 STANDARD; PRT: 856 AA.  
AC P31872;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

DE ENV.

GN Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).

OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC NCBI\_TaxID=31678;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=86218077; Pubmed=2423250;

RX Starch B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RA "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";

RT Cell 45:637-648(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; VCLJ3W.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

SO SEQUENCE 856 AA; 97526 MW; DB68D1E49C0404D89 CRC64;

Query Match 95.1%; Score 174; DB 1; Length 856;  
Best Local Similarity 94.1%; Pred. No. 8.3e-14;  
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIEESONOQEKNEOLELIDKWSLWNMF 34  
||||:|||||

Db 640 SLIYNLIESONQOEKNEDELTDKWSLWNF 673

RESULT 11

ID	ENV_HV1S1	STANDARD	PRT	852 AA
AC	P19549			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).			
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11690;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=90317906; PubMed=2370688;			
	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;			
	"Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";			
RT	J. Virol. 64:4016-4020(1990).			
CC	-----			
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CC	-----			
DR	EMBL: M38427; AAA45072.1; -			
DR	HIV: M38427; ENVSEF33.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120.1.			
DR	Pfam: PF00517; GP41.1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	156	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	331	BY SIMILARITY.
FT	DISULFID	377	439	BY SIMILARITY.
FT	DISULFID	384	412	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	159	159	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	189	189	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	385	385	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 852 AA; 96663 MW; EE7BFB8D23C9910D CRC64.

Query Match 94.0%; Score 172; DB 1; Length 852;

Best Local Similarity 91.2%; Pred. No. 1.5e-13;

Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSIESONQOEKNEDELTDKWSLWNF 34

Db 636 SLIYNLIESONQOEKNEDELTDKWSLWNF 669

RESULT 12

ID	ENV_HV1S1	STANDARD	PRT	847 AA
AC	P19550			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).			
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11691;			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=90347835; PubMed=2384920;			
RA	Cheng-Mayer C., Quitoza M., Tung J.W., Dina D., Levy J.;			
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";			
RT	J. Virol. 64:4390-4398(1990).			
CC	-----			
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CC	-----			
DR	EMBL: M65024; AAA45072.1; -			
DR	HIV: M38428; ENVSEF162.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120.1.			
DR	Pfam: PF00517; GP41.1.			
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	30	502	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	503	847	BY SIMILARITY.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	203	BY SIMILARITY.
FT	DISULFID	125	194	BY SIMILARITY.
FT	DISULFID	130	155	BY SIMILARITY.
FT	DISULFID	216	245	BY SIMILARITY.
FT	DISULFID	226	237	BY SIMILARITY.
FT	DISULFID	294	328	BY SIMILARITY.
FT	DISULFID	374	435	BY SIMILARITY.
FT	DISULFID	381	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 847 AA; 96135 MW; 0A901317FD7FF2AB CRC64;

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Query Match 93.4%; Score 171; DB 1; Length 847;
Best Local Similarity 91.2%; Pred. No. 1,9e-13;
Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLIHSLSIESQNOGKNEQELLELDKWSLIMNF 34
Db 631 SLIHSLSIESQNOGKNEQELLELDKWSLIMNF 664

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RESULT 13
ENV_HV1W2 STANDARD; PRT; 847 AA.
ID ENV_HV1W2
AC P05860.01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP MEDLINE=86235450; PubMed=3012778;
Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HIV-1/LAV over time in patients with AIDS or
at risk for AIDS.";
Science 237:1548-1553(1986).

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CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAIRIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M12507; AAB12990.1; -
CC DR HIV; M12507; ENV:WMJ2.
CC DR InterPro: IPR000328; Env_GP41.
CC DR Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.

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FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 847 847
FT DISULFID 502 501
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 135 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
FT CARBOHYD 194 194
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
FT CARBOHYD 286 286
FT CARBOHYD 292 292
FT CARBOHYD 327 327
FT CARBOHYD 334 334
FT CARBOHYD 350 350
FT CARBOHYD 356 356
FT CARBOHYD 380 380
FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA; 96466 MW; CDIE33D73A5BCAE CRC64;

Query Match 91.8%; Score 168; DB 1; Length 847;
Best Local Similarity 91.2%; Pred. No. 4.5e-13;
Matches 31; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 SLIHSLSIESQNOGKNEQELLELDKWSLIMNF 34
Db 631 SLIHSLSIESQNOGKNEQELLELDKWSLIMNF 664

```

```

RESULT 14
ENV_HV1J3 STANDARD; PRT; 867 AA.
ID ENV_HV1J3
AC P12489.01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP MEDLINE=89352108; PubMed=2669897;
Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria.";
AIDS Res. Hum. Retroviruses 5:411-419(1989).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA: 97140 MM: D197D809940BE732 CRC64;

Query Match 90.2%; Score 165; DB 1; Length 856;  
 Best Local Similarity 88.2%; Pred. No. 1, 1e-12;  
 Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SLIHSLEBSQNOEKNEQELLELDKWSLWNWF 34  
 |||:||||:|||||  
 Db 641 SLIYSLEKSKTOEKNEQELLELDKWSLWNWF 674

Search completed: May 16, 2003, 11:13:33  
 Job time: 5.73494 secs

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GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 24.7831 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-118

Perfect score: 183

Sequence: 1 SLIHSILIESONQOEKNEDELLELDKMASLWNWF 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	645	15	Q993A6 human immun
2	183	100.0	747	15	Q70607 human immun
3	183	100.0	748	15	Q70606 human immun
4	183	100.0	752	15	Q70604 human immun
5	183	100.0	752	15	Q70605 human immun
6	183	100.0	752	15	Q70608 human immun
7	183	100.0	851	15	Q78243 human immun
8	183	100.0	852	15	Q89797 human immun
9	183	100.0	854	15	Q85582 human immun
10	183	100.0	854	15	Q72502 human immun
11	183	100.0	856	15	Q92877 simian-huma
12	183	100.0	856	15	Q74599 human immun
13	183	100.0	856	15	Q74090 human immun
14	179	97.8	854	15	Q90178 human immun
15	179	97.8	854	15	Q78705 human immun
16	178	97.3	856	15	Q905m7 human immun

17	177	96.7	616	15	Q993B0 human immun
18	177	96.7	618	15	Q993B2 human immun
19	177	96.7	757	15	Q90722 human immun
20	177	96.7	848	15	Q69990 human immun
21	175	95.6	838	15	Q03806 human immun
22	175	95.6	854	15	Q78225 human immun
23	175	95.6	855	15	Q03805 human immun
24	174	95.1	42	15	Q69910 human immun
25	174	95.1	443	15	Q80023 human immun
26	174	95.1	841	15	Q41556 human immun
27	174	95.1	849	15	Q77368 human immun
28	174	95.1	849	15	Q8Q851 human immun
29	174	95.1	851	15	Q61110 human immun
30	174	95.1	851	15	Q8Q852 human immun
31	174	95.1	856	15	Q72993 human immun
32	174	95.1	856	15	Q41539 human immun
33	174	95.1	857	15	Q8UL70 human immun
34	174	95.1	858	15	Q8UL90 human immun
35	174	95.1	858	15	Q8UL88 human immun
36	174	95.1	859	15	Q8UL85 human immun
37	174	95.1	859	15	Q8UL80 human immun
38	174	95.1	859	15	Q8UL79 human immun
39	174	95.1	859	15	Q8UL77 human immun
40	174	95.1	859	15	Q8UL73 human immun
41	174	95.1	859	15	Q8Q850 human immun
42	174	95.1	862	15	Q8UL84 human immun
43	174	95.1	862	15	Q8UL83 human immun
44	174	95.1	862	15	Q8UL82 human immun
45	174	95.1	862	15	Q8UL78 human immun

## ALIGNMENTS

RESULT 1  
Q993A6 PRELIMINARY; PRT; 645 AA.  
AC Q993A6;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Suman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env-GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW Aids; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;

Query Match 100.0%; Score 183; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 3.3e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSILIESONQOEKNEDELLELDKMASLWNWF 34  
DB 609 SLIHSILIESONQOEKNEDELLELDKMASLWNWF 642

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RESULT 2
ID 070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP STRAIN-LM87-1.
RC MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12034; AAA76669.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
FT AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ NON_TER 747 AA; 84250 MW; 732B836A52245F14 CRC64;
SEQUENCE

Query Match 100.0%; Score 183; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOEKNEQELLELDKWSIMNF 34
DB 635 SLHSLIESQNOEKNEQELLELDKWSIMNF 668

RESULT 3
ID 070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RC MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12032; AAA76668.1;
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
FT AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ NON_TER 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
SEQUENCE

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOEKNEQELLELDKWSIMNF 34
DB 640 SLHSLIESQNOEKNEQELLELDKWSIMNF 673

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DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 183; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOEKNEQELLELDKWSIMNF 34
DB 636 SLHSLIESQNOEKNEQELLELDKWSIMNF 669

RESULT 4
ID 070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RC MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12030; AAA76666.1;
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR Pfam: PF00517; GP41. 1.
FT AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ NON_TER 752 AA; 84894 MW; 8B30AE894013B45A CRC64;
SEQUENCE

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOEKNEQELLELDKWSIMNF 34
DB 640 SLHSLIESQNOEKNEQELLELDKWSIMNF 673

RESULT 5
ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12031; AA76667.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA: 84894 MW: 8830AE894013B45A CRC64:

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673

RESULT 6
O70608 PRELIMINARY; PRT: 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-2;
RL MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12035; AA76670.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 752
SEQUENCE 752 AA: 84780 MW: 708672A2D0C0E8F8 CRC64:

Query Match 100.0%; Score 183; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673
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Db 640 SLHSLIESONQOEKNEDELLELDKMASLWNMF 673

RESULT 7
O78243 PRELIMINARY; PRT: 851 AA.
AC 078243;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,
  Verani P., Rossi G.B.;
RT "Sequence analysis of HIV-1 proviral DNA from a non producer
  chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Macchi B., Mangiano N., Verani P., Rossi G.;
RT "Biological and molecular characterization of producer and non
  AIDS Res. Hum. Retroviruses 5:385-396(1989).
RN [3]
RP SEQUENCE FROM N.A.
RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Borsetti A., Saggio I., Verani P., Rossi G.;
RT "Variability of HIV-1 virus: characteristics of an infected but not
  productive clone.";
RL Int. J. Immunopharmacol. 3:17-23(1990).
DR EMBL: Z11530; CA47628.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
NON_TER 851
SEQUENCE 851 AA: 96630 MW: 1A3767B9B7E98027 CRC64:

Query Match 100.0%; Score 183; DB 15; Length 851;
Best Local Similarity 100.0%; Pred. No. 4.4e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLHSLIESONQOEKNEDELLELDKMASLWNMF 34
Db 635 SLHSLIESONQOEKNEDELLELDKMASLWNMF 668

RESULT 8
O89797 PRELIMINARY; PRT: 852 AA.
AC 089797;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW90-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
```

RT Infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12053; AAA76685.1; -;  
 DR EMBL: U12036; AAA76671.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Envelope protein; Glycoprotein; Polypotein;  
 KW Transmembrane.  
 SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4E833CF CRC64;  
 Query Match 100.0%; Score 183; DB 15; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-14;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 34  
 636 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 669  
 Db  
 RESULT 9  
 OS 085582; PRELIMINARY; PRT; 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope polypeptide.  
 GN ENV  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.; Buckler-White A.J., Willey R.L., McCoy J.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92219406; PubMed-1373204;  
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes."  
 RL J. Virol. 66:3151-3154(1992).  
 DR EMBL: M19921; AAA44992.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
 Query Match 100.0%; Score 183; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-14;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 34  
 638 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 671  
 Db  
 RESULT 10  
 OS 072502; PRELIMINARY; PRT; 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE ENV polypeptide.  
 GN ENV  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 DR EMBL: U26942; AAB60578.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW CONFLICT 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 G -> D (IN REF. 2).  
 SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
 Query Match 100.0%; Score 183; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-14;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 34  
 638 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 671  
 Db  
 RESULT 11  
 OS 092877; PRELIMINARY; PRT; 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV  
 OS Simian-human immunodeficiency virus.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OS NCBI\_Taxid=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99098984; PubMed-9882298;

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
RA Sodroski J.G.;  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHIV-HXBc2).";  
RL J. Virol. 73:976-984(1999).  
RN [12]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;  
  
Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 34  
Db 640 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 673  
  
RESULT 12  
O74599 PRELIMINARY; PRT; 856 AA.  
AC O74599;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL Virology 174:103-116(1990).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN-MCK1;  
RA Iwatai Y.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86068; BAA12995.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;  
  
Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 34  
Db 640 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 673  
  
RESULT 13  
O74090

ID O74090 PRELIMINARY; PRT; 856 AA.  
AC O74090;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PM213;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL Virology 174:103-116(1990).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PM213;  
RA Iwatai Y.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86069; BAA13003.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;  
  
Query Match 100.0%; Score 183; DB 15; Length 856;  
Best Local Similarity 100.0%; Pred. No. 4,4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 34  
Db 640 SLIHSLSIESNQOQKNEQELLELDKWSLWNMF 673  
  
RESULT 14  
O90178 PRELIMINARY; PRT; 854 AA.  
AC O90178;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT selected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells.";  
RL J. Virol. 69:75-81(1995).  
RN [12]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;  
RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF070521; AAC28452.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.8%; Score 179; DB 15; Length 854;  
 Best Local Similarity 97.1%; Pred. No. 1.3e-13;  
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OY 1 SLIHSIESQNOQENQELLEDKWSLWNF 34  
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 DB 638 SLIHSIESQNOQENQELLEDKWSLWNF 671

## RESULT 15

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 AC 078705;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 VS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.,  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1."  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AA896326.1;  
 DR InterPro; IPR000328; ENV\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
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Query Match 97.8%; Score 179; DB 15; Length 854;  
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OY 1 SLIHSIESQNOQENQELLEDKWSLWNF 34  
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 DB 638 SLIHSIESQNOQENQELLEDKWSLWNF 671

Search completed: May 16, 2003, 11:19:45  
 Time : 24.8546 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.62651 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-118

Perfect score: 183  
Sequence: 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	100.0	34	1 US-08-073-028-73	Sequence 73, Appl
2	183	100.0	34	4 US-08-554-616-73	Sequence 73, Appl
3	183	100.0	34	4 US-09-082-279B-800	Sequence 800, App
4	183	100.0	34	4 US-09-315-304B-800	Sequence 800, App
5	183	100.0	35	1 US-08-073-028-74	Sequence 74, Appl
6	183	100.0	35	4 US-08-484-223B-234	Sequence 234, App
7	183	100.0	35	4 US-08-554-616-74	Sequence 74, Appl
8	183	100.0	35	4 US-09-082-279B-638	Sequence 638, App
9	183	100.0	35	4 US-09-082-279B-799	Sequence 799, App
10	183	100.0	35	4 US-08-474-349A-416	Sequence 416, App
11	183	100.0	35	4 US-09-315-304B-638	Sequence 638, App
12	183	100.0	35	4 US-09-315-304B-799	Sequence 799, App
13	183	100.0	36	1 US-08-073-028-1	Sequence 1, Appli
14	183	100.0	36	1 US-08-486-059-1	Sequence 1, Appli
15	183	100.0	36	3 US-09-071-877-1	Sequence 1, Appli
16	183	100.0	36	3 US-08-360-107A-1	Sequence 1, Appli
17	183	100.0	36	3 US-08-484-223B-1	Sequence 1, Appli
18	183	100.0	36	3 US-08-484-223B-231	Sequence 231, App
19	183	100.0	36	3 US-08-484-223B-232	Sequence 232, App
20	183	100.0	36	3 US-08-919-597-1	Sequence 1, Appli
21	183	100.0	36	3 US-08-475-668A-1	Sequence 1, Appli
22	183	100.0	36	3 US-08-485-551A-1	Sequence 1, Appli
23	183	100.0	36	3 US-08-471-913A-1	Sequence 1, Appli
24	183	100.0	36	4 US-08-554-616-1	Sequence 1, Appli
25	183	100.0	36	4 US-08-485-264A-1	Sequence 15, Appl
26	183	100.0	36	4 US-09-082-279B-15	Sequence 497, App
27	183	100.0	36	4 US-09-082-279B-497	

28	183	100.0	36	4 US-09-082-279B-498	Sequence 498, App
29	183	100.0	36	4 US-09-082-279B-560	Sequence 560, App
30	183	100.0	36	4 US-09-082-279B-561	Sequence 561, App
31	183	100.0	36	4 US-09-082-279B-603	Sequence 603, App
32	183	100.0	36	4 US-09-082-279B-630	Sequence 630, App
33	183	100.0	36	4 US-09-082-279B-631	Sequence 631, App
34	183	100.0	36	4 US-09-082-279B-705	Sequence 705, App
35	183	100.0	36	4 US-09-082-279B-834	Sequence 834, App
36	183	100.0	36	4 US-09-082-279B-1076	Sequence 1076, App
37	183	100.0	36	4 US-09-082-279B-1121	Sequence 1121, App
38	183	100.0	36	4 US-09-082-279B-1161	Sequence 1161, App
39	183	100.0	36	4 US-08-965-056-1	Sequence 1, Appli
40	183	100.0	36	4 US-08-965-056-108	Sequence 108, App
41	183	100.0	36	4 US-09-045-920-1	Sequence 1, Appli
42	183	100.0	36	4 US-08-474-349A-1	Sequence 1, Appli
43	183	100.0	36	4 US-08-474-349A-399	Sequence 399, App
44	183	100.0	36	4 US-08-474-349A-400	Sequence 400, App
45	183	100.0	36	4 US-08-474-349A-401	Sequence 401, App

#### ALIGNMENTS

RESULT 1  
US-08-073-028-73  
Sequence 73, Application US/08073028  
Patent No. 5464933

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.

APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

NUMBER OF SEQUENCES: 74  
TRANSMISSION

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas

CITY: New York  
STATE: New York

COUNTRY: USA  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-004-999  
TELEPHONE/COMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741

INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids  
TYPE: amino acid

TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-073-028-73

Query Match 100.0%; Score 183; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34  
DB 1 SLHSLIESQNOQEKNEOELLELDKWSLWNF 34

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SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 800
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-800

Query Match
Best Local Similarity 100.0%; Score 183; DB 4; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIESQNOQEKNEQLLELDKWSLWNMF 34
|||||
DB 1 SLIHSLIESQNOQEKNEQLLELDKWSLWNMF 34

RESULT 4
US-09-315-304B-800
Sequence 800, Application US/09315304B
Patent No. 6348568
GENERAL INFORMATION:
APPLICANT: Barney, S.
APPLICANT: Guthrie, K.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REFERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 800
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-315-304B-800

Query Match
Best Local Similarity 100.0%; Score 183; DB 4; Length 34;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLIESQNOQEKNEQLLELDKWSLWNMF 34
|||||
DB 1 SLIHSLIESQNOQEKNEQLLELDKWSLWNMF 34

RESULT 5
US-08-073-028-74
Sequence 74, Application US/08073028
Patent No. 5464933
GENERAL INFORMATION:
APPLICANT: Bolognesi, Danl P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073.028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-74

Query Match 100.0%; Score 183; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 34  
|||||  
Db 2 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 35

RESULT 6  
US-08-484-223B-234  
Sequence 234, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484.223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-234

Query Match 100.0%; Score 183; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 34  
|||||  
Db 2 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 35

RESULT 7  
US-08-554-616-74  
Sequence 74, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554.616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073.028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-74

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 34  
|||||  
Db 2 SLIHSLIESONQOEKNEDELLELDKMASLWNWF 35

RESULT 8  
US-09-082-279B-638  
; Sequence 638, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082, 279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 638  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-638

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 34  
Db 2 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 35

RESULT 9  
US-09-082-279B-799  
; Sequence 799, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082, 279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 799  
; LENGTH: 35  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-799

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 34  
Db 2 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 35

RESULT 10  
US-08-474-349A-416  
; Sequence 416, Application US/08474349A  
; Patent No. 6333395  
; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
NUMBER OF SEQUENCES: 517  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474, 349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 416:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
\* MOLECULE TYPE: peptide  
US-08-474-349A-416

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 34  
Db 2 SLIHSLSIESQNOQEKNEQLELDKMSLWNWF 35

RESULT 11  
US-09-315-304B-638  
; Sequence 638, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315, 304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082, 279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 638

LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-638

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 34  
|||||  
DB 2 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 35

RESULT 12  
US-09-315-304B-799  
Sequence 799, Application US/09315304B  
Patent No. 6348568

GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 799  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-799

Query Match 100.0%; Score 183; DB 4; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 34  
|||||  
2 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 35

RESULT 13  
US-08-073-028-1  
Sequence 1, Application US/08073028  
Patent No. 5464933

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1

Query Match 100.0%; Score 183; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 34  
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DB 3 SLIHSLESQNOQEKNEQELLELDKWSIWMNF 36

RESULT 14  
US-08-486-099-1  
Sequence 1, Application US/08486099  
Patent No. 6013263

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-1

Query Match 100.0%; Score 183; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,8e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 34  
|||||  
DB 3 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 36

## RESULT 15

US-09-071-877-1  
Sequence 1, Application US/09071877  
Patent No. 6015881

## GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol  
APPLICANT: Bray, Brian  
APPLICANT: Lichey, Maynard  
APPLICANT: Mader, Catherine  
APPLICANT: Merutka, Gene  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS  
FILE REFERENCE: 7872-050  
CURRENT APPLICATION NUMBER: US/09/071,877  
CURRENT FILING DATE: 1998-05-01  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-09-071-877-1

Query Match 100.0%; Score 183; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,8e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 34  
|||||  
DB 3 SLIHSLEESQNOEKNEQELLELDKWSIWMNF 36

Job completed: May 16, 2003, 11:22:11  
Time: 9.62651 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 14,8835 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-118  
Perfect score: 183  
Sequence: 1 SLIHSLEESONQOEKNEQELLELDKWSLWVNF 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 segs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	100.0	36	9	US-09-874-475-16
2	183	100.0	36	9	US-10-116-797-1
3	183	100.0	36	9	US-09-493-346-1
4	183	100.0	36	10	US-09-796-202-10
5	183	100.0	36	10	US-09-779-451-5
6	183	100.0	36	10	US-09-834-628-1
7	183	100.0	36	10	US-09-834-816-1
8	183	100.0	36	10	US-09-854-816-108
9	183	100.0	37	9	US-09-848-616-176
10	183	100.0	46	10	US-09-779-451-41
11	183	100.0	56	10	US-09-779-451-41
12	183	100.0	177	9	US-10-040-349B-2
13	183	100.0	221	9	US-10-059-271-84
14	183	100.0	232	9	US-10-059-271-81
15	183	100.0	254	9	US-10-059-271-82
16	183	100.0	256	9	US-10-059-271-97
17	183	100.0	268	10	US-09-854-816-16
18	183	100.0	268	10	US-09-854-816-17
19	183	100.0	268	10	US-09-854-816-18

20	183	100.0	344	9	US-10-040-349B-1	Sequence 1, Appli
21	183	100.0	345	9	US-10-026-741-49	Sequence 49, Appl
22	183	100.0	345	10	US-09-779-451-8	Sequence 8, Appli
23	183	100.0	391	9	US-10-059-271-93	Sequence 93, Appl
24	183	100.0	519	10	US-09-756-551A-8	Sequence 8, Appli
25	183	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
26	183	100.0	856	10	US-09-476-242-1	Sequence 1, Appli
27	183	100.0	861	9	US-10-026-741-103	Sequence 103, App
28	183	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
29	183	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
30	180	98.4	36	10	US-09-912-824-1	Sequence 1, Appli
31	180	98.4	268	10	US-09-854-816-19	Sequence 19, Appl
32	177	96.7	1231	9	US-10-059-271-94	Sequence 94, Appl
33	175	95.6	268	10	US-09-854-816-13	Sequence 13, Appl
34	174	95.1	233	10	US-09-854-816-50	Sequence 50, Appl
35	174	95.1	268	10	US-09-854-816-9	Sequence 9, Appli
36	174	95.1	269	10	US-09-854-816-12	Sequence 12, Appl
37	173	94.5	269	10	US-09-854-816-46	Sequence 46, Appl
38	172	94.0	269	10	US-09-854-816-28	Sequence 28, Appl
39	171	93.4	268	10	US-09-854-816-26	Sequence 26, Appl
40	171	93.4	619	10	US-09-891-609-4	Sequence 4, Appli
41	171	93.4	646	10	US-09-891-609-2	Sequence 2, Appli
42	171	93.4	847	10	US-09-476-242-2	Sequence 2, Appli
43	170	92.9	46	10	US-09-854-816-109	Sequence 109, App
44	170	92.9	267	10	US-09-854-816-38	Sequence 38, Appl
45	170	92.9	268	10	US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
  
Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 SLIHSLEESONQOEKNEQELLELDKWSLWVNF 34  
Db 3 SLIHSLEESONQOEKNEQELLELDKWSLWVNF 36  
  
RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US20030044411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 34  
|||||  
DB 3 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Patent No. US20030082185A1  
GENERAL INFORMATION:  
APPLICANT: OLSON, William C  
APPLICANT: MADDON, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 100.0%; Score 183; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 34  
|||||  
DB 3 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 36

PLT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: OLSON, William  
TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 34  
|||||  
DB 3 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 34  
|||||  
DB 3 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 100.0%; Score 183; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 34  
|||||  
DB 3 SLIHSLSIESQNOQEKNEQELLELDKWSLWMNF 36

```

RESULT 7
US-09-854-816-1
; Sequence 1, Application US/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 100.0%; Score 183; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2,7e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SLIHSLSIESQNOQEKNEDELLELDKMSLWNMF 34
|||||
Db 3 SLIHSLSIESQNOQEKNEDELLELDKMSLWNMF 36
|||||

RESULT 8
US-09-854-816-108
; Sequence 108, Application US/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-09-854-816-108
Query Match 100.0%; Score 183; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 2,7e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SLIHSLSIESQNOQEKNEDELLELDKMSLWNMF 34
|||||
Db 3 SLIHSLSIESQNOQEKNEDELLELDKMSLWNMF 36
|||||

RESULT 9
US-09-848-616-176
; Sequence 176, Application US/09848616
; Publication No. US20030054010A1
GENERAL INFORMATION:
APPLICANT: Seibel, Peter
Dunant, Nicolas
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
CURRENT APPLICATION NUMBER: US/09/848,616
CURRENT FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 176
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DP178c peptide
US-09-848-616-176
Query Match 100.0%; Score 183; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,8e-15;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 SLIHSLSIESQNOQEKNEDELLELDKMSLWNMF 34
|||||

```

Db 4 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 37

RESULT 10  
US-09-779-451-41  
; Sequence 41, Application US/09779451  
; Patent No. US20020094521A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
; FILE REFERENCE: 1900.0300003  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/235,901  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/181,543  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 41  
; LENGTH: 46  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-41

Query Match 100.0%; Score 183; DB 10; Length 46;  
Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 13 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 46

RESULT 11  
US-09-779-451-4  
; Sequence 4, Application US/09779451  
; Patent No. US20020094521A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
; FILE REFERENCE: 1900.0300003  
; CURRENT FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/235,901  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/181,543  
; PRIOR FILING DATE: 2000-02-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 56  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-4

Query Match 100.0%; Score 183; DB 10; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.3e-15;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 18 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 51

RESULT 12  
US-10-040-349B-2  
; Sequence 2, Application US/10040349B  
; Publication No. US20030082521A1  
; GENERAL INFORMATION:  
; APPLICANT: Brasseur, Robert

APPLICANT: Charlotteaux, Benoit  
APPLICANT: Chevalier, Michel  
APPLICANT: El Habib, Raphaelle  
APPLICANT: Krell, Tino  
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV  
FILE REFERENCE: 01-078-A  
CURRENT APPLICATION NUMBER: US/10/040.349B  
CURRENT FILING DATE: 2002-07-09  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: (1)...(177)  
OTHER INFORMATION: polypeptide derived from gp41 LAI  
US-10-040-349B-2

Query Match 100.0%; Score 183; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 1.4e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 106 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 139

RESULT 13  
US-10-059-271-84  
; Sequence 84, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPE, HEINRICH  
; APPLICANT: BUDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-059-271-84

Query Match 100.0%; Score 183; DB 9; Length 221;  
Best Local Similarity 100.0%; Pred. No. 1.8e-14;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 34  
Db 133 SLIHSLEESQNOQEKNEQELLELDKMASLWNMF 166

RESULT 14  
US-10-059-271-81  
; Sequence 81, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPE, HEINRICH  
; APPLICANT: BUDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

```

; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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Query Match          100.0%; Score 183; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 34
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Db 146 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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```

Query Match          100.0%; Score 183; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 34
|||||
Db 168 SLIHSLEESQNOQEKNEQELLELDKASLWNMF 201

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Search completed: May 16, 2003, 12:10:23  
Job time : 14.8835 secs

**THIS PAGE BLANK (uspto)**

C:Genetics: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-861/Product: env polypeptide #status predicted <EPP>  
F:87,129,139,140,143,159,163,167,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 89.5%; Score 179; DB 1; Length 861;  
Best Local Similarity 86.1%; Pred. No. 2,le-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESONQOEKNEDELLELDKAMLMNMF 36  
||:||||:||||||||||||||||||||||||||||||  
Db 643 YTSIIYLIIESONQOEKNEDELLELDKAMLMNMF 678

RESULT 8  
S22004  
slope protein gp120/gp41 - human immunodeficiency virus type 1  
Accession: S22004  
Species: human immunodeficiency virus type 1, HIV-1  
Variety: isolate 4B  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S22004; S70419  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
Submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR  
A:Reference number: S21990  
A:Accession: S22004  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>  
A:Cross-references: EMBL:X61353; NID:960188; PIDN:CAM3618.1; PID:960189  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:11736940  
A:Accession: S70419  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-292,'X',294-357 <STE2>  
A:Cross-references: EMBL:X61353; NID:960188  
C:Superfamily: type E retrovirus env polypeptide

Query Match 89.0%; Score 178; DB 2; Length 357;  
Best Local Similarity 86.1%; Pred. No. 1e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 YTGIIYNLLEESONQOEKNEDELLELDKAMLMNMF 36  
||:||||:||||||||||||||||||||||||||||||  
139 YTDLIYLIIESONQOEKNEDELLELDKAMLMNMF 174

RESULT 9  
VCLJIA2  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
A:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Stickney, J.  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666  
C:Genetics: env  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide  
F:1-30/Domain: signal sequence #status predicted <SIG>

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F:510-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
E:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,368,394,400,408,445,
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          89.0%; Score 178; DB 1; Length 855;
Best Local Similarity 88.9%; Pred. No. 2,7e-13;
Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 YTGIIYNLLEESQNQEKNQEQLLELDKMANLMWNF 36
        ||| | | | | | | | | | | | | | | | | | | |
DB     637 YTNITVTLLEESQNQEKNQEQLLELDKMANLMWNF 672

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:11756940
A:Accession: S70420
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-357 <S72>
A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAAA3620.1; PID:960191
A:Experimental source: patient L
A>Note: Submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match          88.5%; Score 177; DB 2; Length 357;
Best Local Similarity 86.1%; Pred. No. 1,3e-13;
Matches 31; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 YTGIIYNLLEESQNQEKNQEQLLELDKMANLMWNF 36
        ||| | | | | | | | | | | | | | | | | | | |
DB     139 YTDLIYTLLEESQNQEKNQEQLLELDKMANLMWNF 174

RESULT 11
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A>Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as deter
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAAA3622.1; PID:960180
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:11756940
A:Accession: S70421
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:960179
C:Superfamily: type E retrovirus env polyprotein

Query Match          88.5%; Score 177; DB 2; Length 357;
Best Local Similarity 86.1%; Pred. No. 1,3e-13;
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 YTGIIYNLLEESQNQEKNQEQLLELDKMANLMWNF 36

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FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 275 275 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 646 646 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 825 825 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCA6 CRC64;

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Query Match 100.0%; Score 200; DB 1; Length 865;
Best Local Similarity 100.0%; Pred. No. 3.8e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTGIIYNLEESONOENKNEOELLELDKMANLWNMF 36
DB 647 YTGIIYNLEESONOENKNEOELLELDKMANLWNMF 682

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RESULT 2
ENV_HV1M1 STANDARD; PRT; 856 AA.
AC P31872; 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=31678;
OX NCI [1]
RP MEDLINE=86218077; PubMed=2423250;
RX Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
AIDS";
RL Cell 45:637-648(1986).
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC PIR: A24774; VCLJ3M.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.

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FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E9C404DE9 CRC64;

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Query Match 92.5%; Score 185; DB 1; Length 856;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTGIIYNLEESONOENKNEOELLELDKMANLWNMF 36
DB 638 YTSIIYNLEESONOENKNEOELLELDKMANLWNMF 673

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RESULT 3
ENV_HV1S3 STANDARD; PRT; 852 AA.
AC P19549; 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11690;
OX NCI [1]
RP MEDLINE=90317906; PubMed=2370688;
RX York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RA "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
the viral genome";
RL J. Virol. 64:4016-4020(1990).
CC -----
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DR EMBL: M38427; AAA5067.1; -  
 DR HIV: M38427; ENVSEF33.  
 DR InterPro: IPR000328; Env-GP41.  
 DR Pfam: PF00516; GP120.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 31 BY SIMILARITY.  
 FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 156 BY SIMILARITY.  
 FT DISULFID 219 248 BY SIMILARITY.  
 FT DISULFID 229 240 BY SIMILARITY.  
 FT DISULFID 297 331 BY SIMILARITY.  
 FT DISULFID 377 439 BY SIMILARITY.  
 FT DISULFID 384 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 813 813 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 852 AA; 96663 MW; E77BBFBD23C9910D CRC64;  
 Query Match 90.5%; Score 181; DB 1; Length 852;  
 Best Local Similarity 88.9%; Pred. No. 6,6e-14;  
 Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 YTGIIYNLEESQNOEKNEQELLEDKMANLNMNF 36  
 Db 634 YTSLLTYTLLSESONOEKNEQELLEDKMASLNMNF 669  
 RESULT 4  
 ENV\_HYIMA STRAND: PRT: 859 AA.  
 AC P04563;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 glycoprotein (GP120), Transmembrane glycoprotein (GP41)].

GN ENV.  
 OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).  
 OC Viruses; Retrod virus; Retroviridae; Lentivirus.  
 OK NCBI\_TaxID=11697;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86245056; PubMed=2424612;  
 RA Allison M., Main-Hobson S., Montagnier L., Sonigo P.;  
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis  
 of two isolates from African patients";  
 RL Cell 46:63-74(1986).  
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DR EMBL: X04415; CAA28016.1; -  
 DR EMBL: A07116; CAA00623.1; -  
 DR HIV: K03456; ENVSMAL.  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 513 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 514 859 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 210 BY SIMILARITY.  
 FT DISULFID 125 201 BY SIMILARITY.  
 FT DISULFID 130 162 BY SIMILARITY.  
 FT DISULFID 223 252 BY SIMILARITY.  
 FT DISULFID 233 244 BY SIMILARITY.  
 FT DISULFID 301 334 BY SIMILARITY.  
 FT DISULFID 380 445 BY SIMILARITY.  
 FT DISULFID 387 418 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 618 618 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 859 AA; 97109 MW; DBCF9A5A253ABF29 CRC64;  
 Query Match 90.0%; Score 180; DB 1; Length 859;

F1	CARBOHY
F1	CARBOHY

FT	CARBOHYD	157	157
FT	CARBOHYD	185	185

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FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 855 AA; 97043 MW; 849B0B8CBAF7008 CRC64;

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Query Match 89.5%; Score 179; DB 1; Length 853;
Best Local Similarity 86.1%; Pred. No. 1,1e-13;
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 YNGIYNLLEESONOENKNEDELLDKRANLMMNF 36
DB 635 YTGILYRLIEESOTOENKNEDELLDKRWSLMMNF 670

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RESULT 7
ENV_HV126

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ID ENV_HV126 STANDARD: PRT: 855 AA.

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AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11708;

```

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RA SETHI, N.A.
RA MEDLINE=87248097; PubMed=3036660;
RA Sridivasan A., Anand R., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman, V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RA "Molecular characterization of human immunodeficiency virus from
RA Zaire: nucleotide sequence analysis identifies conserved and variable
RA domains in the envelope gene.";
RL Gene 52:71-82(1987).

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CC EMBL: K03458; AAA45380.1;
CC PIR: D26192; VCLJZR.
CC HIV: K03458; ENV526.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.

```

```

KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 31 510
FT CHAIN 511 855
FT DISULFID 53 73
FT DISULFID 118 207
FT DISULFID 125 198
FT DISULFID 130 155
FT DISULFID 220 249
FT DISULFID 220 241
FT DISULFID 258 332
FT DISULFID 378 444
FT DISULFID 385 417
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 145 145
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 186 186
FT CARBOHYD 189 189
FT CARBOHYD 199 199
FT CARBOHYD 236 236
FT CARBOHYD 243 243
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FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 673 673
SQ SEQUENCE 855 AA; 96971 MW; 3B4D3D6E239C457 CRC64;

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Query Match 89.5%; Score 179; DB 1; Length 855;
Best Local Similarity 86.1%; Pred. No. 1,1e-13;
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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OY 1 YNGIYNLLEESONOENKNEDELLDKRANLMMNF 36
DB 637 YTGILYRLIEESOTOENKNEDELLDKRWSLMMNF 672

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RESULT 8
ENV_HV15C

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ID ENV_HV15C STANDARD: PRT: 856 AA.

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AC P05678;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;

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```

RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=86219542; PubMed=3369091;

```

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Colliati E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates";  
 RL Virology 164:531-536(1988)  
 CC -i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 KM Signal. 1 29  
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.  
 FT SITE 760 760 IN-FRAME TERMINATION CODON.  
 FT SITE 53 73 BY SIMILARITY.  
 FT DISULFID 118 206 BY SIMILARITY.  
 FT DISULFID 125 197 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 219 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 330 BY SIMILARITY.  
 FT DISULFID 376 439 BY SIMILARITY.  
 FT DISULFID 383 412 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97055 MM; DAF4DA600EBA7A08 CRC64;  
 Query Match 89.5%; Score 179; DB 1; Length 856;  
 Best Local Similarity 86.1%; Pred. No. 1.le-13;

Matches 31; Conservative 3; Mismatches 2; Indels .0; Gaps 0;  
 Oy 1 YTGIIYNLLEESNOQEKNEQELLELDKRWANIMWF 36  
 Db 638 YTSIIYTLIEESNOQEKNEQELLELDKRWASIMWF 673  
 RESULT 9  
 ENV\_HVIA2 STANDARD: PRT; 855 AA.  
 ID ENV\_HVIA2  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85090453; PubMed=2578227;  
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
 RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,  
 RA Levy J.A., Dina D., Luciw P.A.;  
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus.  
 RT (ARV-2).";  
 RT Science 227:484-492(1985).  
 CC -----  
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 CC -----  
 CC EMBL: K02007; AAB59882.1; -  
 DR PIR: A03976; VCLJAZ.  
 DR HIV: K02007; ENVSS2.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 KM Signal. 1 29  
 FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 208 BY SIMILARITY.  
 FT DISULFID 125 199 BY SIMILARITY.  
 FT DISULFID 130 155 BY SIMILARITY.  
 FT DISULFID 221 250 BY SIMILARITY.  
 FT DISULFID 231 242 BY SIMILARITY.  
 FT DISULFID 299 333 BY SIMILARITY.  
 FT DISULFID 380 442 BY SIMILARITY.  
 FT DISULFID 387 415 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 855 AA: 97438 MW: A3BC20573AAC41A2 CRC64:

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Query Match 89.0%; Score 178; DB 1; Length 855;  
 Best Local Similarity 88.9%; Pred. No. 1,5e-13;  
 Matches 32; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 1 YTGIIYNLLEESQNOEKNEDELLEDKWAMNMNF 36
Db 637 YNTIYTLLEESQNOEKNEDELLEDKWAMNMNF 672

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ENV_HV1EL STANDARD: PRT: 853 AA.
ID ENV_HV1EL
AC P04581:

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.

```

```

OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;

```

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RN [1]
RP MEDLINE=86245056; PubMed=2424612;
RX Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RA "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients."
RT Cell 46:63-74(1986).

```

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 -----

```

DR EMBL: K03454; AAA4329.1;
DR EMBL: A07108; CA00616.1;
DR HIV_K03454; ENVSELT.
DR InterPro: IPR000328; ENV_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.

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KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.

```

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FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 BY SIMILARITY.
FT CHAIN 509 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFD 53 73 BY SIMILARITY.
FT DISULFD 118 206 BY SIMILARITY.
FT DISULFD 125 197 BY SIMILARITY.
FT DISULFD 130 154 BY SIMILARITY.

```

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FT DISULFD 219 248 BY SIMILARITY.
FT DISULFD 229 240 BY SIMILARITY.
FT DISULFD 297 330 BY SIMILARITY.
FT DISULFD 376 442 BY SIMILARITY.
FT DISULFD 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA: 96721 MW: F9CD864DAAD07A5 CRC64:

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Query Match 88.0%; Score 176; DB 1; Length 853;  
 Best Local Similarity 83.3%; Pred. No. 2.6e-13;  
 Matches 30; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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OY 1 YTGIIYNLLEESQNOEKNEDELLEDKWAMNMNF 36
Db 635 YTGIIYNLLEESQNOEKNEDELLEDKWAMNMNF 670

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ENV_HV1W2 STANDARD: PRT: 847 AA.
ID ENV_HV1W2
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.

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OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;

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RN [1]
RP MEDLINE=86235450; PubMed=3012778;
RX Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS."
RT Science 232:1548-1553(1986).

```

```

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.

```

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DT 13-AUG-1987 (Rel. 05, last sequence update)  
DT 15-JUL-1999 (Rel. 38, last annotation update)

FT	669	N-LINKED (GLCNAC...)	(POTENTIAL).
FT CARBOHYD	032	N-LINKED (GLCNAC...)	(POTENTIAL).
FT CARBOHYD	032	N-LINKED (GLCNAC...)	(POTENTIAL).
FT CARBOHYD	669	N-LINKED (GLCNAC...)	(POTENTIAL).



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CC -----  
 DR EMBL: K03455; AAB50262.1; -  
 DR EMBL: AF038399; AAB99976.1; -  
 DR EMBL: AF038399; AAC82596.1; -  
 DR HIV: K03455; ENVSHXB2  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 624 624  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97212 MW; 6FA816AF85107FE0 CRC64;

Query Match 87.5%; Score 175; DB 1; Length 856;  
 Best Local Similarity 83.3%; Pred. No. 3.4e-13;  
 Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLESQNOQEKNEDELELDKWMANIMWNF 36  
 Db 638 YTSLSHSLIBESONOQEKNEDELELDKWMANIMWNF 673  
 RESULT 15  
 ENV\_HV1H3

ID ENV\_HV1H3 STANDARD: PRT; 856 AA.  
 AC P04624;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Staal F., Reddy E.P.;  
 RT "HIV-III env gene products synthesized in E. coli are recognized by  
 RT antibodies present in the sera of AIDS patients";  
 RL Cell 41:979-986(1985).  
 CC -----  
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CC -----  
 DR EMBL: M14100; AAA44679.1; -  
 DR HIV: M14100; ENVSHXB3.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
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 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 SO SEQUENCE 856 AA; 97212 MW; 6FA816AF85107FE0 CRC64;

FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	674	674	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	856 AA;	97188 MW;	3373C68B884C1AFC CRC64;

Query Match 87.5%; Score 175; DB 1; Length 856;  
 Best Local Similarity 83.3%; Pred. No. 3.4e-13;  
 Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy	1	YTGIIYNLLEESONOQEKNDQELLELDKMANIMNMF	36
		: : :     :     :     :     :	
Db	638	YTSLSHSLIEESONOQEKNDQELLELDKMANIMNMF	673

Search completed: May 16, 2003, 11:13:32  
 Job time : 7.07229 secs

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GenCore version 5.1.4\_P5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-4

Perfect score: 200  
Sequence: 1 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 36

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	99.0	122	15	Q9QIW9 human immun
2	196	98.0	122	15	Q9QIV1 human immun
3	194	97.0	117	15	Q9YRS7 human immun
4	193	96.5	122	15	Q9YXPI human immun
5	193	96.5	123	15	Q9EAA3 human immun
6	193	96.5	854	15	Q56566 human immun
7	193	96.5	861	15	Q41560 human immun
8	192	96.0	50	15	Q69898 human immun
9	192	96.0	122	15	Q9QD37 human immun
10	191	95.5	122	15	Q9YXR1 human immun
11	191	95.5	122	15	Q9IXR1 human immun
12	191	95.5	122	15	Q9IJO3 human immun
13	190	95.0	122	15	Q9EAB9 human immun
14	189	94.5	122	15	Q9IJK3 human immun
15	189	94.5	122	15	Q9QDK9 human immun
16	188	94.0	122	15	Q9YXR6 human immun

17	188	94.0	122	15	Q9YXN0 human immun
18	188	94.0	122	15	Q9QIW0 human immun
19	188	94.0	857	15	Q92823 human immun
20	188	94.0	857	15	Q71013 human immun
21	188	94.0	857	15	Q92821 human immun
22	188	94.0	857	15	Q89654 human immun
23	187	93.5	117	15	Q9QON2 human immun
24	187	93.5	117	15	Q9QON1 human immun
25	187	93.5	122	15	Q9YXW9 human immun
26	187	93.5	122	15	Q9IJP7 human immun
27	187	93.5	122	15	Q9IUN5 human immun
28	187	93.5	852	15	Q92761 human immun
29	187	93.5	852	15	Q73303 human immun
30	187	93.5	857	15	Q8UL89 human immun
31	187	93.5	859	15	Q73307 human immun
32	186	93.0	50	15	Q69900 human immun
33	186	93.0	118	15	Q9E5R0 human immun
34	186	93.0	122	15	Q9YXP7 human immun
35	186	93.0	122	15	Q9QIW6 human immun
36	186	93.0	122	15	Q9EAA5 human immun
37	186	93.0	122	15	Q9EAA0 human immun
38	186	93.0	122	15	Q9EAA4 human immun
39	186	93.0	122	15	Q9IJO0 human immun
40	186	93.0	122	15	Q9IJP9 human immun
41	186	93.0	856	15	Q73295 human immun
42	186	93.0	861	15	Q56109 human immun
43	186	93.0	866	15	Q9E1R5 human immun
44	185	92.5	122	15	Q9YXR2 human immun
45	185	92.5	122	15	Q9YXR8 human immun

## ALIGNMENTS

RESULT 1  
Q9QIW9 PRELIMINARY; PRT; 122 AA.  
AC Q9QIW9;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=GP41ERRJ02;  
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
RA Machado E., de Sa C.A.M., Eyer W., Passoni L.F.C., Meneses J.A.,  
RA Calzans A.R., Tenuri A.;  
RT "Genotyping and phenotyping analysis of B and non-B human  
RT immunodeficiency virus type 1 subtypes from patients under HAART";  
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF165535; AAF08480.1; -  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14744 MW; 02F0BE9F79AEC75 CRC64;

Query Match 99.0%; Score 198; DB 15; Length 122;  
Best Local Similarity 97.2%; Pred. No. 1.5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 36  
||:|||||  
Db 78 YTGIIYNLEESQNOEKNEQELLEDKRWANLWNMF 113

RESULT 2



```
Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36
|||||:|||||:|||||:|||||:|||||
Db 79 YTGIIYNLLEESQNOEKNEQELLELDKRWASLNMNF 114

RESULT 6
ID 056566 PRELIMINARY; PRT; 854 AA.
AC 056566;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PIH309;
MEDLINE=99372987; PubMed=10445815;
Alman-Onal Y., Colffier C., Giraud A., Babic-Ercog A., Biron F.,
Verrier B.;
RT "Comparison of complete env gene sequences from individuals with
RT symptomatic primary HIV type 1 infection.";
RL AIDS Res. Hum. Retroviruses 15:1035-1039(1999).
DR EMBL: AF041132; AAC02523.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97062 MW; 58B012C83A0C3DA2 CRC64;

Query Match 96.5%; Score 193; DB 15; Length 854;
Best Local Similarity 94.4%; Pred. No. 4.3e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36
|||||:|||||:|||||:|||||:|||||
Db 636 YTGIIYNLLEESQNOEKNEQELLELDKRWASLNMNF 671

RESULT 7
ID 041560 PRELIMINARY; PRT; 861 AA.
AC 041560;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE - Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C24;
MEDLINE=98105804; PubMed=9445059;
Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
Walker B.D., Neumann A.U., Vermund S.H., Westleky J., Jackson S.,
Fenamore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,
McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines.";
RL J. Virol. 72:1552-1576(1998).
DR EMBL: U84817; AAC58848.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
```

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FT NON_TER 1 1
SQ SEQUENCE 861 AA; 97500 MW; 98C2DFADEAC76539 CRC64;

Query Match 96.5%; Score 193; DB 15; Length 861;
Best Local Similarity 91.7%; Pred. No. 4.4e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36
|||||:|||||:|||||:|||||:|||||
Db 643 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 678

RESULT 8
ID 069898 PRELIMINARY; PRT; 50 AA.
AC 069898;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94211861; PubMed=7512731;
Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emimi E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAW-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL: U06728; AAA19141.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;

Query Match 96.0%; Score 192; DB 15; Length 50;
Best Local Similarity 94.4%; Pred. No. 3.3e-16;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 36
|||||:|||||:|||||:|||||:|||||
Db 15 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMNF 50

RESULT 9
ID 090DJ7 PRELIMINARY; PRT; 122 AA.
AC 090DJ7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DG;
Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Bityahwa B., Sempaia S.D.K., Rayfield M.A., Dondero T.J., Lai R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307734; AAL08795.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
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KW Transmembrane.
FT NON_TER 1
KW NON_TER 122
SQ SEQUENCE 122 AA: 14743 MW: FBB3D55A1B1482A2 CRC64:

Query Match
Best Local Similarity 96.0%; Score 192; DB 15; Length 122;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 36
DB 78 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 113

RESULT 10
O9YXR1 PRELIMINARY: PRT: 122 AA.
AC O9YXR1:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ96BRP019;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF034042; AAC79294.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14835 MW: 396EA258E3BAABD5 CRC64:

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 36
DB 78 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 113

RESULT 11
O9IJRO PRELIMINARY: PRT: 122 AA.
AC O9IJRO:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ARI;
RA MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggis J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL: AF220672; AAF74224.1; -

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DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14808 MW: ADDACE746A9C757 CRC64:

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 36
DB 78 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 113

RESULT 12
O9IJQ3 PRELIMINARY: PRT: 122 AA.
AC O9IJQ3:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AR46;
RA MEDLINE=20346416; PubMed=10890362;
RA Masciotra S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggis J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL: AF220679; AAF74231.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA: 14478 MW: A548C7BE0315D851 CRC64:

Query Match
Best Local Similarity 95.5%; Score 191; DB 15; Length 122;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 36
DB 78 YTGIIYNLLEESQNOOEKNEQELLELDKKNALMNMF 113

RESULT 13
O9EA89 PRELIMINARY: PRT: 122 AA.
AC O9EA89:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX774;
RA MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B

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RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States."
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL: AF190963; AAG02325.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 122 AA; 14892 MW; 8EF45DAF0E5FAFA7 CRC64;

Query Match
Best Local Similarity 95.0%; Score 190; DB 15; Length 122;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKWNALMNWF 36
DB 78 YTNLIYNLLEESQNOQEKNEQELLELDKWNALMNWF 113

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AC O9JTN3;
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DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AR48;
RX MEDLINE-20346416; PubMed-10890362;
RA Masciocla S., Livellara B., Belloso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014(2000).
DR EMBL: AF220699; AAF76818.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14748 MW; 2B120F6B47730DFD CRC64;

Query Match
Best Local Similarity 94.5%; Score 189; DB 15; Length 122;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKWNALMNWF 36
DB 78 YTGIIYNLLEESQNOQEKNEQELLELDKWNALMNWF 113

RESULT 15
O90DK9 PRELIMINARY; PRT; 122 AA.
AC O90DK9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UG;

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RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
RA Biryahwaho B., Sempala S.D.K., Rayfield M.A., Dondero T.J., Lal R.;
RT "Similar distribution and continued predominance of HIV-1 subtypes A
RT and D infections in Uganda.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307722; AAL08783.1; -.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14675 MW; 2FFD0A7866F3BB37 CRC64;

Query Match
Best Local Similarity 94.4%; Score 189; DB 15; Length 122;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKWNALMNWF 36
DB 78 YTGIIYNLLEESQNOQEKNEQELLELDKWNALMNWF 113

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Search completed: May 16, 2003, 11:19:44  
Job time : 27.3124 secs

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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-4

Perfect score: 200

Sequence: 1 YTGIIYNLIEESQNOEKNEQELLDKRWANLWNF 36

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Issued\_Patents\_AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUTS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	1	US-08-073-028-4
2	200	100.0	36	3	US-08-486-099-4
3	200	100.0	36	3	US-08-360-107A-4
4	200	100.0	36	3	US-08-484-223B-4
5	200	100.0	36	3	US-08-919-597-4
6	200	100.0	36	3	US-08-475-668A-4
7	200	100.0	36	3	US-08-485-551A-4
8	200	100.0	36	3	US-08-471-913A-4
9	200	100.0	36	4	US-08-534-616-4
10	200	100.0	36	4	US-08-485-264A-4
11	200	100.0	36	4	US-09-082-279B-1358
12	200	100.0	36	4	US-09-082-279B-1359
13	200	100.0	36	4	US-08-474-349A-4
14	200	100.0	36	4	US-09-315-304B-1358
15	200	100.0	36	4	US-09-315-304B-1359
16	200	100.0	36	4	US-08-255-208A-4
17	200	100.0	36	4	US-09-570-921-18
18	200	100.0	269	4	US-08-965-056-13
19	200	100.0	865	4	US-07-956-483-13
20	200	100.0	887	4	US-08-472-240A-4
21	185	92.5	138	4	US-09-570-921-27
22	185	92.5	233	4	US-08-965-056-50
23	185	92.5	267	4	US-08-965-056-38
24	185	92.5	268	4	US-08-965-056-41
25	184	92.0	36	1	US-08-073-028-3
26	184	92.0	36	3	US-08-360-107A-3
27	184	92.0	36	4	US-08-554-616-3

28	183	91.5	269	4	US-08-965-056-43	Sequence 43, Appl
29	182	91.0	46	4	US-08-965-056-110	Sequence 110, App
30	182	91.0	268	4	US-08-965-056-13	Sequence 13, Appl
31	182	91.0	269	4	US-08-965-056-48	Sequence 48, Appl
32	182	91.0	270	4	US-08-965-056-67	Sequence 67, Appl
33	182	91.0	855	1	US-08-022-835-6	Sequence 6, Appl1
34	182	91.0	855	2	US-08-388-809-6	Sequence 6, Appl1
35	182	91.0	855	2	US-08-647-714-6	Sequence 19, Appl
36	181	90.5	138	4	US-08-570-921-19	Sequence 28, Appl
37	181	90.5	269	4	US-08-965-056-28	Sequence 28, Appl
38	180	90.0	36	4	US-09-082-279B-642	Sequence 642, App
39	180	90.0	36	4	US-09-315-304B-642	Sequence 5, Appl1
40	180	90.0	138	4	US-09-570-921-5	Sequence 14, Appl
41	180	90.0	613	4	US-09-257-490-14	Sequence 28, Appl
42	180	90.0	850	2	US-08-448-603A-28	Sequence 28, Appl
43	180	90.0	850	3	US-09-134-075-28	Sequence 28, Appl
44	180	90.0	850	4	US-09-492-739-28	Sequence 28, Appl
45	179	89.5	138	4	US-09-570-921-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-073-028-4  
; Sequence 4, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Mathews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO. 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-4  
Query Match 100.0%; Score 200; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLIEESQNOEKNEQELLDKRWANLWNF 36  
|||||

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLWNMF 36

RESULT 2

US-08-486-099-4

Sequence 4, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-4

Query Match 100.0%; Score 200; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1,8e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLWNMF 36

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLWNMF 36

RESULT 3

US-08-360-107A-4

Sequence 4, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-4

Query Match 100.0%; Score 200; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1,8e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLWNMF 36

Db 1 YTGIIYNLLESQNOQEKNEQELLELDKRWANLWNMF 36

RESULT 4

US-08-484-223B-4

Sequence 4, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
DB-484-223B-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36  
Db 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36

RESULT 5  
US-08-919-597-4  
Sequence 4, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36  
Db 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36

RESULT 6  
US-08-475-668A-4  
Sequence 4, Application US/08475668A  
Patent No. 606065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-4

Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36  
Db 1 YTGIIYNLEESONQOEKNEDELLELDKWNANLWNMF 36

RESULT 7  
US-08-485-551A-4  
Sequence 4, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
RESULT 8  
US-08-471-913A-4  
Sequence 4, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
RESULT 9  
US-08-554-616-4  
Sequence 4, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993

US-08-485-551A-4  
Sequence 4, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
RESULT 8  
US-08-471-913A-4  
Sequence 4, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-4  
Query Match 100.0%; Score 200; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
DB 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLNMWF 36  
RESULT 9  
US-08-554-616-4  
Sequence 4, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-554-616-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36  
 1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36

RESULT 10  
 US-08-485-264A-4  
 Sequence 4, Application US/08485264A  
 Patent No. 6228983

GENERAL INFORMATION:  
 APPLICANT: Bolognesi, Dani P.  
 APPLICANT: Matthews, Thomas J.  
 APPLICANT: Wild, Carl T.  
 APPLICANT: Barney, Shawn O.  
 APPLICANT: Lambert, Dennis M.  
 APPLICANT: Peteway, Stephen R.  
 APPLICANT: Langlois, Alphonse J.  
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
 TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
 NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
 ADDRESS: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,264A  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide

US-08-485-264A-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36  
 1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36

RESULT 11  
 US-09-082-279B-1358  
 Sequence 1358, Application US/09082279B  
 Patent No. 6258782

GENERAL INFORMATION:  
 APPLICANT: Barney, Shawn  
 APPLICANT: Guthrie, Kelly  
 APPLICANT: Merutka, Gene  
 APPLICANT: Anwer, Mohamed  
 APPLICANT: Lambert, Dennis  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
 FILE REFERENCE: 7872-043  
 CURRENT APPLICATION NUMBER: US/09/082,279B  
 CURRENT FILING DATE: 1998-05-20  
 NUMBER OF SEQ ID NOS: 1515  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1358  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-082-279B-1358

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36  
 1 YTGIIYNLLESQNOQEKNEQELLELDKWNLMNMF 36

RESULT 12  
 US-09-082-279B-1359  
 Sequence 1359, Application US/09082279B  
 Patent No. 6258782

GENERAL INFORMATION:  
 APPLICANT: Barney, Shawn  
 APPLICANT: Guthrie, Kelly  
 APPLICANT: Merutka, Gene  
 APPLICANT: Anwer, Mohamed  
 APPLICANT: Lambert, Dennis  
 TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
 TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
 FILE REFERENCE: 7872-043  
 CURRENT APPLICATION NUMBER: US/09/082,279B  
 CURRENT FILING DATE: 1998-05-20  
 NUMBER OF SEQ ID NOS: 1515  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 1359  
 LENGTH: 36  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Core polypeptide  
 US-09-082-279B-1359

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 13  
US-08-474-349A-4  
Sequence 4, Application US/08474349A  
Patent No. 6333395

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petterway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
NUMBER OF SEQUENCES: 517  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,349A  
FILING DATE: 07-JUN-1995

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-024  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-474-349A-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 14  
US-09-315-304B-1358

Sequence 1358, Application US/09315304B  
Patent No. 6348568

GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.

APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1358  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1358

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

RESULT 15  
US-09-315-304B-1359

Sequence 1359, Application US/09315304B  
Patent No. 6348568

GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1359  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1359

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.8e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36  
|||||  
Db 1 YTGIIYNLLEESQNOEKNEQELLELDKRWANLWNMF 36

Search completed: May 16, 2003, 11:22:10  
Job time : 10.1928 secs

GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-4  
Perfect score: 200  
Sequence: 1 YTGIIYNLIEESQNOQEKNEQELLELDKWMNIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

al number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	269	10	US-09-854-816-33
2	185	92.5	233	10	US-09-854-816-50
3	185	92.5	267	10	US-09-854-816-38
4	185	92.5	268	10	US-09-854-816-41
5	183	91.5	269	10	US-09-854-816-43
6	182	91.0	46	10	US-09-854-816-110
7	182	91.0	268	10	US-09-854-816-113
8	182	91.0	269	10	US-09-854-816-48
9	182	91.0	270	10	US-09-854-816-67
10	181	90.5	269	10	US-09-854-816-28
11	179	89.5	268	10	US-09-854-816-9
12	179	89.5	268	10	US-09-854-816-26
13	179	89.5	269	10	US-09-854-816-12
14	179	89.5	619	10	US-09-891-609-4
15	179	89.5	646	10	US-09-891-609-2
16	179	89.5	847	10	US-09-476-242-2
17	178	89.0	46	10	US-09-854-816-109
18	178	89.0	145	12	US-10-000-321-11
19	178	89.0	268	10	US-09-854-816-40

20	178	89.0	269	10	US-09-854-816-6	Sequence 6, Appl
21	178	89.0	269	10	US-09-854-816-30	Sequence 30, Appl
22	178	89.0	269	10	US-09-854-816-31	Sequence 31, Appl
23	178	89.0	269	10	US-09-854-816-42	Sequence 42, Appl
24	177	88.5	223	10	US-09-854-816-49	Sequence 49, Appl
25	176	88.0	36	10	US-09-779-451-44	Sequence 44, Appl
26	176	88.0	46	10	US-09-779-451-42	Sequence 42, Appl
27	176	88.0	268	10	US-09-854-816-68	Sequence 68, Appl
28	176	88.0	268	10	US-09-854-816-71	Sequence 71, Appl
29	176	88.0	269	10	US-09-854-816-21	Sequence 21, Appl
30	176	88.0	269	10	US-09-854-816-22	Sequence 22, Appl
31	176	88.0	269	10	US-09-854-816-44	Sequence 44, Appl
32	176	88.0	269	10	US-09-854-816-46	Sequence 46, Appl
33	175	87.5	36	9	US-09-874-475-16	Sequence 16, Appl
34	175	87.5	36	9	US-10-116-797-1	Sequence 1, Appl
35	175	87.5	36	9	US-09-493-246-1	Sequence 1, Appl
36	175	87.5	36	10	US-09-796-202-10	Sequence 10, Appl
37	175	87.5	36	10	US-09-779-451-5	Sequence 5, Appl
38	175	87.5	36	10	US-09-834-628-1	Sequence 1, Appl
39	175	87.5	36	10	US-09-854-816-1	Sequence 1, Appl
40	175	87.5	36	10	US-09-854-816-108	Sequence 108, App
41	175	87.5	37	9	US-09-848-616-176	Sequence 176, App
42	175	87.5	46	10	US-09-779-451-41	Sequence 41, Appl
43	175	87.5	56	10	US-09-779-451-4	Sequence 4, Appl
44	175	87.5	177	9	US-10-040-349B-2	Sequence 2, Appl
45	175	87.5	221	9	US-10-059-271-84	Sequence 84, Appl

## ALIGNMENTS

RESULT 1  
US-09-854-816-33  
; Sequence 33, Application US/09854816  
; Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasinik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:



CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-09-854-816-41  
Query Match 92.5%; Score 185; DB 10; Length 268;  
Best Local Similarity 88.9%; Pred. No. 1,8e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGIIYNLEESQNOEKNEQELLELDKRWANIMWNF 36  
Db 168 YTGIIYNLEESQNOEKNEQELLELDKRWASIMWNF 203  
RESULT 5  
US-09-854-816-43  
Sequence 43; Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-854-816-43  
Query Match 91.5%; Score 183; DB 10; Length 269;  
Best Local Similarity 86.1%; Pred. No. 3.1e-14;  
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTGIIYNLEESQNOEKNEQELLELDKRWANIMWNF 36  
Db 169 YTGIIYNLEESQNOEKNEQELLELDKRWASIMWNF 204  
RESULT 6  
US-09-854-816-110  
Sequence 110; Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-09-854-816-110  
Query Match 91.0%; Score 182; DB 10; Length 46;

Qy	1	YTGIIYNLLEESQNOQEKNEDELLEDDKANLMMNF	36
		:             :	
Db	11	YTXIIYNLLEESQNOQEKNEQDLDLADKANLMMNF	46

RESULT 7  
US-09-854-816-13  
; Sequence 13, Application US/09854816  
; Patent No. US20020151473a1  
; GENERAL INFORMATION:  
; Application 13, 2002-01-13, 2002-01-13

Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

```

?      COMPUTER READABLE FORM:
?      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
?      COMPUTER: IBM PC compatible
?      OPERATING SYSTEM: PC-DOS/MS-DOS
?      SOFTWARE: WinPatIn (Genentech)
?      CURRENT APPLICATION DATA:
?      APPLICATION NUMBER: US/09/854, 816
?      FILING DATE: 15-May-2001
?      CLASSIFICATION: <Unknown>
?      PRIOR APPLICATION DATA:

```

1 APPLICATION NUMBER: 08/965,.056  
2 FILING DATE: <unknown>  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Torchia, PhD., Timothy E.  
5 REGISTRATION NUMBER: 36,700  
6 REFERENCE/DOCKET NUMBER: P1005RR  
7 TELECOMMUNICATION INFORMATION:  
8 TELEPHONE: 650/225-8674  
9 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 266 amino acids  
 TYPE: Amino acid  
 TOPOLOGY: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-854-816-13

Query Match	91.0%	Score 183	DB 10	Length 268
Best Local	88.9%	Pred. No. 4	1e-14	
Matches 32, Conservative		3, Mismatches 1,	Indels 0,	Gaps 0;

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Qy      1 YTGITVNLIEESQNOQEKNEQELLELDKMWLIMWF 36
        |||:::|||||:|||||:|||||
Db     168 YTSITVSLIEESQNOQEKNEQELLELDKWSLIMWF 203

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RESULT 8  
US-09-854-816-48  
Sequence 48, Application US/09864816  
Patent No. US20020151473A1  
GENERAL INFORMATION  
APPLICANT: Andrew C. Braisteece  
J. Kevin Judice  
Robert S. McDowell

J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

```

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001

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? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: 08/965,056  
 ? FILING DATE: <unknown>  
 ?  
 ? ATTORNEY/AGENT INFORMATION:  
 ? NAME: Torchia, Phd., Timothy E  
 ? REGISTRATION NUMBER: 36,700  
 ? REFERENCE/DOCKET NUMBER: P1005?

```

1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: 650/225-8674
3 TELEFAX: 650/952-9881
4
5 INFORMATION FOR SEQ ID NO: 48:
6
7     SEQUENCE CHARACTERISTICS:
8         LENGTH: 269 amino acids
9         TYPE: Amino Acid
10        TOPOLOGY: Linear
11
12     SEQUENCE DESCRIPTION: SEQ ID NO: 48:
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Query Match	91.0%;	Score 182;	DB 10;	Length 269;
Best Local Similarity	86.1%;	Pred. No. 4, 1e-14;		
Matches	31;	Conservative	4;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1	YTGITYNNLEESQNOOEKNEDELEELDKRANIMNMF	36	
		: : : : : : : : : : : : : : : : :		
Db	169	YTGIFNLIIEFAQNOOEKNEEDLLLEDKRWAGIMNMF	204	

RESULT 9  
US-09-854-816-67  
; Sequence 67, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted

Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik

```

; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113

```

STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-854-816-67

Query Match 91.0%; Score 182; DB 10; Length 270;  
Best Local Similarity 88.9%; Pred. No. 4,1e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 36  
DB 170 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 205

RESULT 10  
US-09-854-816-28  
Sequence 28, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-854-816-28

Query Match 90.5%; Score 181; DB 10; Length 269;  
Best Local Similarity 88.9%; Pred. No. 5.4e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 36  
DB 169 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 204

RESULT 11  
US-09-854-816-9  
Sequence 9, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-854-816-9

Query Match 89.5%; Score 179; DB 10; Length 268;  
Best Local Similarity 86.1%; Pred. No. 9.3e-14;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 36  
DB 168 YTGIIYNLLEESONQOEKNEDELLEDKWANLWNMF 203

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: RESULT 12
: US-09-854-816-26
: Sequence 26, Application US/09854816
: Patent No. US20020151473A1
: GENERAL INFORMATION:
: APPLICANT: Andrew C. Braisted
: J. Kevin Judice
: Robert S. McDowell
: J. Christopher Phelan
: Melissa A. Starovasnik
: James A. Wells
: TITLE OF INVENTION: Constrained Helical Peptides and Methods of
: Making Same
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/854,816
: FILING DATE: 15-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/965,056
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, PhD., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P1005R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 268 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 26:
: US-09-854-816-26
: Query Match 89.5%; Score 179; DB 10; Length 268;
: Best Local Similarity 86.1%; Pred. No. 9,3e-14;
: Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0
: QY 1 YTCIYNLEESONOEKNEOELLIEDKXANLWNWF 36
: 11:11111111111111111111111111111111
: Db 168 YTNLIVTLIEESONOEKNEOELLIEDKXANLWNWF 203
: RESULT 13
: US-09-854-816-12
: Sequence 12, Application US/09854816
: Patent No. US20020151473A1
: GENERAL INFORMATION:
: APPLICANT: Andrew C. Braisted
: J. Kevin Judice
: Robert S. McDowell
: J. Christopher Phelan
: Melissa A. Starovasnik
: James A. Wells
: TITLE OF INVENTION: Constrained Helical Peptides and Methods of
: Making Same
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P100542

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-854-816-12

Query Match      89.5%; Score 179; DB 10; Length 269;
Best Local Similarity 86.1%; Pred. NO. 9.3e-14;
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy      1 YTGIIYNLLEESONOEKNEOELLELDKMANIMNF 36
      ||:||||:||||:||||:||||:||||:||||:||||:
Db      169 YTNLIYTLLEESONOEKNEOELLELDKMASIMNF 204

RESULT 14
US-09-891-609-4
; Sequence 4, Application US/09891609
; Patent No. US20020127238A1
; GENERAL INFORMATION:
; APPLICANT: Stamatatos, Leonidas
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
; FILE REFERENCE: 2570-1-002N
; CURRENT APPLICATION NUMBER: US/09/891,609
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,608
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-4

Query Match      89.5%; Score 179; DB 10; Length 619;
Best Local Similarity 86.1%; Pred. No. 2.2e-13;
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy      1 YTGIIYNLLEESONOEKNEOELLELDKMANIMNF 36
      ||:||||:||||:||||:||||:||||:||||:||||:
Db      574 YTNLIYTLLEESONOEKNEOELLELDKMASIMNF 609

```

; Sequence 2, Application US/09891609  
; Patent No. US20020127238A1  
; GENERAL INFORMATION:  
; APPLICANT: Stamatos, Leonidas  
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR  
; FILE REFERENCE: 2570-1-002N  
; CURRENT APPLICATION NUMBER: US/09/891,609  
; CURRENT FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: 60/214,608  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 646  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-891-609-2

Query Match 89.5%; Score 179; DB 10; Length 646;  
Best Local Similarity 86.1%; Pred. No. 2.3e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YTCIITNLEESQNOQKNEQELLELDKWNLMNMF 36  
DB 601 YTNLIYTLLEESQNOQKNEQELLELDKWNLMNMF 636

Search completed: May 16, 2003, 12:10:22  
Job time: 15.759 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193

Sequence: 1 YNSLIYSLLEKSGTQOEKNEDELLDKWASLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_101002:\*

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- 2: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:\*
- 3: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:\*
- 4: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*
- 5: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*
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- 10: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:\*
- 11: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:\*
- 12: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:\*
- 13: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:\*
- 14: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:\*
- 15: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:\*
- 16: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:\*
- 17: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:\*
- 18: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:\*
- 19: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:\*
- 20: /SID52/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*
- 21: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*
- 22: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*
- 23: /SID52/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	100.0	36	17 AAR98401	Peptide correspond
2	193	100.0	36	18 AAM17014	DP-178-like peptid
3	193	100.0	36	22 AAG67042	HIV-1 gp41 peptide
4	193	100.0	36	22 AAU14014	DP178 homologue de
5	193	100.0	36	22 AAB92247	Virus related pept
6	193	100.0	36	22 AAB54788	HIV antiviral acti
7	193	100.0	267	19 AAY22819	SEQ ID NO. 15 from
8	193	100.0	267	23 AAG68290	Envelope protein g
9	193	100.0	854	19 AAM43068	HIV-1 gp120 protei
10	193	100.0	856	12 AAR14903	HIV-1(MN) env prot

11	193	100.0	856	16 AAR79173	HIV virus-1 isolat
12	193	100.0	856	18 AAM11579	Human immunodefici
13	193	100.0	856	19 AAM58805	HIV-1 isolate MN e
14	193	100.0	856	20 AAR88111	Predicted amino ac
15	193	100.0	1188	17 AAR94622	HIV-1 gp160-NY5 p5
16	187	96.9	36	21 AAR98940	Core polypeptide f
17	187	96.9	36	21 AAY89841	Core polypeptide f
18	187	96.9	36	22 AAU70182	HIV viral envelope
19	187	96.9	36	22 ABB01248	Viral DP178/107-1i
20	187	96.9	36	22 ABB01249	Viral DP178/107-1i
21	187	96.9	36	22 ABB02833	Viral core polypep
22	187	96.9	36	22 AAU13794	DP178-1-like/DP107-1
23	187	96.9	36	22 AAU13795	Core polypeptide T
24	187	96.9	36	22 AAB78241	Core polypeptide T
25	187	96.9	36	22 AAB78242	Core polypeptide T
26	187	96.9	160	21 AAB12265	HIV-1 gp41 ectodom
27	187	96.9	857	12 AAR14904	HIV-1(MN-ST1) env
28	187	96.9	857	18 AAM11580	Human Immunodefici
29	187	96.9	857	20 AAB08112	Predicted amino ac
30	184	95.3	36	22 ABB02834	Viral core polypep
31	182	94.3	36	22 ABB00638	Viral DP178/107-1i
32	182	94.3	36	22 ABB02115	Viral core polypep
33	182	94.3	36	22 AAU13186	DP178-1-like/DP107-1
34	182	94.3	36	22 AAB77633	Core polypeptide T
35	182	94.3	850	16 AAB67724	Core polypeptide T
36	181	93.8	36	16 AAR67700	DP-178 homologue d
37	181	93.8	36	22 ABB00639	Viral DP178/107-1i
38	181	93.8	36	22 ABB02116	Viral core polypep
39	181	93.8	36	22 AAU13187	DP178-1-like/DP107-1
40	181	93.8	36	22 AAB77634	Core polypeptide T
41	181	93.8	269	19 AAY22832	SEQ ID NO. 28 from
42	181	93.8	269	23 AAG68303	Envelope protein g
43	180	93.3	268	19 AAY22817	SEQ ID NO. 13 from
44	180	93.3	268	23 AAG68288	Envelope protein g
45	180	93.3	855	12 AAR14905	HIV-1 BA-L clone-e

## ALIGNMENTS

RESULT 1

ID	Score	Query Match	Length	ID	Description
17 AAR98401	193	100.0	36	17 AAR98401	Peptide correspond
18 AAM17014	193	100.0	36	18 AAM17014	DP-178-like peptid
22 AAG67042	193	100.0	36	22 AAG67042	HIV-1 gp41 peptide
22 AAU14014	193	100.0	36	22 AAU14014	DP178 homologue de
22 AAB92247	193	100.0	36	22 AAB92247	Virus related pept
22 AAB54788	193	100.0	36	22 AAB54788	HIV antiviral acti
19 AAY22819	267	100.0	267	19 AAY22819	SEQ ID NO. 15 from
23 AAG68290	267	100.0	267	23 AAG68290	Envelope protein g
19 AAM43068	854	100.0	854	19 AAM43068	HIV-1 gp120 protei
12 AAR14903	856	100.0	856	12 AAR14903	HIV-1(MN) env prot

Human immunodeficiency virus type 1.

W09619495-A1.

27-JUN-1996.

20-DEC-1995; 95WO-US16733.

06-JUN-1995; 95US-0470896.

20-DEC-1994; 94US-0360107.

(TRIM-) TRIMERIS INC.

(UYDU-) UNIV DUKE.

Barney SO, Bologna DP, Lambert DM, Langlois AJ, Matthews TJ, Petteway SR, Wild CT, WPT, 1996-309517/31.

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 PS  
 XX Disclosure: Fig 1; 471pp; English.  
 CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 100.0%; Score 193; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 2  
 ID AAM17014 standard; peptide; 36 AA.  
 XX AAM17014:  
 AC  
 XX  
 DT 01-JUL-1997 (first entry)  
 XX  
 DE DP-178-like peptide useful for treatment of HIV infection.  
 XX  
 KW HIV: STV: human; simian immunodeficiency virus; glycoprotein 41;  
 KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition.  
 KW replication; transmission.  
 XX  
 OS Human immunodeficiency virus type 1 MN isolate.  
 XX  
 PN WO9640191-A1.  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US039499.  
 XX  
 PP 07-JUN-1995; 95US-0481957.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Johnson RM, Lambert DM;  
 XX  
 DR WPI; 1997-099886/09.  
 XX  
 PT Compsns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Disclosure: Figure 1; 84pp; English.  
 XX  
 CC AAM17012-WI7016 are DP-178 homologues that are useful in the  
 CC treatment of HIV infection. DP-178 is a peptide corresponding to  
 CC residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane  
 CC protein. DP-178 and its derivatives/homologues are used in combination  
 CC with a therapeutic agent, e.g. a reverse transcriptase, viral protease,  
 CC cytokine, glycosylation or viral mRNA processing inhibitor or a  
 CC nucleoside inhibitor. The peptides work by inhibiting viral replication  
 CC or inhibiting transmission. They may also be used in vaccines for  
 CC protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 193; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 3  
 ID AAG67042 standard; Peptide; 36 AA.  
 XX AAG67042:  
 AC  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE HIV-1 gp41 peptide DP178 homologue.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection; DP178.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200164013-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 07-FEB-2001; 2001WO-US03988.  
 XX  
 PR 29-FEB-2000; 2000US-0515965.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX  
 DR WPI; 2001-514829/56.  
 XX  
 PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 PS Disclosure: Fig 1; 587pp; English.  
 XX  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1/IIA1 transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 100.0%; Score 193; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 DB 1 YTSLIYSLEKSTQOEKNEQELLELDKNASLWNMF 36  
 RESULT 4  
 ID AAU14014 standard; peptide; 36 AA.  
 XX AAU14014:  
 AC AAU14014:

[illegible]

XX	Homo sapiens.
OS	Synthetic.
PN	WO200069900-A2.
XX	
PD	23-NOV-2000.
XX	
PF	17-MAY-2000; 2000WO-US13576.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
PR	15-OCT-1999; 99US-0159783.
XX	
PA	(CONJ-) CONJUCHEM INC.
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX	
DR	WPI: 2001-112059/12.
XX	
PT	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity
PS	
XX	
PS	Disclosure: Page 663; 733pp; English.
CC	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (II) and a
CC	reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptidease stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specifically as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB92441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 36 AA:
	Query Match 100.0%; Score 193; DB 22; Length 36;
	Best Local Similarity 100.0%; Pred. No. 2,9e-17;
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSLIYSLLKESQTOOEKNEOELLELDKWSLMMNF 36
DB	1 YTSLIYSLLKESQTOOEKNEOELLELDKWSLMMNF 36
RESULT 6	
AAB54788	
ID	AAB54788 standard; Peptide; 36 AA.
XX	
AC	AAB54788;
XX	
DT	05-MAR-2001 (first entry)
XX	
XX	HIV antiviral activity exhibiting peptide SEQ ID NO:5.
XX	
KW	Long lasting fusion peptide inhibitor; viral infection; antiviral;
KW	antifusogenic; mobile blood component; measles virus; MeV; SIV;
KW	simian immunodeficiency virus; human parainfluenza virus; HIV;
KW	human respiratory syncytial virus; human immunodeficiency virus; HIV.
OS	Human immunodeficiency virus type 1.
PN	WO200069902-A1.

XX 23-NOV-2000.  
PD  
XX 17-MAY-2000; 2000WO-US13651.  
XX  
XX 17-MAY-1999; 99US-0134406.  
PR 10-SEP-1999; 99US-0153406.  
XX  
XX (CONF-) CONJUCHEM INC.  
XX  
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;  
XX WPI; 2001-007496/01.  
XX  
XX A modified peptide and a reactive group which is reactive with amino  
PT groups, hydroxyl groups, or thiol groups on blood components to form  
PT stable covalent bonds useful for treatment of viral infections, e.g.  
PT human immunodeficiency virus  
XX  
XX Claim 6; Page 174; 211pp; English.

XX The present invention describes a modified anti-viral peptide (I)  
XX comprising a peptide that exhibits anti-viral activity and a reactive  
XX group which is reactive with amino groups, hydroxyl groups, or thiol  
XX groups on blood components to form stable covalent bonds. (I) has  
XX anti-viral and anti-fusogenic activities. (I) inhibits viral infection  
XX of cells by inhibiting cell-cell fusion or free virus infection or to  
XX reduce the level of membrane fusion events between two or more entities,  
XX e.g., virus-cell or cell-cell, relative to the level of membrane fusion  
XX that occurs in the absence of the peptide. (I) is useful in the  
XX treatment of patients who are suffering from viral infection, e.g. HIV,  
XX RSV, HPIV, MeV, and SIV. (I) may be administered prophylactically to  
XX previously uninfected individuals. This is useful in cases where an  
XX individual has been subjected to a high risk of exposure to a virus.  
XX By bonding of long-lived components of the blood, such as immunoglobulin,  
XX serum albumin, red blood cells and platelets the activity is extended  
XX for days to weeks. This is due to improved stability in vivo and a  
XX reduced susceptibility to peptidase or protease degradation. This  
XX minimises the need for more frequent, or even continual, administration  
XX of the peptides. AAB54784 to AAB55431 represent peptides used in the  
XX exemplification of the present invention.

XX Sequence 36 AA:

Query Match 100.0%; Score 193; DB 22; Length 36;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSOQOQEKNEDELLELDKWSLMMNF 36  
1 YTSLSLSLEKSOQOQEKNEDELLELDKWSLMMNF 36

RESULT 7

AY22819  
ID AY22819 standard; Protein: 267 AA.

AY22819;

19-AUG-1999 (first entry)

SEQ ID NO. 15 from WO9820036.

XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
XX vaccine; antibody; viral membrane fusion; viral infectivity;  
XX ligand affinity purification; protein A replacement;  
XX immunoglobulin purification; epitope mimic.

OS Human immunodeficiency virus.

XX WO9820036-A1.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US20069.  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH) GENENTECH INC.  
XX  
XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
PI Wells JA;  
XX WPI; 1998-286866/25.  
XX

XX Production of constrained helical peptide(s) by linking side chains  
PT on terminl of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX Claim 11; Page 155; 279pp; English.

XX Peptides AAY2805-Y22917 are derived from Human immunodeficiency virus  
XX (HIV). Specifically, AAY2810-Y22910 are derived from gp41 proteins  
XX of known HIV virus strains (AAY2871, AAY22871, AAY22880, AAY22888 and  
XX AAY22903 represent consensus sequences of various sections of the gp41  
XX protein). Sequences derived from the peptides are used to produce  
XX constrained helical peptides of the invention. The constrained helical  
XX peptide is produced by synthesising an octapeptide in which both terminal  
XX amino acids have a side-chain that includes a group able to form an amide  
XX bond, and cyclizing the octapeptide by reacting the specified side-chain  
XX residues with a difunctional linker to produce two amide bonds.  
XX The constrained helical peptides are used to treat or prevent HIV  
XX infection, especially as vaccines that generate antibodies that  
XX prevent viral membrane fusion or infectivity. Vaccines may contain  
XX constrained helical peptides derived from several different strains of  
XX HIV. The antibodies are also useful for diagnosing HIV infection. Other  
XX uses for the constrained helical peptides are in affinity purification  
XX of ligands (particularly where complete binding protein is not readily  
XX available, e.g. replacements for protein A in immunoglobulin  
XX purification); as epitope mimics for antibody production; for isolation  
XX of synthetic antibody clones from phage display libraries, or as stable  
XX forms of "floppy" peptides or proteins.

XX Sequence 267 AA:

Query Match 100.0%; Score 193; DB 19; Length 267;  
Best Local Similarity 100.0%; Pred. NO. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSOQOQEKNEDELLELDKWSLMMNF 36  
167 YTSLSLSLEKSOQOQEKNEDELLELDKWSLMMNF 202

RESULT 8

ABG68290  
ID ABG68290 standard; Protein: 267 AA.

ABG68290;

07-OCT-2002 (first entry)

Envelope protein gp41 from HIV clade B strain #9.

XX HIV; glycoprotein; gp41; antigen; helical conformation;  
XX virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
XX viral envelope protein; vaccine; virucide; anti-HIV.

OS Human immunodeficiency virus type 1 clade B.

XX US6271198-B1.

XX 07-AUG-2001.

PF 05-NOV-1997; 97US-0965056.  
 XX  
 PR 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-JUN-1997; 97US-0876698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasiluk MA;  
 PI Wells JA;  
 XX WPI: 2002-487624/52.  
 DR  
 XX  
 PR New cyclic peptides from human immune deficiency virus gp41, useful for  
 PR treatment or prevention of HIV infection, are constrained to have  
 PR alpha-helical conformation -  
 PS Disclosure: Column 151-152; 175pp; English.  
 XX  
 CC The invention relates to cyclic peptides (A) with a constrained helical  
 CC conformation, derived from gp41 (glycoprotein 41), a viral envelope  
 CC protein of human immunodeficiency virus (HIV). The cyclic  
 CC peptides have formulas given in the specification part of which are  
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
 CC C, D, E or O. The peptides are used to cause induction of a specific  
 CC immune response, resulting in antibodies that prevent virus-induced  
 CC membrane fusion. The peptides are used to treat subjects with, or at risk  
 CC of, HIV infection, either as antiretroviral/anti-infection agents or,  
 CC preferably where associated with a carrier, as an immunogen (including as  
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
 CC cases of health care accidents. The peptides can be based on specific HIV  
 CC strains, e.g. breakthrough isolates of HIV that have developed during  
 CC vaccine trials, so a combination of them should cover a wide range of  
 CC protection. The present sequence is gp41 protein from a particular  
 CC HIV clade used to derive a consensus sequence of gp41.  
 XX  
 SQ Sequence 267 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 23; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 167 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 202  
 XX  
 ULT 9  
 AAW43068  
 ID AAW43068 standard; peptide; 854 AA.  
 XX  
 AC AAW43068;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE HIV-1 gp120 protein fragment from isolate MN.  
 XX  
 KW gp120 protein: purification; fractionation; ion exchange; chromatography;  
 KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.  
 XX  
 OS Human immunodeficiency virus type 1.  
 OS  
 PN US5696238-A.  
 XX  
 PD 09-DEC-1997.  
 XX  
 PF 11-MAY-1995; 95US-0439286.  
 XX  
 PR 20-AUG-1991; 91US-0684963.  
 PR 16-AUG-1993; 93US-0109002.  
 PR 09-MAY-1994; 94US-0240073.

PR 11-MAY-1995; 95US-0439286.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Haigwood NL, Scandella C;  
 XX  
 DR WPI: 1998-041353/04.  
 XX  
 PT Purification of HIV gp120 - using chromatographic methods  
 XX  
 PS Disclosure: Fig 2A-W; 53pp; English.  
 XX  
 CC AAW43066-W43080 are fragments of the gp120 protein from different human  
 CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used  
 CC in a novel method for purifying HIV gp120 so as to provide a purified  
 CC gp120 glycoprotein having protein/protein binding properties  
 CC substantially identical to natural viral HIV gp120. The method involves  
 CC fractionating a crude gp120 preparation containing full-length,  
 CC glycosylated gp120 using ion exchange chromatography so as to provide a  
 CC first collection of fractions. A fraction from the first collection is  
 CC selected that exhibits specific binding affinity for CD4 peptide.  
 CC thereby producing a first fractionated material. The first fractionated  
 CC material is fractionated by hydrophobic interaction chromatography so as  
 CC to provide a second collection of fractions from which a second  
 CC collection is selected that exhibits specific binding affinity for CD4  
 CC peptide. This second fraction is fractionated by size exclusion  
 CC chromatography so as to provide a third collection of fractions  
 CC exhibiting specific binding affinity for CD4 peptide, thereby providing  
 CC the purified gp120. The purified gp120 can be used for antibody  
 CC production and in vaccines.  
 XX  
 SQ Sequence 854 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 19; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 637 YTSLSLSLEKSTQOEKNEQELLELDKWSLWNMF 672  
 XX  
 RESULT 10  
 AAR14903  
 ID AAR14903 standard; Protein; 856 AA.  
 XX  
 AC AAR14903;  
 XX  
 DT 17-DEC-2001 (updated)  
 DT 05-FEB-1992 (first entry)  
 XX  
 DE HIV-1(MN) env protein.  
 XX  
 KW human immunodeficiency virus; United States; MN isolate; AIDS;  
 KW envelope protein.  
 XX  
 OS Human immunodeficiency virus-1 (MN).  
 OS  
 PN USN7599491-N.  
 XX  
 PD 15-OCT-1991.  
 XX  
 PF 17-OCT-1990; 90US-0183830.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 XX  
 PA (USSH ) NAT INST OF HEALTH.  
 XX  
 PI Reitz M;  
 PI  
 DR WPI: 1991-346752/47.  
 DR N-PSDB; AAO14751.  
 XX

PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are  
 XX useful in therapeutics, vaccines and diagnostic tests  
 PS Example 1; Fig 3; 61pp; English.  
 XX  
 CC The permuted circular unintegrated viral DNA representing the  
 CC complete HIV-1(MN) genome was cloned into the EcoRI site of lambda  
 CC gTWS.Lambda B DNA from total DNA of H9 cells producing HIV-1 (MN).  
 CC This clone was designated lambda MN-PH1; it was subcloned in M13mp18  
 CC and M13mp19 and the DNA sequence of the entire clone was obtained  
 CC the amino acid sequence of the env protein was deduced from it.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 12; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 36  
 DB 639 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 674  
 RESULT 11  
 AAR79173  
 ID AAR79173 standard; protein; 856 AA.  
 AC AAR79173;  
 XX  
 DT 09-MAR-1996 (first entry)  
 XX  
 DE HIV virus-1 isolate MN gp120 sequence.  
 XX  
 KM HIV virus-1; gp120; therapeutic; immunogen; diagnostic; peptomer.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT Protein 1..856  
 FT Misc-difference 301..400 /note= "HIV-1 isolate MN gp120 sequence"  
 FT Region 401..800 /note= "V3 loop"  
 FT Region 419..436 /note= "CD4 binding region"  
 FT Region 801..856 /note= "CD4 binding region consensus sequence"  
 FT Region 824..830 /note= "MHC II homology region"  
 FT Region /note= "MHC II homology region consensus sequence"  
 XX  
 FN WO9520162-A1.  
 XX  
 PD 27-JUL-1995.  
 XX  
 PF 19-JAN-1995; 95WO-US00760.  
 XX  
 PR 19-JAN-1994; 94US-0184330.  
 XX  
 PA (USSH ) US SEC DEPT HEALTH.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Harris-Kelson TA, Robert-Guioff M, Robey FA;  
 XX  
 DR WPI; 1995-269543/35.  
 XX  
 PT Peptide analogues useful as therapeutic agents, immunogens, or for  
 PT diagnosis of disease - maintain conformation of native protein,  
 PT e.g. HIV gp120 peptide.

XX  
 PS Disclosure; Fig 1; 55pp; English.  
 XX  
 CC Peptide analogues of HIV virus antigen contain a plurality of  
 CC peptide monomers, each comprising the gp120 CD4 binding region  
 CC consensus sequence (amino acids 419-436) (see AAR79173). The  
 CC synthetic peptomers are useful as therapeutic agents, immunogens  
 CC in vaccine compositions or for the diagnosis of disease.  
 CC Since the analogues maintain the conformation of the native proteins  
 CC from which they are derived (the consensus sequence), they are  
 CC useful against infection by various HIV-1 and HIV-2 isolates (see  
 CC AAR79174-84).  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 16; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 36  
 DB 639 YTSLYSLEKSOTOEKNQELLEDKWSLWMPF 674  
 RESULT 12  
 AAW1579  
 ID AAW1579 standard; Protein; 856 AA.  
 AC AAW1579;  
 XX  
 DT 25-MAR-1997 (first entry)  
 XX  
 DE Human Immunodeficiency Virus-1 strain MN-PH1 envelope protein.  
 XX  
 KM Acquired immune deficiency syndrome; AIDS; envelope protein;  
 KM env gene; vaccine.  
 XX  
 OS Human immunodeficiency virus type 1 (strain MN-PH1).  
 XX  
 PN US5576000-A.  
 XX  
 PD 19-NOV-1996.  
 XX  
 PF 17-OCT-1990; 90US-0599491.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 PR 25-FEB-1993; 93US-0022835.  
 PR 15-FEB-1995; 95US-0388809.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX  
 DR WPI: 1997-011206/01.  
 DR N-PSDB: AAT58549.  
 XX  
 PD New isolated envelope protein of HIV-1 strain BA-L and recombinant  
 PT equivalents - useful as immunogens for vaccines and antibody prodn.,  
 PT typical of US clinical isolates  
 XX  
 PS Example; Fig 3; 86pp; English.  
 XX  
 CC The permuted circular unintegrated viral DNA representing the  
 CC complete HIV-1(MN) genome was cloned into the EcoRI site of lambda  
 CC gTWS.Lambda B DNA from total DNA of H9 cells producing HIV-1(MN)  
 CC isolate. The clone was designated lambda MN-PH1. The present sequence  
 CC was deduced from the env gene region of the MN-PH1 genome.  
 CC  
 SQ Sequence 856 AA:  
 XX  
 Query Match 100.0%; Score 193; DB 18; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 639 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 674

RESULT 13  
 AAM58805  
 ID AAM58805 standard; protein; 856 AA.  
 XX  
 AC AAM58805;  
 XX  
 DT 23-JUL-1998 (first entry)  
 XX  
 DE HIV-1 isolate MN envelope protein gp120.  
 XX  
 KM Envelope protein; gp120; peptomer; peptides oligomer; detection;  
 KM CD4-binding region; anti-HIV antibody; therapeutic; infection;  
 KM inhibition; T cell; immunogenic agent; antibody; vaccine; epitope.  
 XX  
 FT Human immunodeficiency virus type 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 301..335  
 FT /label= V3 loop  
 FT 401..800  
 FT /label= CD4-binding\_region  
 FT 801..855  
 FT /note= "region with MHC II homology"  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Harris-Kelson TA, Robert-Guroff M, Robey FA;  
 DR WPI; 1998-296756/26.  
 XX  
 PT HIV gp120 peptide oligomers - useful as diagnostic, immunogenic or  
 PT therapeutic agents  
 XX  
 XX Disclosure: Fig 1; 25pp; English.  
 XX  
 CC This sequence represents the Human Immunodeficiency Virus Type I (HIV-1)  
 CC isolate MN envelope protein gp120. This protein is used in a novel  
 CC method to produce and analyse peptides oligomers, "peptomers", consisting  
 CC of several peptide monomers arranged head to tail, each monomer  
 CC comprising a sequence from a CD4-binding region of HIV gp120. Such  
 CC peptides are useful as assay reagents for detecting anti-HIV antibodies  
 CC in biological samples, e.g. blood samples, or as a therapeutic agent for  
 CC inhibiting infection of T cells by HIV and as an immunogenic agent for  
 CC antibody production e.g. in vaccines. They are preferably synthetically  
 CC produced and thus are consistent in their sequence and structure. Most  
 CC HIV vaccines and detection peptides used currently rely on fragments of  
 CC inactivated live viruses and thus may not contain the correct epitopes  
 CC to elicit an immune response.  
 XX  
 SQ Sequence 856 AA:

Query Match 100.0%; Score 193; DB 19; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 639 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 674

DB 639 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 674

RESULT 14  
 AAM88111  
 ID AAM88111 standard; protein; 856 AA.  
 XX  
 AC AAM88111;  
 XX  
 DT 09-APR-1999 (first entry)  
 XX  
 DE Predicted amino acid sequence of the MN-PH1 envelope (env) protein.  
 XX  
 KM MN-PH1 clone; HIV-1; HIV-1 strain BA-L; envelope protein; vaccine;  
 KM immunotherapy; HIV infection; immunogen; HIV-1 diagnosis; env; ds.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN US5869313-A.  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 14-MAY-1996; 96US-0647714.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 PR 25-FEB-1993; 93US-0022835.  
 PR 15-FEB-1995; 95US-0388809.  
 PR 14-MAY-1996; 96US-0647714.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX  
 DR WPI; 1999-152779/13.  
 XX  
 PT DNA encoding env protein of the human immune deficiency virus  
 PT isolate BA-L - useful for producing protein for use in vaccines, as  
 PT assay reagent and to generate antibodies  
 XX  
 PS Example 1; Fig 3A-C; 87pp; English.  
 XX  
 CC The present sequence represents the predicted amino acid sequence  
 CC of the MN-PH1 clone envelope (env) protein. MN-PH1 is a Human  
 CC immunodeficiency virus type 1 (HIV-1) clone. The specification  
 CC also describes the env and rev coding sequences of the HIV-1  
 CC strain BA-L (ATCC 40890). BA-L is more typical of United States  
 CC isolates of HIV-1 than previously known strains. Recombinant,  
 CC complete env protein of the BA-L strain is used as a vaccine  
 CC component and for immunotherapy of existing HIV infections, to  
 CC detect HIV-specific antibodies, e.g. in donated blood, and as  
 CC an immunogen to raise specific antibodies, for HIV-1 diagnosis.  
 XX  
 SQ Sequence 856 AA:

Query Match 100.0%; Score 193; DB 20; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 36  
 DB 639 YTSLYSLEKSTQOEKNEQELLELDKWSLWNMF 674

RESULT 15  
 AAR94622  
 ID AAR94622 standard; protein; 1188 AA.  
 XX  
 AC AAR94622;  
 XX  
 DT 29-AUG-1996 (first entry)  
 XX  
 DE HIV-1 gp160-NY5 p55 protein fusion.

[illegible]

Search completed: May 16, 2003, 11:12:02  
Job time : 32.4578 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193  
Sequence: 1 YTSLYSLLEKSGTQOEKNEDELLELDKWSLNMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

PIR73: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	100.0	859	1 VCLJMN	env polypotein pr
2	179	92.7	358	2 S21998	envelope protein g
3	179	92.7	443	2 C41621	env polypotein p
4	179	92.7	856	1 VCLJ3W	env polypotein pr
5	179	92.7	861	1 VCLJ3C	env polypotein pr
6	178	92.2	853	2 S54384	envelope polypote
7	178	92.2	855	1 VCLJZR	env polypotein pr
8	177	91.7	851	2 S33985	env polypotein -
9	177	91.7	854	2 S13288	env protein - huma
10	177	91.7	856	1 VCLJH3	env polypotein pr
11	177	91.7	861	1 VCLJLV	env polypotein pr
12	176	91.2	357	2 S21994	envelope protein g
13	175	90.7	357	2 S21996	envelope protein g
14	173	89.6	846	1 VCLJMD	env polypotein pr
15	173	89.6	855	1 VCLJ42	env polypotein pr
16	172	89.1	847	2 T09448	envelope glycoprot
17	172	89.1	847	2 S13289	env protein - huma
18	172	89.1	852	1 VCLJBR	env polypotein -
19	171	88.6	445	2 A41621	env polypotein M
20	170	88.1	357	2 S21992	envelope protein g
21	170	88.1	358	2 S22002	envelope protein g
22	170	88.1	358	2 S22000	envelope protein g
23	170	88.1	358	2 S70417	envelope protein g
24	170	88.1	352	2 T12016	envelope glycoprot
25	169	87.6	357	2 S22004	envelope protein g
26	169	87.6	843	1 H44001	env polypotein pr
27	168	87.0	856	1 T01672	env polypotein pr
28	168	87.0	859	1 VCLJVL	envelope polypote
29	166	86.0	357	2 S22006	envelope protein g

30	161	83.4	729	1 VCLJRX	env polypotein pr
31	161	83.4	861	1 VCLJRB	env polypotein pr
32	159	82.4	136	2 J00266	envelope polypote
33	159	82.4	136	2 J00954	envelope polypote
34	157	81.3	454	2 B41621	env polypotein D
35	156	80.8	868	1 VCLJH4	env polypotein -
36	153	79.3	854	1 VCLJST	env polypotein pr
37	153	79.3	856	1 A44963	env polypotein pr
38	143	74.1	357	2 S21990	envelope protein g
39	134	69.4	877	2 S49197	envelope protein p
40	129	66.8	863	2 A53034	gag polypotein -
41	86	44.6	366	2 B41365	env polypotein -
42	86	44.6	881	1 VCLJG3	env polypotein -
43	86	44.6	881	2 S03068	env protein - huma
44	86	44.6	889	1 VCLJG5	env polypotein -
45	85	44.0	151	2 S30448	env protein - huma

#### ALIGNMENTS

##### RESULT 1

VCLJMN

env polypotein precursor - human immunodeficiency virus type 1 (isolate MN)  
N:Alternate names: coat polypotein

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997

C:Accession: A28922

R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Vitrology 164, 531-536, 1988

A:Title: Envelope sequences of two new United States HIV-1 isolates.

A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: A28922

A:Molecule type: DNA

A:Residues: 1-859 <GUR>

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypotein

C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane pr

F:1-29/Domain: signal sequence #status predicted <Strg>

F:30-859/Product: env polypotein #status predicted <EPP>

F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,

Query Match 100.0%; Score 193; DB 1; Length 859;

Best Local Similarity 100.0%; Pred. No. 1.1e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLLEKSGTQOEKNEDELLELDKWSLNMWF 36

DB 642 YTSLYSLLEKSGTQOEKNEDELLELDKWSLNMWF 677

##### RESULT 2

S21998

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 28

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S21998; S70425

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21998

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70425

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222,'X',224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.7%; Score 179; DB 2; Length 358;  
 Best Local Similarity 88.9%; Pred. No. 2,2e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWNNF 36  
 |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|  
 Db 140 YTSLLYTLIESQNOEQKNEQELLELDKWSLWNNF 175

## RESULT 3

env polyprotein p - human immunodeficiency virus type 1 (fragment)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)  
 C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
 C:Accession: C41621  
 R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
 A:Reference number: A41621; MUID:92107924; PMID:1763038  
 A:Accession: C41621  
 A:Molecule type: DNA  
 A:Residues: 1-443 <BUR>  
 A:Cross-references: GB:M77230; NID:9328631; PIDN:AB03792.1; PID:9555015  
 A:Note: this virus was isolated from the mother's sexual partner

C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro  
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <TMN>  
 F:424-443/Product: transmembrane #status predicted <TMN>  
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ce

Query Match 92.7%; Score 179; DB 2; Length 443;  
 Best Local Similarity 88.9%; Pred. No. 2.8e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWNNF 36  
 |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|  
 378 YTSLLYTLIESQNOEQKNEQELLELDKWSLWNNF 413

## RESULT 4

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
 N:Contains: coat protein gp120; coat protein gp41  
 C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
 C:Accession: A24774  
 R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STRA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:91906382

C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,  
 Query Match 92.7%; Score 179; DB 1; Length 856;  
 Best Local Similarity 88.9%; Pred. No. 5.9e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWNNF 36  
 |||||:|:|:| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 638 YTSLLYTLIESQNOEQKNEQELLELDKWSLWNNF 673

## RESULT 5

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Gurgoo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
 Virolgy 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091

A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-861/Product: env polyprotein #status predicted <EBP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

Query Match 92.7%; Score 179; DB 1; Length 861;  
 Best Local Similarity 88.9%; Pred. No. 5.9e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWNNF 36  
 |||||:|:~|| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 643 YTSLLYTLIESQNOEQKNEQELLELDKWSLWNNF 678

## RESULT 6

envelope polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 C:Accession: S54384  
 R:Theodore, T.; Buckler-White, A.J.  
 submitted to the EMBL Data Library, July 1989  
 A:Reference number: S54377  
 A:Accession: S54384  
 A:Status: preliminary  
 A:Molecule type: genomic RNA  
 A:Residues: 1-853 <THE>  
 A:Cross-references: EMBL:M22639; NID:9329377; PIDN:AAA45370.1; PID:9329385  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: polyprotein

Query Match 92.2%; Score 178; DB 2; Length 853;  
 Best Local Similarity 88.9%; Pred. No. 7.8e-14;  
 Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 YTSLLYSLEKSQTQOEKNEQELLELDKWSLWNNF 36  
 |||||:|:~|| |||||:|:~|| |||||:|:~|| |||||:|:~||  
 Db 635 YTGLLYTLIESQNOEQKNEQELLELDKWSLWNNF 670

## RESULT 7

env polyprotein precursor - human immunodeficiency virus Zr-6  
 N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus Zr-6  
C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: D26192  
R:Strinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot  
A:Reference number: A26192; MUID:87248097; PMID:3036660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRI>  
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA5380.1; PID:g329403  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot  
F:1-19/Domain: signal sequence #status predicted <STIG>  
F:20-855/Product: env polypotein #status predicted <MNT>  
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>  
F:87,129,140,145,154,158,186,189,199,226,243,264,278,291,297,333,340,355,386,392,398,404  
Query Match 92.2%; Score 178; DB 1; Length 855;  
Best Local Similarity 88.9%; Pred. No. 7.8e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 36  
DB 637 YTGILYRIEESQTOQEKNEQELLEDKWASLMNMF 672

RESULT 8  
S33985  
env polypotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAN>  
A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.7%; Score 177; DB 2; Length 851;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 36  
DB 633 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 668

RESULT 9  
S33288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S33288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S33288; MUID:91043044; PMID:2172833  
A:Accession: S33288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.7%; Score 177; DB 2; Length 854;  
Best Local Similarity 88.9%; Pred. No. 1e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 36  
DB 636 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 671

RESULT 10  
VCLJH3  
env polypotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; D  
Nberger, J.A.; Pappas, T.S.; Chryabeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A03353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <STIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 91.7%; Score 177; DB 1; Length 856;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 36  
DB 638 YTSLSLEKSOQOQEKNEQELLEDKWASLMNMF 673

RESULT 11  
VCLJH3  
env polypotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:8509333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAT>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AA59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <STIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TMM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 91.7%; Score 177; DB 1; Length 861;  
Best Local Similarity 88.9%; Pred. No. 1e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSYSLSEKSOEQEKNQELLEDKWSLWNNF 36  
 |||||:||||:|||||  
 Db 643 YTSLSHSLSESONQOEKNEQELLEDKWSLWNNF 678

## RESULT 12

S21994  
 envlope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variatey: isolate 278  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STE1>  
 A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180  
 Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebri  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:960179  
 C:Superfamily: type E retrovirus env polypotein

Query Match 91.2%; Score 176; DB 2; Length 357;  
 Best Local Similarity 86.1%; Pred. No. 5.1e-14;  
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSYSLSEKSOEQEKNQELLEDKWSLWNNF 36  
 |||||:||||:|||||  
 Db 139 YTTLLTYTLLESQNOEKNQELLEDKWSLWNNF 174

## RESULT 13

S21996  
 envlope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebri  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:91067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991  
 C:Superfamily: type E retrovirus env polypotein

Query Match 90.7%; Score 175; DB 2; Length 357;  
 Best Local Similarity 86.1%; Pred. No. 6.8e-14;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYSLSEKSOEQEKNQELLEDKWSLWNNF 36  
 |||||:||||:|||||  
 Db 139 YTTLLTYTLLESQNOEKNQELLEDKWSLWNNF 174

## RESULT 14

VCLJND  
 env polypotein precursor - human immunodeficiency virus type 1 (isolate NDK)  
 N:Alternate names: coat polypotein  
 N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999  
 C:Accession: J00066

R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,  
 Gene 81, 275-284, 1989  
 A:Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human imm  
 A:Reference number: J00065; MUID:90034200; PMID:2806917  
 A:Accession: J00066  
 A:Molecule type: DNA

A:Residues: 1-846 <SPI>  
 A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162  
 A:Note: the authors translated the codon GCG for residue 523 as Arg  
 C:Genetics:

C:Superfamily: type E retrovirus env polypotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <CP1>  
 F:502-846/Product: coat protein gp41 #status predicted <CP2>  
 F:502-520/Domain: transmembrane #status predicted <TM1>  
 F:674-692/Domain: transmembrane #status predicted <TM2>  
 F:87-129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,  
 F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

Query Match 89.6%; Score 173; DB 1; Length 846;  
 Best Local Similarity 86.1%; Pred. No. 3.2e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYSLSEKSOEQEKNQELLEDKWSLWNNF 36  
 |||||:||||:|||||  
 Db 628 YTTLLTYTLLESQNOEKNQELLEDKWSLWNNF 663

## RESULT 15

VCLJND  
 env polypotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
 N:Alternate names: coat polypotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03976  
 R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
 Science 227, 484-492, 1985  
 A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
 A:Reference number: A04003; MUID:85090453; PMID:2578227  
 A:Accession: A03976  
 A:Molecule type: DNA  
 A:Residues: 1-855 <SAN>  
 A:Cross-references: GB:K02007; NID:9328658; PIDN:AB59882.1; PID:9328666  
 C:Genetics:

Query Match 89.6%; Score 173; DB 1; Length 855;  
 Best Local Similarity 86.1%; Pred. No. 3.2e-13;  
 Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSLSYSLSEKSOEQEKNQELLEDKWSLWNNF 36  
 |||||:||||:|||||  
 Db 637 YTTLLTYTLLESQNOEKNQELLEDKWSLWNNF 672

Search completed: May 16, 2003, 11:25:07  
 Job time : 13.1446 secs



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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97140 MW; D197D80940BE732 CRC64;

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Query Match 100.0%; Score 193; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2.3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 YTSLYSLEKSOEQOENKNEQLLELDKWSLMMNF 36
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DB 639 YTSLYSLEKSOEQOENKNEQLLELDKWSLMMNF 674

```

```

RESULT 2
ENV_HV1S3 STANDARD; PRT: 852 AA.
ID ENV_HV1S3 STANDARD; PRT: 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.

```

```

Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11690;

```

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OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=90317906; PubMed=2370688;
RX York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).

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CC EMBL: M38427; AAA45067.1; -.
CC DR HIV; M38427; ENV$SEF3.
CC DR InterPro: IPR000328; ENV_GP41.
CC DR InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.

```

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DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

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Query Match 93.8%; Score 181; DB 1; Length 852;
Best Local Similarity 91.7%; Pred. No. 7e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTSLYSLEKSOEQOENKNEQLLELDKWSLMMNF 36
    |||||
DB 634 YTSLYSLEKSOEQOENKNEQLLELDKWSLMMNF 669

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```

RESULT 3
ENV_HV1E1 STANDARD; PRT: 853 AA.
ID ENV_HV1E1 STANDARD; PRT: 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.

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Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11689;

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CC SEQUENCE FROM N.A.
CC RP MEDLINE=86245056; PubMed=2424612;
CC RX Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;
CC "Genetic variability of the AIDS virus: nucleotide sequence analysis

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FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAFADA60DEBA7A08 CRC64;

Query Match
Best Local Similarity 92.7%; Score 179; DB 1; Length 856;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DE9 CRC64;

Query Match
Best Local Similarity 92.7%; Score 179; DB 1; Length 856;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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1 YTSLYISLEKSOQOEKNEDELLELDKNASLWNMF 36  
 638 YTSLYITLIEESONQOEKNEDELLELDKNASLWNMF 673

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RESULT 5
ENV_HV1W1 STANDARD; PRT; 856 AA.
ID ENV_HV1W1
AC P31872;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=31678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
RL Cell 45:637-648(1986).
CC -I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
CC PIR: A24774; VCLJ3W.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 51 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 247 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

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RESULT 6
ENV_HV122 STANDARD; PRT; 853 AA.
ID ENV_HV122
AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (22/DCD-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -----
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CC -----
CC EMBL: M22639; AAA5370.1; -.
CC HIV: M22639; ENV8226.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 31
FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.

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FT	CARBOHYD	620	620	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	632	632	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	669	669	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1 CRC64;	
Oy	1 YTSILYSLEKSQFOOEKNEQELLELDKWASIMNMF	36			
Db	633 YTSLHSLIEESQNOEKNEDELLELDKWASIMNMF	668			
RESULT 9					
ID	ENV_HVIB1	STANDARD:	PRT:	856 AA.	
AC	P03375:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
DE	ENV.				
OS	Human immunodeficiency virus type 1 (BH10 isolate) (HTLV-I).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11678;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85111123; PubMed=2578615;				
RA	Raher L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Laumenberger K., Ivanoff L., Peteway S.R. Jr., Pearson M.L., Laumenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C., Wong-Straal F.				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III."				
RL	Nature 313:277-284(1985).				
RM	[2]				
RN	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.				
RX	MEDLINE=90285159; PubMed=2355006;				
RA	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.				
RT	"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type I recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells."				
RT	J. Biol. Chem. 265:10373-10382(1990).				
CC	-----				
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CC	-----				
DR	EMBL, M15654; AAA44205.1; -				
DR	PIR: A03973; VCLJH3.				
DR	HIV: M15654; ENVSBH102.				
DR	InterPro: IPRO00328; Env.GP41.				
DR	InterPro: IPRO00777; GP120.				
DR	pfam: PF00516; GP120; 1.				
DR	pfam: PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL.	1	30		
FT	CHAIN	31	511		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	512	856		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74		
FT	DISULFID	119	205		
FT	DISULFID	126	196		

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FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97224 MW; 08F61A18931BB27 CRC64;

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Query Match 91.7%; Score 177; DB 1; Length 856;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTSLSYLSLEKSQTOQEKNEDELLELDKWSLWNF 36
Db 638 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNF 673

HIV-10
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1989 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
virus."
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RP REVISIONS.
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;

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RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
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DR EMBL; K03455; AAB50262.1; -
DR EMBL; AF038399; AAB9976.1; -
DR EMBL; AF033819; AAC82596.1; -
DR HIV; K03455; ENVSHXB2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT DISULFID 54 856 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 119 74 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 385 BY SIMILARITY.
FT DISULFID 385 448 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97212 MW; 6FA816A8F5107FED CRC64;

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Query Match 91.7%; Score 177; DB 1; Length 856;
Best Local Similarity 88.9%; Pred. No. 2.2e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTSLSYLSLEKSQTOQEKNEDELLELDKWSLWNF 36
Db 638 YTSLSHLSLEESQNOQEKNEDELLELDKWSLWNF 673

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FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	754	754	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	856 AA;	97188 MW;	337368BB84C1A9C	CRC64;
Query Match	Best Local Similarity	91.7%;	Score 177;	DB 1;	Length 856;
Matches	32; Conservative	88.9%;	Pred. No. 2.2e-14;	1; Indels	0; Gaps
Oy	1	YTSLIYSLEKSOQOQENKEOELLELDKWSIMNMF	36		
Db	638	YTSLIHSLIEESQNOQEKNEOELLELDKWSIMNMF	673		
RESULT 12					
ENV_HV1LM					
ID	ENV_HV1LM	STANDARD;	PRT;	856 AA.	
AC	070626;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	15-JUL-1999 (Rel. 36, Last annotation update)				
DE	Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=82834;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95127297; PubMed=7826699;				
RA	Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;				
RT	"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIIB).".				
RL	AIDS Res. Hum. Retroviruses 10:1143-1153(1994).				
CC	-----				
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CC	-----				
DR	EMBL: U12055; AAA76690.1; -				
DR	GLYCOSITEDB: Q70626; -				
DR	InterPro: IPR000328; Env GP41.				
DR	InterPro: IPR000772; GP120.				
DR	Pfam: PF00517; GP120; 1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
KM	SIGNAL	1	30		
FT	CHAIN	31	511		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	512	856		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74		BY SIMILARITY.
FT	DISULFID	119	205		BY SIMILARITY.
FT	DISULFID	126	196		BY SIMILARITY.
FT	DISULFID	131	157		BY SIMILARITY.
FT	DISULFID	218	247		BY SIMILARITY.
FT	DISULFID	228	239		BY SIMILARITY.
FT	DISULFID	256	331		BY SIMILARITY.
FT	DISULFID	378	445		BY SIMILARITY.
FT	DISULFID	385	418		BY SIMILARITY.
FT	CARBOHYD	88	88		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	156	156		N-LINKED (GLCNAC. . .) (POTENTIAL).



```

RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RL macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RU J. Virol. 64:4396-4398(1990)
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CC -----
CC EMBL: M65024; AAA45072.1;
DR HIV; M38428; ENVSF162.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
CC -----
CC Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
CC Signal.
FT SIGNAL. 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN..
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.
FT CARBOHYD 87 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7F22AB CRC64;
Query Match 91.2%; Score 176; DB 1; Length 847;
Best Local Similarity 86.1%; Pred. No. 2.9e-14;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

AC P19551.
DT 01-FEB-1991 (Rel. 17, Created)
DR 01-FEB-1991 (Rel. 17, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317877; PubMed=1695254;
RA Wasiaik A.;
RA Stevenson M., Haggerty S., Lamontica C., Mann A.M., Meier C.,
RT "Cloning and characterization of human immunodeficiency virus type 1
RT variants diminished in the ability to induce syncytium-independent
RT cytolysis.";
RL J. Virol. 64:3792-3803(1990).
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M33943; AAA44850.1;
DR HIV; M33943; ENVSF162.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
CC -----
CC Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
FT SIGNAL. 1 30
FT CHAIN 31 509 EXTERIOR MEMBRANE GLYCOPROTEIN..
FT CHAIN 510 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 203 BY SIMILARITY.
FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT	CARBOHYD	635	635	N-LINKED (GLCNAC. . .)	(POTENTIAL.)
FT	CARBOHYD	672	672	N-LINKED (GLCNAC. . .) <td>(POTENTIAL.)</td>	(POTENTIAL.)
FT	CARBOHYD	748	748	N-LINKED (GLCNAC. . .) <td>(POTENTIAL.)</td>	(POTENTIAL.)
FT	CARBOHYD	814	814	N-LINKED (GLCNAC. . .) <td>(POTENTIAL.)</td>	(POTENTIAL.)
SQ	SEQUENCE	853 AA:	96912 MM:	3377B933B6F22ABA	CRC64;

Query Match	90.28;	Score 174;	DB 1;	Length 853;
Post Local Similarity	86.18;	Prod No	5	30-14.

Best Local Similarity 86.1%; Pred. No. 5.2e-14;  
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 YTSLSLLEKSQTQOEKNEQELLLELDKWSLWNWF 36
          |||||:::| | | | | | | | | | | | | | | |
Db      636 YTSLSLSDIDESQNOEKNEQELLLELDKWSLWNWF 671

```

Search completed: May 16, 2003, 11:13:32  
Job time : 6.07229 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-5  
Perfect score: 193  
Sequence: 1 YTSLIYSLEKSOEQEKNEQELLEDKWASLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriophage:\*  
17: sp-archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	857	15	Q9YUL5 human immun
2	193	100.0	861	15	Q90294 human immun
3	193	100.0	861	15	Q90295 human immun
4	184	95.3	117	15	Q9YXW3 human immun
5	184	95.3	122	15	Q9YXW3 human immun
6	183	94.8	127	15	Q9YXW3 human immun
7	183	94.8	129	15	Q9YXW3 human immun
8	183	94.8	852	15	Q9YXW3 human immun
9	182	94.3	848	15	Q9YXW3 human immun
10	181	93.8	49	15	Q9YXW3 human immun
11	181	93.8	122	15	Q9YXW3 human immun
12	181	93.8	851	15	Q9YXW3 human immun
13	181	93.8	851	15	Q9YXW3 human immun
14	181	93.8	855	15	Q9YXW3 human immun
15	181	93.8	857	15	Q9YXW3 human immun
16	181	93.8	858	15	Q9YXW3 human immun

17	181	93.8	858	15	Q9YXW3 human immun
18	181	93.8	864	15	Q9YXW3 human immun
19	180	93.3	49	15	Q9YXW3 human immun
20	180	93.3	117	15	Q9YXW3 human immun
21	180	93.3	122	15	Q9YXW3 human immun
22	180	93.3	122	15	Q9YXW3 human immun
23	180	93.3	122	15	Q9YXW3 human immun
24	180	93.3	122	15	Q9YXW3 human immun
25	180	93.3	122	15	Q9YXW3 human immun
26	180	93.3	127	15	Q9YXW3 human immun
27	180	93.3	127	15	Q9YXW3 human immun
28	180	93.3	128	15	Q9YXW3 human immun
29	180	93.3	838	15	Q9YXW3 human immun
30	180	93.3	848	15	Q9YXW3 human immun
31	180	93.3	854	15	Q9YXW3 human immun
32	180	93.3	855	15	Q9YXW3 human immun
33	180	93.3	857	15	Q9YXW3 human immun
34	180	93.3	857	15	Q9YXW3 human immun
35	180	93.3	860	15	Q9YXW3 human immun
36	179	92.7	42	15	Q9YXW3 human immun
37	179	92.7	122	15	Q9YXW3 human immun
38	179	92.7	122	15	Q9YXW3 human immun
39	179	92.7	122	15	Q9YXW3 human immun
40	179	92.7	122	15	Q9YXW3 human immun
41	179	92.7	132	15	Q9YXW3 human immun
42	179	92.7	358	15	Q9YXW3 human immun
43	179	92.7	443	15	Q9YXW3 human immun
44	179	92.7	807	15	Q9YXW3 human immun
45	179	92.7	841	15	Q9YXW3 human immun

## ALIGNMENTS

## RESULT 1

Q9YUL5 PRELIMINARY: PRT; 857 AA.  
AC Q9YUL5;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NM;  
RA MEDLINE:98362112; PubMed:9696803;  
RX Park E.J., Vujoic L.K., Anand R., Theodore T.S., Quinn G.V. Jr.;  
RT "Mutations in both gp120 and gp41 are responsible for the broad  
RT neutralization resistance of variant human immunodeficiency virus type  
RT 1 MN to antibodies directed at V3 and non-V3 epitopes.";  
RL J. Virol. 72:7099-7107(1998).  
DR EMBL: AF075722; AAC31819.1;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; Gp120.  
DR Pfam: PF00516; Gp120\_1.  
KW Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 857 AA; 97095 MW; 922D362E10C60DA8 CRC64;

Query Match 100.0%; Score 193; DB 15; Length 857;

Best Local Similarity 100.0%; Pred. No. 3e-15; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSOEQEKNEQELLEDKWASLWNMF 36  
Db 639 YTSLIYSLEKSOEQEKNEQELLEDKWASLWNMF 674

RESULT 2

```

090294
ID 090294 PRELIMINARY: PRT: 861 AA.
AC 090294:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
EN Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MN;
RX MEDLINE=98362112; PubMed=9696803;
RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V., Jr.;
RT "Mutations in both gp120 and gp41 are responsible for the broad
neutalization resistance of variant human immunodeficiency virus type
1 MN to antibodies directed at V3 and non-V3 epitopes.";
RJ J. Virol. 72:7099-7107(1998).
[2]
SEQUENCE FROM N.A.
RC STRAIN=MN;
RA Park E.J., Quinnan G.V., Jr., Theodore T.S.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF075719; AAC33788.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 861 AA; 97671 MW; 8136732E44445E56 CRC64;

Query Match 100.0%; Score 193; DB 15; Length 861;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36
DB 639 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 674

RESULT 3
090295
ID 090295 PRELIMINARY: PRT: 861 AA.
AC 090295:
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
EN Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MN;
RX MEDLINE=98362112; PubMed=9696803;
RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinnan G.V., Jr.;
RT "Mutations in both gp120 and gp41 are responsible for the broad
neutalization resistance of variant human immunodeficiency virus type
1 MN to antibodies directed at V3 and non-V3 epitopes.";
RJ J. Virol. 72:7099-7107(1998).
DR EMBL: AF075720; AAC31817.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 861 AA; 97617 MW; 36593D08429DC700 CRC64;

Query Match 100.0%; Score 193; DB 15; Length 861;
Best Local Similarity 100.0%; Pred. No. 3e-15;

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Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36
DB 639 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 674

RESULT 4
09YWM3
ID 09YWM3 PRELIMINARY: PRT: 117 AA.
AC 09YWM3:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
EN Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=501.045;
RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,
RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;
RT "Serologic and Phylogenetic Characterization of HIV-1 Subtypes in
Uganda.";
RJ Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF006947; AAD01391.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14014 MW; 507434356041176E CRC64;

Query Match 95.3%; Score 184; DB 15; Length 117;
Best Local Similarity 91.7%; Pred. No. 5.1e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 36
DB 82 YTSLIYSLEKSQTQOEKNEQELLELDKNASLWNMF 117

RESULT 5
09EA81
ID 09EA81 PRELIMINARY: PRT: 122 AA.
AC 09EA81:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
EN Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McCowan J.P.,
RA Olivo N., Ramos A., Schable C., Lai R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
diversity in the United States.";
RJ J. Infect. Dis. 181:470-475(2000).
DR EMBL: AF190971; AAG02333.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
KW NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1EB85BCBD CRC64;

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[illegible]



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GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-5

Perfect score: 193

Sequence: 1 YTSLSYSLKSKQTQOEKNEQELLELDKASLMMWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2.6/ptodata/1/1aa/PCUTS.COMB.pep.\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	36	1 US-08-073-028-5	Sequence 5, Appli
2	193	100.0	36	3 US-08-486-099-5	Sequence 5, Appli
3	193	100.0	36	3 US-08-360-107A-5	Sequence 5, Appli
4	193	100.0	36	3 US-08-484-223B-5	Sequence 5, Appli
5	193	100.0	36	3 US-08-919-597-5	Sequence 5, Appli
6	193	100.0	36	3 US-08-475-668A-5	Sequence 5, Appli
7	193	100.0	36	3 US-08-485-551A-5	Sequence 5, Appli
8	193	100.0	36	3 US-08-471-913A-5	Sequence 5, Appli
9	193	100.0	36	4 US-08-554-616-5	Sequence 5, Appli
10	193	100.0	36	4 US-08-485-264A-5	Sequence 5, Appli
11	193	100.0	36	4 US-08-474-349A-5	Sequence 5, Appli
12	193	100.0	36	4 US-08-255-208A-5	Sequence 5, Appli
13	193	100.0	138	4 US-09-570-921-15	Sequence 15, Appli
14	193	100.0	267	4 US-08-965-056-15	Sequence 15, Appli
15	193	100.0	856	1 US-08-022-835-2	Sequence 2, Appli
16	193	100.0	856	1 US-08-388-809-2	Sequence 2, Appli
17	193	100.0	856	1 US-08-375-100-1	Sequence 1, Appli
18	193	100.0	856	2 US-08-647-714-2	Sequence 11, Appli
19	193	100.0	856	4 US-07-956-483-11	Sequence 2, Appli
20	193	100.0	887	4 US-08-472-240A-2	Sequence 2, Appli
21	187	96.9	36	3 US-08-484-223B-240	Sequence 240, App
22	187	96.9	36	4 US-09-082-279B-1360	Sequence 1360, Ap
23	187	96.9	160	4 US-09-315-304B-1360	Sequence 1360, Ap
24	187	96.9	160	4 US-09-433-428D-70	Sequence 70, Appli
25	187	96.9	857	1 US-08-022-835-4	Sequence 4, Appli
26	187	96.9	857	1 US-08-388-809-4	Sequence 4, Appli
27	187	96.9	857	2 US-08-647-714-4	Sequence 4, Appli

28	184	95.3	36	4 US-09-082-279B-1361	Sequence 1361, Ap
29	184	95.3	36	4 US-09-315-304B-1361	Sequence 1361, Ap
30	182	94.3	36	4 US-09-082-279B-642	Sequence 642, App
31	182	94.3	36	4 US-09-315-304B-642	Sequence 642, App
32	182	94.3	850	2 US-08-448-603A-28	Sequence 28, Appli
33	182	94.3	850	3 US-09-134-075-28	Sequence 28, Appli
34	182	94.3	850	4 US-09-492-739-28	Sequence 28, Appli
35	181	93.8	36	4 US-09-082-279B-643	Sequence 643, App
36	181	93.8	36	4 US-09-315-304B-643	Sequence 643, App
37	181	93.8	138	4 US-09-570-921-19	Sequence 19, Appli
38	181	93.8	269	4 US-08-965-056-28	Sequence 28, Appli
39	180	93.3	268	4 US-08-965-056-13	Sequence 13, Appli
40	180	93.3	855	1 US-08-022-835-6	Sequence 6, Appli
41	180	93.3	855	1 US-08-388-809-6	Sequence 6, Appli
42	180	93.3	855	2 US-08-647-714-6	Sequence 6, Appli
43	179	92.7	138	4 US-09-570-921-3	Sequence 3, Appli
44	179	92.7	138	4 US-09-570-921-12	Sequence 12, Appli
45	179	92.7	138	4 US-09-570-921-27	Sequence 27, Appli

## ALIGNMENTS

RESULT 1  
US-08-073-028-5  
; Sequence 5, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Danl P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; TELEPHONE: (212) 869-8864/9741  
; TELEFAX: (212) 869-8864/9741  
; TELE: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-5

Query Match 100.0%; Score 193; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLSYSLKSKQTQOEKNEQELLELDKASLMMWF 36  
|||||

DB 1 YTSLYSLEKSQTQOEKNEDELLEIDKWSLWMP 36

RESULT 2

US-08-486-099-5

Sequence 5, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-5

Query Match 100.0%; Score 193; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSQTQOEKNEDELLEIDKWSLWMP 36

DB 1 YTSLYSLEKSQTQOEKNEDELLEIDKWSLWMP 36

RESULT 3

US-08-360-107A-5

Sequence 5, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-5

Query Match 100.0%; Score 193; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYSLEKSQTQOEKNEDELLEIDKWSLWMP 36

DB 1 YTSLYSLEKSQTQOEKNEDELLEIDKWSLWMP 36

RESULT 4

US-08-484-223B-5

Sequence 5, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 869-9741/8864  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-484-223B-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36  
|||||  
DB 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36

RESULT 5  
US-08-919-597-5  
Sequence 5, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36  
|||||  
DB 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36

RESULT 6  
US-08-475-668A-5  
Sequence 5, Application US/08475668A  
Patent No. 606065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-5

Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36  
|||||  
DB 1 YTSLIYSLEKSOQTOEKNEDELELDKWSLWNNF 36

RESULT 7  
US-08-485-551A-5  
Sequence 5, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-5  
Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity: 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYISLLEKSOTOEKNQELLELDKWSLWNMF 36  
DB 1 YTSLYISLLEKSOTOEKNQELLELDKWSLWNMF 36  
RESULT 8  
US-08-471-913A-5  
Sequence 5, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-5  
Query Match 100.0%; Score 193; DB 3; Length 36;  
Best Local Similarity: 100.0%; Pred. No. 2.9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYISLLEKSOTOEKNQELLELDKWSLWNMF 36  
DB 1 YTSLYISLLEKSOTOEKNQELLELDKWSLWNMF 36  
RESULT 9  
US-08-554-616-5  
Sequence 5, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 10  
US-08-485-264A-5  
Sequence 5, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-485-264A-5  
Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 11  
US-08-474-349A-5  
Sequence 5, Application US/08474349A  
Patent No. 6333395  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: POSITION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
TITLE OF INVENTION: VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 517  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,349A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-024  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-474-349A-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36  
1 YTSLSLSLEKSTQTOEKNEDELLDKWASLWNF 36

RESULT 12  
US-08-255-208A-5  
Sequence 5, Application US/08255208A  
Patent No. 6440656

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteaway Jr., Stephen R.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
NUMBER OF SEQUENCES: 111  
TRANSMISSION  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/255,208A  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-010  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-255-208A-5

Query Match 100.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2,9e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 36  
1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 36

RESULT 13  
US-09-570-921-15  
Sequence 15, Application US/09570921  
Patent No. 6455265  
GENERAL INFORMATION:  
APPLICANT: SERRES, PIERRE-FRANCOIS  
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION  
FILE REFERENCE: 106213  
CURRENT APPLICATION NUMBER: US/09/570,921  
CURRENT FILING DATE: 2000-05-15  
PRIOR APPLICATION NUMBER: PCT/FR98/02447  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: FR/97/14387  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Human  
US-09-570-921-15

Query Match 100.0%; Score 193; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 1,2e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 36  
1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 134

RESULT 14  
US-08-965-056-15  
Sequence 15, Application US/08965056  
Patent No. 6271198  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
APPLICANT: J. Kevin Judice  
APPLICANT: Robert S. McDowell  
APPLICANT: J. Christopher Phelan  
APPLICANT: Melissa A. Starovasnik  
APPLICANT: James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinpatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/965,056  
FILING DATE: 05-NO. 6271198-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-965-056-15

Query Match 100.0%; Score 193; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 36  
1 YTSLLYSLEKSTQTOQEKNEQELLELDKWSLWNNF 202

RESULT 15  
US-08-022-835-2  
Sequence 2, Application US/08022835  
Patent No. 5420030  
GENERAL INFORMATION:  
APPLICANT: Reitz Jr., Marvin S.  
APPLICANT: Franchini, Genoveffa  
APPLICANT: Markham, Phillip D.  
APPLICANT: Gallo, Robert C.  
APPLICANT: Lori, Franco C.

APPLICANT: Popovic, Mikulas  
 APPLICANT: Garnter, Suzanne  
 TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
 STREET: Eleventh Floor, 1615 L. Street, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20036-5601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/022,835  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/599,491  
 FILING DATE: 17-OCT-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Scott, Watson T.  
 REGISTRATION NUMBER: 26,581  
 REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 861-3000  
 TELEFAX: (202) 822-0944  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 856 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-022-835-2

Query Match 100.0%; Score 193; DB 1; Length 856;  
 Best Local Similarity 100.0%; Pred. NO. 8.7e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLEKSTQOEKNEQELLEDKWASLWNP 36  
 DB 639 YTSLSLEKSTQOEKNEQELLEDKWASLWNP 674

Job completed: May 16, 2003, 11:22:11  
 Job time: 11.1928 secs

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-5  
Perfect score: 193  
Sequence: 1 YTSLSYSLERSQTOEKNEQELLDKRWASIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 segs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	100.0	267	10	US-09-854-816-15 Sequence 15, Appl
2	181	93.8	269	10	US-09-854-816-28 Sequence 28, Appl
3	180	93.3	268	10	US-09-854-816-13 Sequence 13, Appl
4	179	92.7	233	10	US-09-854-816-50 Sequence 50, Appl
5	179	92.7	268	10	US-09-854-816-9 Sequence 9, Appl
6	179	92.7	269	10	US-09-854-816-12 Sequence 12, Appl
7	178	92.2	269	10	US-09-854-816-46 Sequence 46, Appl
8	177	91.7	36	9	US-09-874-475-16 Sequence 16, Appl
9	177	91.7	36	9	US-10-116-797-1 Sequence 1, Appl
10	177	91.7	36	9	US-09-493-346-1 Sequence 1, Appl
11	177	91.7	36	10	US-09-796-202-10 Sequence 10, Appl
12	177	91.7	36	10	US-09-779-451-5 Sequence 5, Appl
13	177	91.7	36	10	US-09-834-628-1 Sequence 1, Appl
14	177	91.7	36	10	US-09-834-816-1 Sequence 1, Appl
15	177	91.7	36	10	US-09-854-816-108 Sequence 108, App
16	177	91.7	37	9	US-09-848-616-176 Sequence 176, App
17	177	91.7	46	10	US-09-779-451-41 Sequence 41, Appl
18	177	91.7	56	10	US-09-779-451-4 Sequence 4, Appl
19	177	91.7	177	9	US-10-040-349B-2 Sequence 2, Appl

20	177	91.7	221	9	US-10-059-271-84 Sequence 84, Appl
21	177	91.7	232	9	US-10-059-271-81 Sequence 81, Appl
22	177	91.7	254	9	US-10-059-271-82 Sequence 82, Appl
23	177	91.7	256	9	US-10-059-271-97 Sequence 97, Appl
24	177	91.7	268	10	US-09-854-816-16 Sequence 16, Appl
25	177	91.7	268	10	US-09-854-816-17 Sequence 17, Appl
26	177	91.7	268	10	US-09-854-816-18 Sequence 18, Appl
27	177	91.7	344	9	US-10-040-349B-1 Sequence 1, Appl
28	177	91.7	345	9	US-10-026-741-49 Sequence 49, Appl
29	177	91.7	345	10	US-09-779-451-8 Sequence 8, Appl
30	177	91.7	391	9	US-10-059-271-93 Sequence 93, Appl
31	177	91.7	519	10	US-09-756-551A-8 Sequence 8, Appl
32	177	91.7	853	9	US-10-003-035-33 Sequence 33, Appl
33	177	91.7	856	10	US-09-476-242-1 Sequence 1, Appl
34	177	91.7	861	9	US-10-026-741-103 Sequence 103, App
35	177	91.7	1101	9	US-10-003-035-53 Sequence 53, Appl
36	177	91.7	1186	9	US-10-003-035-55 Sequence 55, Appl
37	176	91.2	36	10	US-09-779-451-50 Sequence 50, Appl
38	176	91.2	46	10	US-09-779-451-48 Sequence 48, Appl
39	176	91.2	268	10	US-09-854-816-26 Sequence 26, Appl
40	176	91.2	268	10	US-09-854-816-40 Sequence 40, Appl
41	176	91.2	269	10	US-09-854-816-45 Sequence 45, Appl
42	176	91.2	619	10	US-09-891-609-4 Sequence 4, Appl
43	176	91.2	646	10	US-09-891-609-9 Sequence 2, Appl
44	176	91.2	847	10	US-09-476-242-2 Sequence 2, Appl
45	175	90.7	46	10	US-09-854-816-109 Sequence 109, App

## ALIGNMENTS

RESULT 1  
US-09-854-816-15  
Sequence 15, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasknik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: I DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854, 816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION NUMBER: 08/965, 056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

LENGTH: 267 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-854-816-15

Query Match 100.0%; Score 193; DB 10; Length 267;  
Best Local Similarity 100.0%; Pred. No. 6.8e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLYLSLEKSOTQOEKNEDELLELDKWSLWNMF 36  
DB 167 YTSLYLSLEKSOTQOEKNEDELLELDKWSLWNMF 202

## RESULT 2

US-09-854-816-28  
Sequence 28, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 28:

US-09-854-816-28

Query Match 93.8%; Score 181; DB 10; Length 269;

Best Local Similarity 91.7%; Pred. No. 1.9e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYLSLEKSOTQOEKNEDELLELDKWSLWNMF 36

DB 169 YTSLYLSLEKSOTQOEKNEDELLELDKWSLWNMF 204

RESULT 3

## US-09-854-816-13

Sequence 13, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-854-816-13

Query Match 93.3%; Score 180; DB 10; Length 268;

Best Local Similarity 88.9%; Pred. No. 2.5e-14;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

## RESULT 4

US-09-854-816-50

Sequence 50, Application US/09854816

Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way





Query Match 91.7%: Score 177; DB 9; Length 36;  
Best Local Similarity 88.9%: Pred. No. 6,7e-15;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36

## RESULT 11

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olsson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 91.7%: Score 177; DB 10; Length 36;  
Best Local Similarity 88.9%: Pred. No. 6,7e-15;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36

## RESULT 12

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT FILING DATE: 2001-08-17  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 91.7%: Score 177; DB 10; Length 36;  
Best Local Similarity 88.9%: Pred. No. 6,7e-15;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36

RESULT 13  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT FILING DATE: 2001-04-16  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 91.7%: Score 177; DB 10; Length 36;  
Best Local Similarity 88.9%: Pred. No. 6,7e-15;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSEKSGTOQEKNEQELLELDKWSLWNNF 36

## RESULT 14

US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: DP178  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-854-816-1

Query Match 91.7%; Score 177; DB 10; Length 36;  
 Best Local Similarity 88.9%; Pred. No. 6.7e-15;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSLEKSOEQEKNQELLDKWSLWNF 36  
 |||||:||||:|||||  
 Db 1 YTSLSLEKSOEQEKNQELLDKWSLWNF 36

LT 15

US-854-816-108  
 Sequence 108, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
 J. Kevin Judice  
 Robert S. McDowell  
 J. Christopher Phelan  
 Melissa A. Starovansnk  
 James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 Making Same

NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/854,816  
 FILING DATE: 15-May-2001  
 CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/965,056  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, Ph.D., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: P1005R2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 108:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
 US-09-854-816-108

Query Match 91.7%; Score 177; DB 10; Length 36;  
 Best Local Similarity 88.9%; Pred. No. 6.7e-15;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSLEKSOEQEKNQELLDKWSLWNF 36

Db 1 YTSLSLEKSOEQEKNQELLDKWSLWNF 36  
 |||||:||||:|||||

Search completed: May 16, 2003, 12:10:23  
 Job time : 16.759 secs

PR 07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Peteway SR, Wild CT;  
 XX WPI: 1995-036105/05.  
 DR  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11, Page 133; 182pp; English.  
 XX  
 CC AAR64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
 CC truncated at the amino terminus. DP-178 corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. The peptide derivs. were identified by a computer assisted  
 CC peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype  
 CC specific diagnostic tools.  
 XX  
 SQ Sequence 35 AA;  
 XX  
 Query Match 100.0%; Score 188; DB 16; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSLHSLIEESONQOEKNEQELLELDKWSIMNWF 35  
 Db 1 TSLHSLIEESONQOEKNEQELLELDKWSIMNWF 35  
 II  
 RESULT 2  
 AAB52687  
 ID AAB52687 standard; Peptide: 35 AA.  
 XX  
 AC AAB52687;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #65.  
 XX  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemoattractant.  
 KW  
 XX Human immunodeficiency virus type 1.  
 XX  
 PN WO200066622-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 05-MAY-2000; 2000WO-US12371.  
 XX  
 PR 05-MAY-1999; 99US-0132686.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 DR WPI: 2000-656493/63.  
 XX  
 PT Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation.  
 XX  
 PS Claim 12; Page 25; 148pp; English.  
 XX  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is

CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemoattractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 XX  
 SQ Sequence 35 AA;  
 XX  
 Query Match 100.0%; Score 188; DB 21; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSLHSLIEESONQOEKNEQELLELDKWSIMNWF 35  
 Db 1 TSLHSLIEESONQOEKNEQELLELDKWSIMNWF 35  
 II  
 RESULT 3  
 AAB14670  
 ID AAB14670 standard; peptide: 35 AA.  
 XX  
 AC AAB14670;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #64.  
 XX  
 KW HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 KW isolate LAI.  
 KW  
 XX Human immunodeficiency virus type 1.  
 XX  
 OS  
 XX WO200040616-A1.  
 XX  
 PN 13-JUL-2000.  
 XX  
 PD 10-JAN-2000; 2000WO-US00456.  
 XX  
 PF 08-JAN-1999; 99US-0115404.  
 XX  
 PR 07-JAN-2000; 2000US-0460336.  
 XX  
 PA (WILD/) WILD C T.  
 PA (WEISS/) WEISS C D.  
 XX  
 XX Wild CT, Weiss CD;  
 PI  
 DR WPI: 2000-465959/40.  
 XX  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure.  
 XX  
 PS Disclosure; Page 34; 97pp; English.  
 XX  
 CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralizing antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides

CC can be administered either singly or as a combination (particularly  
CC a combination of N-helical and C-helical peptides), and can be  
CC multimerized. For example, N- and C-helical domain peptides can be  
CC alternately linked together to form a peptide which mimics the core  
CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
CC response, with the production of antibodies against gp41 structures  
CC involved in viral entry. As these portions of gp41 are well conserved,  
CC such antibodies may be effective against a broad range of HIV strains  
CC and isolates. The peptide compositions may be administered as a  
CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
CC or inhibit the ability of HIV to infect uninfected cells. A composition  
CC comprising polyclonal or monoclonal antibodies can be administered to  
CC reduce HIV infection of uninfected cells. Antibodies raised against  
CC entry-relevant gp41 structures may also be used therapeutically and as  
CC tools to further elucidate the mechanism of HIV cell entry.

SO Sequence 35 AA:

Query Match 100.0%; Score 188; DB 21; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35  
1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

DB 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

RESULT 4  
AA89388  
ID AA89388 standard; peptide: 35 AA.  
AC AA89388;  
XX  
XX 23-MAY-2000 (first entry)  
DT  
DE Core polypeptide fragment T No. 923.  
XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
OS  
XX MO9959615-A1.  
PN  
XX 25-NOV-1999.  
PD  
XX 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
PI  
XX WPI: 2000-136792/12.  
DR  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
PT comprises enhancer sequence -  
XX  
XX  
PS Disclosure: Page 35; 14pp; English.  
XX  
XX The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,

CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AA88651-990055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.

SO Sequence 35 AA:

Query Match 100.0%; Score 188; DB 21; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35  
1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

DB 1 TSLHSLIEESQNOQEKNEQELLELDKWSLWNMF 35

RESULT 5  
ABB00634  
ID ABB00634 standard; Peptide: 35 AA.  
AC ABB00634;  
XX  
XX 03-JAN-2002 (first entry)  
DT  
DE Viral DP178/107-like region peptide T715.  
XX  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KW infection.  
XX  
XX Viridiae.  
OS  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "N-terminal is substituted by Ac"  
FT Modified-site 35  
FT /note= "C-terminal amide"  
XX  
XX WO200164013-A2.  
XX  
XX 07-SEP-2001.  
PD  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
PI  
XX WPI: 2001-514829/56.  
DR  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
XX  
PS Disclosure: Page 45; 58pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other,  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.

SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 6

ABB00796 ID ABB00796 standard; Peptide: 35 AA.

XX ABB00796;

XX 03-JAN-2002 (first entry)

XX Viral DP178/107-like region peptide T923.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 infection.

XX Virididae.

XX Key Location/Qualifiers

XX Modified-site 35 /note="C-terminal amide"

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI: 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

XX Disclosure: Page 49; 587pp; English.

CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 7

ABB02111 ID ABB02111 standard; Peptide: 35 AA.

XX ABB02111;

XX 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 638.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 infection.

XX Virididae.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US03988.

XX 29-FEB-2000; 2000US-0515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI: 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

XX Disclosure: Page 336; 587pp; English.

CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX SQ Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEQELLELDKWSLWNMF 35

RESULT 8

ABB02272 ID ABB02272 standard; Peptide: 35 AA.

XX ABB02272;

XX 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 799.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 KW infection.

XX Viridae.  
OS  
XX WO200164013-A2.  
PN  
XX 07-SEP-2001.  
PD  
XX 07-FEB-2001; 2001WO-US03988.  
PF  
XX 29-FEB-2000; 2000US-0515965.  
PR  
XX (TRIM-) TRIMERIS INC.  
PA  
XX Autczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
PI WPI; 2001-514829/56.  
DR  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX Disclosure; Page 379; 587pp; English.  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
XX Sequence 35 AA:  
SQ  
Query Match 100.0%; Score 188; DB 22; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSLIHSLEESONOEKNEOELLELDKWSLWNMF 35  
DB 1 TSLIHSLEESONOEKNEOELLELDKWSLWNMF 35  
RESULT 9  
AAU13182  
AAU13182 standard; Peptide: 35 AA.  
AC  
XX AAU13182;  
XX  
XX 21-NOV-2001 (first entry)  
DT  
XX  
XX DP178-like/DP107-like peptide T-715.  
DE  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KW antitumorogenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1 isolate LAI.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT Modified-site /note= "N-terminal is substituted by Ac"  
FT Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US35727.  
PF

XX  
XX 09-JUL-1999; 99US-0350841.  
PR  
XX (TRIM-) TRIMERIS INC.  
PA  
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
PI WPI; 2001-442157/47.  
DR  
XX  
XX Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antitumorogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex -  
XX  
XX Disclosure; Page 65; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
CC to amino acids 639-673 of the transmembrane protein gp41 from human  
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
CC also relates to a method of identifying compounds that inhibit the  
CC formation of or disrupts a DP107/DP178 complex. The method comprises  
CC detecting the formation of a DP107/DP178 complex, both in the presence  
CC or absence of a test compound, in a reaction mixture containing DP107  
CC and DP178 peptides. The method is useful for identifying compounds,  
CC including small molecule compounds, which may themselves exhibit  
CC antitumorogenic, antiviral or intracellular modulatory activity. The  
CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
CC retroviral, particularly HIV, transmission to uninfected cells. The  
CC present sequence represents one of the DP178-like/DP107-like peptides  
CC of the invention.  
XX  
XX Sequence 35 AA:  
SQ  
Query Match 100.0%; Score 188; DB 22; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSLIHSLEESONOEKNEOELLELDKWSLWNMF 35  
DB 1 TSLIHSLEESONOEKNEOELLELDKWSLWNMF 35  
RESULT 10  
AAU13342  
AAU13342 standard; Peptide: 35 AA.  
AC  
XX AAU13342;  
XX  
XX 21-NOV-2001 (first entry)  
DT  
XX  
XX DP178-like/DP107-like peptide T-923.  
DE  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KW antitumorogenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1 isolate LAI.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
FT Modified-site 35  
FT Modified-site /note= "C-terminal amide"  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US35727.  
PF  
XX  
XX 09-JUL-1999; 99US-0350841.  
PR  
XX

Query Match	Best Local Similarity	Score	DB	Length
Matches	35; Conservative	100.0%; 100.0%;	Pred. No. 2.5e-16;	Mismatches 0; Indels 0; Gaps 0;
Y	1 TSLHSLIEESQNOQEKNEQELLELDKASLWNWF 35	1 TSLHSLIEESQNOQEKNEQELLELDKASLWNWF 35		
Db	1 TSLHSLIEESQNOQEKNEQELLELDKASLWNWF 35			
RESULT 11				
AA877629				
ID	AA877629 standard; Peptide: 35 AA.			
XX	AA877629;			
XX	19-APR-2001 (first entry)			
DE	Core polypeptide T715.			
XX	Core polypeptide: enhancer: antiviral; anti-HIV;			
KW	vitucide; hepatotropic; antiinflammatory; hybrid polypeptide;			
KW	colled-coll peptide interaction; fusion-related disorder;			
KW	bacterial infection; viral infection.			
XX	Unidentified.			
OS	WO200103723-A1.			
XX	18-JAN-2001.			
PN	10-JUL-2000; 2000WO-US18772.			
PD	09-JUL-1999; 99US-0350641.			
PF	(TRIM-) TRIMERIS INC.			
XX	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;			
PI	WPI: 2001-147136/15.			
XX				
XX				
PA	(TRIM-) TRIMERIS INC.			
XX				
PI	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;			
XX	WPI: 2001-442157/47;			
DR				
XX	Identifying a compound that inhibits the formation of or disrupts a			
PT	DP107/DP178 complex, especially compounds with antifeosgenic, antiviral			
PT	or intracellular modulatory activity, by detecting the formation of a			
PT	DP107/DP178 complex -			
XX	Disclosure: Page 68; 259pp; English.			
PS				
CC	The present invention relates to peptides which exhibit anti-retroviral			
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise			
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds			
CC	to amino acids 639-673 of the transmembrane protein gp41 from human			
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide			
CC	also relates to a method of identifying compounds that inhibit the			
CC	formation of or disrupts a DP107/DP178 complex. The method comprises			
CC	detecting the formation of a DP107/DP178 complex, both in the presence			
CC	or absence of a test compound, in a reaction mixture containing DP107			
CC	and DP178 peptides. The method is useful for identifying compounds,			
CC	including small molecule compounds, which may themselves exhibit			
CC	antifeosgenic, antiviral or intracellular modulatory activity. The			
CC	DP178-like/DP107-like peptides are useful to inhibit human and non-human			
CC	retroviral, particularly HIV, transmission to uninfected cells. The			
CC	present sequence represents one of the DP178-like/DP107-like peptides			
CC	of the invention.			
SO	Sequence 35 AA:			

PT	New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide
PS	Disclosure; Page 44; 151pp; English.
XX	The present sequence is a core polypeptide which may be linked to an enhancer peptide to form a novel hybrid polypeptide. The hybrid polypeptide exhibits enhanced pharmacokinetic properties relative to those exhibited by the core polypeptide when introduced into a living system. It is used to increase the in vitro or ex vivo half-life of the core polypeptide. The hybrid and core polypeptides can be used for modulating flogogenic events and intracellular processes involving coiled-coil peptide interactions. Other uses include preventing, treating and/or diagnosing disorders involving fusion events (e.g. modulation of neurotransmitter exchange and sperm-egg fusion), intracellular processes involving coiled-coil peptides (e.g. bacterial infections) and viral infections that involve cell-cell and/or virus-cell fusion (e.g. viral infections caused by human immunodeficiency virus, respiratory syncytial virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and polio virus).
CC	The enhancer peptide sequence increases the half-life and reduces the clearance rate of therapeutic peptides, which increases their efficacy and minimises the incidence and severity of adverse side effects.
CC	In addition, this increases the sensitivity of the diagnostic procedure in which they are used.
CC	
CC	
SQ	Sequence    35 AA:
	Query Match                  100.0%; Score 188; DB 22; Length 35;
	Best Local Similarity        100.0%; Pred. No. 2.5e-16;
	Matches     35; Conservative    0; Mismatches    0; Indels      0; Gaps        0.
Oy	1 TSLHSLIEESONQOEKNQELLELDKNASLNNWF 35       1 TSLHSLIEESONQOEKNQELLELDKNASLNNWF 35
Dd	
	RESULT 12
AAB77789	
ID	AAB77789 standard; Peptide: 35 AA.
XX	
AC	AAB77789;
XX	
DT	19-APR-2001 (first entry)
XX	
DE	Core polypeptide T923.
XX	
KW	Core polypeptide: enhancer; antiviral; anti-HIV; vifucide; hepatotropic; antiinflammatory; hybrid polypeptide: coiled-coil peptide interaction; fusion-related disorder; bacterial infection; viral infection.
KW	
XX	Unidentified.
OS	
XX	WO200103723-A1.
PN	
PD	18-JAN-2001.
XX	
Pf	10-JUL-2000; 2000WO-US18772.
XX	
PR	09-JUL-1999; 99US-0350641.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
P1	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
DR	WPI; 2001-1A7136/15.
XX	
PT	New hybrid polypeptide, useful for preventing, treating and diagnosing e.g. viral infections, comprises an enhancer peptide linked to a core polypeptide -
PT	
XX	

PS Disclosure: Page 48; 151pp; English.  
 XX  
 CC The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC cell-cell peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency B virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.

XX Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEELLELDKWSLWNMF 35

RESULT 13  
 AAB54934

ID AAB54934 standard; Peptide; 35 AA.

XX AAB54934;

DT 05-MAR-2001 (first entry)

DE Anti-HIV peptide DP178 amino truncation peptide #32.

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;

KW antifusogenic; mobile blood component; measles virus; MeV; SIV;

KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX Human immunodeficiency virus type 1.

XX WO200069902-A1.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13651.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX WPI; 2001-007496/01.

XX A modified peptide and a reactive group which is reactive with amino  
 XX groups, hydroxyl groups, or thiol groups on blood components to form  
 XX stable covalent bonds useful for treatment of viral infections, e.g.  
 XX human immunodeficiency virus

XX Disclosure: Page 135; 211pp; English.

CC The present invention describes a modified anti-viral peptide (I)  
 CC comprising a peptide that exhibits anti-viral activity and a reactive  
 CC group which is reactive with amino groups, hydroxyl groups, or thiol  
 CC groups on blood components to form stable covalent bonds. (I) has  
 CC anti-viral and anti-fusogenic activities. (I) inhibits viral infection  
 CC of cells by inhibiting cell-cell fusion or free virus infection or to  
 CC reduce the level of membrane fusion events between two or more entities,  
 CC e.g., virus-cell or cell-cell, relative to the level of membrane fusion  
 CC that occurs in the absence of the peptide. (I) is useful in the  
 CC treatment of patients who are suffering from viral infection, e.g. HIV,  
 CC RSV, HPIV, MeV, and SIV. (I) may be administered prophylactically to  
 CC previously uninfected individuals. This is useful in cases where an  
 CC individual has been subjected to a high risk of exposure to a virus.  
 CC By bonding of long-lived components of the blood, such as immunoglobulin,  
 CC serum albumin, red blood cells and platelets the activity is extended  
 CC for days to weeks. This is due to improved stability in vivo and a  
 CC reduced susceptibility to peptidase or protease degradation. This  
 CC minimises the need for more frequent, or even continual, administration  
 CC of the peptides. AAB54784 to AAB54784 to AAB54784 represent peptides used in the  
 CC exemplification of the present invention.

XX Sequence 35 AA:

Query Match 100.0%; Score 188; DB 22; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLHSLIEESONQOEKNEELLELDKWSLWNMF 35  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 TSLHSLIEESONQOEKNEELLELDKWSLWNMF 35

RESULT 14  
 AAR64364

ID AAR64364 standard; Peptide; 36 AA.

XX AAR64364;

DT 24-AUG-1995 (first entry)

DE DP-178 derived from HIV-1 isolate LAI has antiviral activity.

XX antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;

KW human immunodeficiency virus; transmembrane protein; gp41;

KW alpha helix; leucine zipper; DP-185.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "optionally has an amino, acetyl,  
 9-fluorenylmethoxy-carbonyl, hydrophobic or

FT Modified-site 38  
 FT /note= "optionally has a carboxyl, amido, hydrophobic  
 or macromolecular carrier gp. attached"

XX WO9428920-A.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US05739.

XX 07-JUN-1993; 93US-0073028.

XX (UYDU-) UNIV DUKE.

XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;

XX Peteway SR, Wild CT;

XX WPI; 1995-036105/05.

XX Computer search generated synthetic peptides - are inhibitors of

PT HIV transmission  
 XX  
 PS Claim 11, page 132, 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.  
 CC  
 SO Sequence 36 AA:  
 Query Match 100.0%; Score 188; DB 16; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNP 35  
 ||||||||||||||||||||||||||||  
 2 TSLHSLIEESQNOEKNEQELLELDKWSLWNP 36  
 Db  
 RESULT 15  
 AAR98398  
 ID AAR98398 standard; peptide: 36 AA.  
 AC AAR98398;  
 DT 17-FEB-1997 (first entry)  
 DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
 XX  
 KW Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KW ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KW Influenza virus; hepatitis B virus.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PM W09619495-A1.  
 PD 27-JUN-1996.  
 XX  
 PF 20-DEC-1995; 95WO-US16733.  
 XX  
 06-JUN-1995; 95US-0470896.  
 20-DEC-1994; 94US-0360107.  
 XX  
 (TRIM-) TRIMERIS INC.  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Petteway SR, Wild CT;  
 DR WPI; 1996-309517/31.  
 XX  
 PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure; Fig 1; 471pp; English.  
 CC  
 CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 CC  
 XX

SO Sequence 36 AA:  
 Query Match 100.0%; Score 188; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 0Y 1 TSLHSLIEESQNOEKNEQELLELDKWSLWNP 35  
 ||||||||||||||||||||||||||||  
 Db 2 TSLHSLIEESQNOEKNEQELLELDKWSLWNP 36  
 Search completed: May 16, 2003, 11:12:03  
 Job time : 32.5562 secs

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.8072 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-117

Perfect score: 188  
Sequence: 1 TSLIHSILIESQNOQEKNEOELLELDKWSLWMP 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	100.0	851	2 S33985	env polyprotein -
2	188	100.0	854	2 S13288	env polyprotein - huma
3	188	100.0	856	1 VCLJH3	env polyprotein pr
4	188	100.0	861	1 VCLJLV	env polyprotein pr
5	179	95.2	443	2 C41621	env polyprotein p
6	179	95.2	856	1 VCLJVL	env polyprotein pr
7	179	95.2	856	1 VCLJVC	env polyprotein pr
8	179	95.2	861	1 VCLJSC	env polyprotein pr
9	176	93.6	357	2 S21994	env polyprotein pr
10	176	93.6	358	2 S21998	env polyprotein g
11	175	93.1	357	2 S21996	env polyprotein g
12	172	91.5	847	2 T09448	env polyprotein g
13	172	91.5	847	2 S13289	env polyprotein g
14	171	91.0	445	2 A41621	env polyprotein M
15	170	90.4	358	2 S22002	env polyprotein g
16	170	90.4	358	2 S22000	env polyprotein g
17	170	90.4	358	2 S70417	env polyprotein g
18	170	90.4	852	2 T12016	env polyprotein g
19	169	89.9	357	2 S22004	env polyprotein pr
20	169	89.9	357	2 S22004	env polyprotein pr
21	169	89.9	855	1 VCLJAZ	env polyprotein g
22	167	88.8	853	2 S54384	env polyprotein pr
23	167	88.8	855	1 VCLJZR	env polyprotein pr
24	166	88.3	357	2 S22006	env polyprotein pr
25	166	88.3	843	1 H44001	env polyprotein pr
26	165	87.8	846	1 VCLJND	env polyprotein pr
27	163	86.7	357	2 S21992	env polyprotein g
28	163	86.7	852	1 VCLJBR	env polyprotein -
29	161	85.6	729	1 VCLJIX	env polyprotein pr

30	161	85.6	861	1 VCLJKB	env polyprotein pr
31	160	85.1	859	2 T01672	env polyprotein pr
32	157	83.5	454	2 B41621	env polyprotein D
33	156	83.0	868	1 VCLJH4	env polyprotein -
34	153	81.4	136	2 JU0266	env polyprotein pr
35	153	81.4	136	2 JU0266	env polyprotein pr
36	144	76.6	854	1 VCLJST	env polyprotein pr
37	142	75.5	357	2 S21990	env polyprotein pr
38	140	74.5	357	2 S21990	env polyprotein pr
39	136	72.3	877	2 S49197	env polyprotein p
40	119	63.3	863	2 A53034	env polyprotein -
41	86	45.7	881	1 VCLJG3	env polyprotein -
42	86	45.7	881	1 S03068	env polyprotein -
43	86	45.7	889	1 VCLJG5	env polyprotein -
44	85	45.2	151	2 S30448	env polyprotein -
45	85	45.2	151	2 S30452	env polyprotein -

## ALIGNMENTS

```

RESULT 1
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1.
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 100.0%; Score 188; DB 2; Length 851;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSILIESQNOQEKNEOELLELDKWSLWMP 35
Db 634 TSLIHSILIESQNOQEKNEOELLELDKWSLWMP 668

RESULT 2
S13288
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Narmaze, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack,
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
C:Superfamily: type E retrovirus env polyprotein

Query Match
Best Local Similarity 100.0%; Score 188; DB 2; Length 854;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIHSILIESQNOQEKNEOELLELDKWSLWMP 35
Db 637 TSLIHSILIESQNOQEKNEOELLELDKWSLWMP 671

RESULT 3
VCLJH3

```

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Butler, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; M01D:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; N1D:g326383; PIDN:AAAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:12-856/Product: transmembrane glycoprotein #status predicted <TM>
F:188,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic
Query Match 100.0%; Score 188; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 35
Db 639 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 673

RESULT 4
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; M01D:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: GB:K02013; N1D:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,161,165,191,202,230,246,267,281,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predic
Query Match 100.0%; Score 188; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 35
Db 644 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 678

RESULT 5
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
```

```
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; M01D:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; N1D:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:1-52-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 95.2%; Score 179; DB 2; Length 443;
Best Local Similarity 94.3%; Pred. No. 7e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 35
Db 379 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 413

RESULT 6
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Wensing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; M01D:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; N1D:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,622,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre
Query Match 95.2%; Score 179; DB 1; Length 856;
Best Local Similarity 97.1%; Pred. No. 1.5e-13;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 34
Db 639 TSLIHSLSIESQNOQEKNEDELLELDKWSLWMMF 672

RESULT 7
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
```

C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1  
A:Reference number: A24774; M0ID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 95.2%; Score 179; DB 1; Length 856;  
Best Local Similarity 94.3%; Pred. No. 1.5e-13;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONOQOEKNEDELLELDKWSLWMP 35  
DB 639 TSLIYNLIESONQOEKNEDELLELDKWSLWMP 673

RESULT 8  
VC1JSC  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gargio, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Ska  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; M0ID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote  
F:1-29/Domain: signal sequence #status predicted <Sig>  
F:30-861/Product: env polypeptide #status predicted <GP>  
F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.2%; Score 179; DB 1; Length 861;  
Best Local Similarity 94.3%; Pred. No. 1.5e-13;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONOQOEKNEDELLELDKWSLWMP 35  
DB 644 TSLIYNLIESONQOEKNEDELLELDKWSLWMP 678

RESULT 9  
S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 278  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21994; S70421  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
A:Reference number: S21994  
A:Accession: S21994  
A:Molecule type: DNA  
A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; M0ID:92144209; PMID:1736940  
A:Accession: S70421  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140; 'X', 142-312; 'X', 314-357 <STE2>  
A:Cross-references: EMBL:X61355; NID:g60179  
C:Superfamily: type E retrovirus env polypeptide

Query Match 93.6%; Score 176; DB 2; Length 357;  
Best Local Similarity 91.4%; Pred. No. 1.3e-13;  
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONOQOEKNEDELLELDKWSLWMP 35  
DB 140 TSLIYNLIESONQOEKNEDELLELDKWSLWMP 174

RESULT 10  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 28  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998; S70425  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
A:Reference number: S21990  
A:Accession: S21998  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; M0ID:92144209; PMID:1736940  
A:Accession: S70425  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-222; 'X', 224-358 <STE2>  
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
C:Superfamily: type E retrovirus env polypeptide

Query Match 93.6%; Score 176; DB 2; Length 358;  
Best Local Similarity 91.4%; Pred. No. 1.3e-13;  
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLIHSLESONOQOEKNEDELLELDKWSLWMP 35  
DB 141 TSLIYNLIESONQOEKNEDELLELDKWSLWMP 175

RESULT 11  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; M0ID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
A:Experimental source: patient 27L  
A:Note: submitted to the EMBL Data Library, July 1991



GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 5.90361 seconds  
(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-117  
Perfect score: 188  
Sequence: 1 TSLHSLIEBSONOQEKNEQELLEDKWSLWNF 35

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	100.0	851	ENV_HV1B8	P04582 human immun
2	188	100.0	856	ENV_HV1B1	P03375 human immun
3	188	100.0	856	ENV_HV1B2	P04578 human immun
4	188	100.0	856	ENV_HV1B3	P04624 human immun
5	188	100.0	856	ENV_HV1B4	P070626 human immun
6	188	100.0	856	ENV_HV1B5	P03377 human immun
7	185	98.4	853	ENV_HV1B6	P03551 human immun
8	179	95.2	856	ENV_HV1B7	P03376 human immun
9	179	95.2	856	ENV_HV1B8	P03878 human immun
10	179	95.2	856	ENV_HV1B9	P31872 human immun
11	177	94.1	852	ENV_HV1B10	P19549 human immun
12	176	93.6	847	ENV_HV1B11	P05880 human immun
13	173	92.0	847	ENV_HV1B12	P05880 human immun
14	172	91.5	867	ENV_HV1B13	P12489 human immun
15	170	90.4	856	ENV_HV1B14	P05877 human immun
16	169	89.9	855	ENV_HV1B15	P05877 human immun
17	168	89.4	853	ENV_HV1B16	P04581 human immun
18	168	89.4	865	ENV_HV1B17	P04579 human immun
19	167	88.8	853	ENV_HV1B18	P12487 human immun
20	167	88.8	855	ENV_HV1B19	P04580 human immun
21	166	88.3	843	ENV_HV1B20	P35961 human immun
22	165	87.8	846	ENV_HV1B21	P18799 human immun
23	165	87.8	855	ENV_HV1B22	P18799 human immun
24	163	86.7	852	ENV_HV1B23	P12488 human immun
25	162	86.2	848	ENV_HV1B24	P20871 human immun
26	161	85.6	861	ENV_HV1B25	P31819 human immun
27	160	85.1	859	ENV_HV1B26	P04583 human immun
28	156	83.0	868	ENV_HV1B27	P05879 human immun
29	155	82.4	863	ENV_HV1B28	P05881 human immun
30	144	76.6	854	ENV_HV1B29	P12881 chimpanzee
31	142	75.9	856	ENV_HV1B30	P05881 human immun
32	90	47.9	854	ENV_HV1B31	O02837 simian immun
33	86	45.7	881	ENV_HV1B32	P05884 simian immun

34	86	45.7	882	1	ENV_HV1B33	P05885 simian immun
35	85	45.2	885	1	ENV_HV1B34	P12492 simian immun
36	84	44.7	859	1	ENV_HV1B35	P15831 human immun
37	84	44.7	860	1	ENV_HV1B36	P18094 human immun
38	82	43.6	880	1	ENV_HV1B37	P11267 human immun
39	80	42.6	859	1	ENV_HV1B38	P24105 human immun
40	80	42.6	889	1	ENV_HV1B39	P19503 simian immun
41	77	41.0	846	1	ENV_HV1B40	P12449 human immun
42	77	41.0	851	1	ENV_HV1B41	P17755 human immun
43	77	41.0	851	1	ENV_HV1B42	P18040 human immun
44	77	41.0	858	1	ENV_HV1B43	P04577 human immun
45	77	41.0	859	1	ENV_HV1B44	P20872 human immun

## ALIGNMENTS

RESULT 1	ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582:				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	13-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]				
GN	ENV.				
OC	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OS	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615;				
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumanster K., Ivanoff L., Petteney S.R., Pearson W.L., Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III."				
RL	Nature 313:277-284(1985).				
CC	-----				
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CC	-----				
CC	EMBL: K02011; AAA4461.1; -				
DR	HIV: K02011; ENV5B8.				
DR	GlycositeDB: P04582; -				
DR	InterPro: IPR000328; ENV_GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120.1.				
DR	Pfam: PF00517; GP41.1.				
KW	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	506		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851		TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74		BY SIMILARITY.
FT	DISULFID	119	205		BY SIMILARITY.
FT	DISULFID	126	196		BY SIMILARITY.
FT	DISULFID	131	157		BY SIMILARITY.
FT	DISULFID	218	247		BY SIMILARITY.
FT	DISULFID	228	239		BY SIMILARITY.
FT	DISULFID	296	331		BY SIMILARITY.
FT	DISULFID	378	440		BY SIMILARITY.
FT	DISULFID	385	413		BY SIMILARITY.
FT	CARBOHYD	88	88		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141		N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

```

```

Query Match 100.0%; Score 188; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1,9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 TSLHSLIEESQOEKNEOELLELDKNASLWNMF 35
    |||||||
DB 634 TSLHSLIEESQOEKNEOELLELDKNASLWNMF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_TaxID=11678;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.,
RA Josephs S.F., Doran E.R., Ratafski J.A., Whitehorn E.A.,
RA Baumanster K., Ivanoff L., Petteney S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RA Nature 313:277-284(1985).

```

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RL [2]
RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382(1990).

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DR EMBL; M15654; AAA44205.1;
DR PIR; A03973; VCLJH3.
DR HIV; M15654; ENVBH102.
DR InterPro; IPR000328; ENV GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
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FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

```

```

Query Match 100.0%; Score 188; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1,9e-15;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 TSLHSLIEESQOEKNEOELLELDKNASLWNMF 35
    |||||||
DB 639 TSLHSLIEESQOEKNEOELLELDKNASLWNMF 673

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RESULT 3
ENV_HV1B2 STANDARD; PRT; 856 AA.
AC P04578; O09779;

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

```

```

Query Match Best Local Similarity 100.0%; Score 188; DB 1; Length 856;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Oy 1 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 35
Db 639 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 673

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RESULT 5
ENV_HV1LW STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP MEDLINE=95127297; PubMed=7826699;
RX Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC DR GlycosultedB: Q70626; -
CC DR InterPro: IPR000328; Env_Gp41.

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```

DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT SIGNAL 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 448
FT DISULFID 385 418
FT CARBOHYD 88 136
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

```

```

Query Match Best Local Similarity 100.0%; Score 188; DB 1; Length 856;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Oy 1 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 35
Db 639 TSLHSLIEESONQOEKNEDELLELDKWSLWNMF 673

```

```

RESULT 6
ENV_HV1BR STANDARD; PRT; 861 AA.
ID ENV_HV1BR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

```



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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64;

Query Match
Best Local Similarity 97.1%; Score 185; DB 1; Length 853;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TSLHSLIESONQOEKNEQELLELDKMASLWNMF 35
|||||:|||||:|||||:|||||:|||||:
637 TSLHSLIDESONQOEKNEQELLELDKMASLWNMF 671

RESULT 8
ENV_HV1PV STANDARD: PRT; 856 AA.
ID ENV_HV1PV
AC P03376;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Mueing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/Lymphadenopathy retrovirus.";
RC Nature 313:450-458(1985).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: K02083; AAB59873.1;
CC EMBL: X01762; CA25903.1; ALT_SEQ.
CC PIR: A03974; VCLJVL.
CC HIV: K02083; ENVSPV22.
CC InterPro: IPR000328; Env_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120.1.
CC DR Pfam: PF00517; GP41.1.
CC DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
CC Signal.
CC KMW SIGNAL.
CC FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 512 511 TRANSMEMBRANE GLYCOPROTEIN.
CC FT DISULFID 54 74 BY SIMILARITY.
CC FT DISULFID 119 205 BY SIMILARITY.
CC FT DISULFID 126 196 BY SIMILARITY.
CC FT DISULFID 131 157 BY SIMILARITY.
CC FT DISULFID 218 247 BY SIMILARITY.
CC FT DISULFID 228 239 BY SIMILARITY.

```

```

FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 366 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA: 97339 MW: 5FCDB1DC3C1209B3 CRC64;

Query Match
Best Local Similarity 95.2%; Score 179; DB 1; Length 856;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TSLHSLIESONQOEKNEQELLELDKMASLWNMF 34
|||||:|||||:|||||:|||||:|||||:
639 TSLHSLIDESONQOEKNEQELLELDKMASLWNMF 672

RESULT 9
ENV_HV1SC STANDARD: PRT; 856 AA.
ID ENV_HV1SC
AC P05878;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OC Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldrovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
CC -----
CC MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
CC 1984 IN SOUTHERN CALIFORNIA.
CC -----
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CC -----

DR EMBL: M17450: -; NOT\_ANNOTATED\_CDS.

DR HIV: M17450: ENVSSC.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane;

KM Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 129

FT CARBOHYD 129 135

FT CARBOHYD 135 140

FT CARBOHYD 140 143

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA: 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match

Best Local Similarity 94.3%; Score 179; DB 1; Length 856;

Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLISLIEESONQOEKNEQELLELDKASLWNWF 35

DB 639 TSLIYTLIEESONQOEKNEQELLELDKASLWNWF 673

ENV\_HV1W1

STANDARD: PRT: 856 AA.

AC P31872;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polyprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].

DE ENV.

OS Human immunodeficiency virus type 1 (WM1 isolate) (HIV-1).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=31678;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86218077; PubMed=2423250;

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,

RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."

RL Cell 45:637-648(1986).

CC -i MISCELLANEOUS: ISOLATES WM01, WM02, AND WM03 WERE OBTAINED FROM

CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO

CC WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; VCLJ3W.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Glycoprotein; Transmembrane;

KM Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 97526 MW; DB68D1E49C404DE3 CRC64;

SO SEQUENCE

Query Match

Best Local Similarity 94.3%; Score 179; DB 1; Length 856;

Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLISLIEESONQOEKNEQELLELDKASLWNWF 35

Db 639 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 673

RESULT 11

ENV\_HV153 STANDARD: PRT: 852 AA.

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90317906; PubMed=2370688;

RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome."

RT J. Virol. 64:4016-4020(1990).

CC -----

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CC -----

CC EMBL: M38427; AAA45067.1; -

CC HIV: M38427; EVNSF33.

DR InterPro: IPR000328; Env-GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 31 BY SIMILARITY.

FT CHAIN 507 852 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.

FT DISULFID 331 439 BY SIMILARITY.

FT DISULFID 377 412 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 852 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 852 AA: 96663 MW: EE7BBF8D23C9910D CRC64;

Query Match

Best Local Similarity 94.1%; Score 177; DB 1; Length 852;

Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 35

Db 635 TSLIYNLIESONQOEKNEOELLELDKMSLWNMF 669

RESULT 12

ENV\_HV151 STANDARD: PRT: 847 AA.

AC PI9550:

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-VUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).

OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11691;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90347635; PubMed=2384920;

RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation."

RT J. Virol. 64:4390-4398(1990).

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CC -----

CC EMBL: M65024; AAA5072.1; -

CC HIV: M38428; EVNSF162.

DR InterPro: IPR000328; Env-GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 203 BY SIMILARITY.

FT DISULFID 125 194 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 216 245 BY SIMILARITY.

FT DISULFID 226 237 BY SIMILARITY.

FT DISULFID 294 338 BY SIMILARITY.

FT DISULFID 374 435 BY SIMILARITY.

FT DISULFID 381 408 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 166 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

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Query Match 93.6%; Score 176; DB 1; Length 847;
Best Local Similarity 91.4%; Pred. No. 5.6e-14;
Matches 32; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OY 1 TSLHSLIEESONOEKNEOELELDKMASLWNMF 35
Db 630 TNLITLIEESONOEKNEOELELDKMASLWNMF 664

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RESULT 13
ENV_HV1W2 STANDARD; PRT; 847 AA.
AC POS880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS.";
Science 232:1548-1553(1986).
RL -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SPONTANEOUSLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
WAS PERINATALLY INFECTED BY HER MOTHER.
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CC -----
DR EMBL: M12507; AAB12990.1;
DR HIV: M12507; ENV5WMJ2.
DR InterPro: IPR000328; ENV_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.

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FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFD 53 73
FT DISULFD 118 202
FT DISULFD 125 193
FT DISULFD 130 152
FT DISULFD 130 152
FT DISULFD 215 244
FT DISULFD 225 236
FT DISULFD 293 326
FT DISULFD 372 435
FT DISULFD 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
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FT CARBOHYD 238 238
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FT CARBOHYD 334 334
FT CARBOHYD 350 350
FT CARBOHYD 356 356
FT CARBOHYD 380 380
FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA; 96466 MW; C01E33D73AAB3CAE CRC64;

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Query Match 92.0%; Score 173; DB 1; Length 847;
Best Local Similarity 91.4%; Pred. No. 1.3e-13;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 TSLHSLIEESONOEKNEOELELDKMASLWNMF 35
Db 630 TSLHSLIEESONOEKNEOELELDKMASLWNMF 664

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RESULT 14
ENV_HV1J3 STANDARD; PRT; 867 AA.
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352108; PubMed=2669897;
Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria.";
AIDS Res. Hum. Retroviruses 5:411-419(1989).
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 CC -----  
 DR EMBL; M21138; AAB03526.1; -  
 DR HIV; M21138; ENV5JH3.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 1 516  
 FT CHAIN 517 867  
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 FT DISULFID 118 217  
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 FT DISULFID 130 160  
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 FT CARBOHYD 87 87  
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 FT SEQUENCE 867 AA: 98399 MW: 5F2310146B8E8680 CRC64;  
 Query Match 91.5%; Score 172; DB 1; Length 867;  
 Best Local Similarity 91.4%; Pred. No. 1,8e-13;  
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11696;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;  
 RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reltz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates."  
 RL Virology 164:531-536(1988).  
 CC -I- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS  
 CC PATIENT IN 1984.  
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 CC -----  
 DR EMBL; M17449; AAA44857.1; -  
 DR PIR; A28922; VCLJMN.  
 DR HIV; M17449; ENV5MN.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 513  
 FT CHAIN 514 856  
 FT DISULFID 53 73  
 FT DISULFID 118 210  
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 FT DISULFID 130 162  
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 FT SEQUENCE 867 AA: 98399 MW: 5F2310146B8E8680 CRC64;  
 Query Match 91.5%; Score 172; DB 1; Length 867;  
 Best Local Similarity 91.4%; Pred. No. 1,8e-13;  
 Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97140 MW; D197D80940BE732 CRC64;

Query Match 90.4%; Score 170; DB 1; Length 856;  
 Best Local Similarity 88.6%; Pred. No. 3.1e-13;  
 Matches 31; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLIHSLIESQNOQEKNEQELLELDKRWASLWNF 35  
 |||||:||||:|||||  
 DB 640 TSLIYSLEKSOQOEKNEQELLELDKRWASLWNF 674

Search completed: May 16, 2003, 11:13:33  
 Job time : 6.90361 secs

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F:424-443/Domain: transmembrane #status predicted <TMN>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 92.5%; Score 185; DB 2; Length 443;  
Best Local Similarity 88.9%; Pred. No. 1,9e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 36  
DB 378 YTSLIYNLEESONQOEKNEDELLELDKMANLNMWF 413

RESULT 3  
VCLJ3M  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
F:45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382

C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.5%; Score 185; DB 1; Length 856;  
Best Local Similarity 88.9%; Pred. No. 3,9e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 36  
DB 638 YTSLIYNLEESONQOEKNEDELLELDKMANLNMWF 673

RESULT 4  
T01672  
envelope polyprotein precursor - human immunodeficiency virus type 1

Species: human immunodeficiency virus type 1, HIV-1  
A:Note: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: T01672  
R:Alison, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.  
Cell 46, 63-74, 1986  
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol  
A:Reference number: Z14389; MUID:86245056; PMID:2424612  
A:Accession: T01672  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-859 <ALII>  
A:Cross-references: EMBL:K03456; NID:g60228; PIDN:CAA28016.1; PID:g60234  
C:Superfamily: type E retrovirus env polyprotein

Query Match 90.0%; Score 180; DB 2; Length 859;  
Best Local Similarity 88.9%; Pred. No. 1,6e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 36  
DB 640 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 675

RESULT 5  
S54384

envelope polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
C:Accession: S54384  
R:Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989

A:Reference number: S54377  
A:Accession: S54384  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-853 <THE>  
A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 89.5%; Score 179; DB 2; Length 853;  
Best Local Similarity 86.1%; Pred. No. 2e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 36  
DB 635 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 670

RESULT 6  
VCLJ2R  
env polyprotein precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus Zr-6  
C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999  
C:Accession: D26192  
R:Srivatsan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorlino, P.; Schochetman, G.;  
Gene 52, 71-82, 1987  
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucle  
A:Reference number: A26192; MUID:87248097; PMID:3036660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRID>  
A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-855/Product: env polyprotein #status predicted <MAT>  
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-855/Product: transmembrane glycoprotein #status predicted <TMN>  
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,

Query Match 89.5%; Score 179; DB 1; Length 855;  
Best Local Similarity 86.1%; Pred. No. 2e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 36  
DB 637 YTGIIYNLEESONQOEKNEDELLELDKMANLNMWF 672

RESULT 7  
VCLJSC  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
Virollogy 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-4

Perfect score: 200  
Sequence: 1 YTGIIYNLEESQNOEKNEDELLEDKWANLNMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185	92.5	357	2 S21996	envelope protein g
2	185	92.5	443	2 C41621	env polypeptide P
3	185	92.5	856	1 VCLJ3W	env polypeptide pr
4	180	90.0	859	2 T01672	envelope glycoprote
5	179	89.5	853	2 S54384	envelope polypeptide
6	179	89.5	855	1 VCLJ2R	env polypeptide pr
7	179	89.5	861	1 VCLJ3C	env polypeptide pr
8	178	89.0	855	1 VCLJ2A	envelope protein g
9	178	89.0	855	2 S22004	env polypeptide pr
10	177	88.5	357	2 S22006	envelope protein g
11	177	88.5	357	2 S21994	envelope protein g
12	177	88.5	445	2 A41621	env polypeptide M
13	176	88.0	358	2 S21928	envelope protein g
14	175	87.5	851	2 S33985	envelope protein g
15	175	87.5	854	2 S13288	env polypeptide -
16	175	87.5	856	1 VCLJ3H	env protein - huma
17	175	87.5	861	1 VCLJ3V	env polypeptide pr
18	174	87.0	357	2 T09448	env polypeptide pr
19	174	87.0	847	2 S21992	envelope protein g
20	174	87.0	856	2 S13289	envelope glycoprote
21	174	87.0	856	1 VCLJ3L	env polypeptide pr
22	173	86.5	846	1 VCLJ3D	env polypeptide pr
23	172	86.0	859	1 VCLJ3N	env polypeptide pr
24	171	85.5	843	1 H44001	env polypeptide pr
25	170	85.0	358	2 S22002	envelope protein g
26	170	85.0	358	2 S22000	envelope protein g
27	170	85.0	358	2 S70417	envelope protein g
28	170	85.0	729	1 VCLJ3X	env polypeptide pr
29	170	85.0	861	1 VCLJ3B	env polypeptide pr

30	168	84.0	852	2 T12016	envelope glycoprote
31	164	82.0	852	1 VCLJBR	env polypeptide -
32	163	81.5	454	2 B41621	env polypeptide D
33	162	81.0	136	2 J70266	envelope polypeptide
34	162	81.0	136	2 J70954	envelope polypeptide
35	162	81.0	856	1 A44963	env polypeptide pr
36	159	79.5	854	1 VCLJ3I	env polypeptide pr
37	159	79.5	868	1 VCLJ3H	env polypeptide -
38	143	71.5	357	2 S21990	envelope protein g
39	132	66.0	877	2 S49197	envelope protein p
40	115	57.5	863	2 A53034	gag polypeptide -
41	86	43.0	151	2 S30448	env protein - huma
42	86	43.0	151	2 S30452	env protein - huma
43	86	43.0	151	2 S30451	env polypeptide -
44	86	43.0	366	2 B41565	env polypeptide -
45	86	43.0	885	2 S04322	env polypeptide -

## ALIGNMENTS

## RESULT 1

S21996

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S70422; S21996

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70422

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:613156; NID:960181; PIDN:CAAA3624.1; PID:g1067129

A:Experimental source: Patient 27L

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.5% Score 185; DB 2; Length 357;  
Best Local Similarity 88.9% Pred. No. 1.5e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOEKNEDELLEDKWANLNMWF 36  
DB 139 YTGIIYNLEESQNOEKNEDELLEDKWANLNMWF 174

## RESULT 2

C41621 env polypeptide P - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: C41621

A:Molecule type: DNA

A:Residues: 1-443 <BUR>

A:Cross-references: GB:M77230; NID:9328631; PIDN:AA03792.1; PID:g555015

A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: C41621

A:Note: this virus was isolated from the mother's sexual partner

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyg

F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI: 2001-147136/15.  
 XX

PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide -  
 XX  
 PS

Disclosure: Page 58; 151pp: English.

XX The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating flogogenic events and intracellular processes involving  
 CC coiled-coil peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure  
 CC in which they are used.  
 XX

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQNOQEKNEQELLELDKWNANLMMWF 36  
 II  
 DB 1 YTGIIYNLEESQNOQEKNEQELLELDKWNANLMMWF 36

Search completed: May 16, 2003, 11:12:02  
 Job time : 33.4578 secs



XX AAU13793;  
 AC Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 XX antifusogenic; antiviral; HIV transmission; mutant; mutein.  
 DT 21-NOV-2001 (first entry)  
 XX DP178-like/DP107-like peptide T-1408.  
 DE  
 XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 XX antifusogenic; antiviral; HIV transmission; mutant; mutein.  
 KM  
 XX Human immunodeficiency virus 1 isolate LAI.  
 OS Synthetic.  
 OS WO200151673-A2.  
 XX  
 XX 19-JUL-2001.  
 PD  
 XX 05-JUL-2000; 2000WO-US35727.  
 PF  
 XX 09-JUL-1999; 99US-0350841.  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 PI WPI: 2001-442157/47.  
 DR  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 PS Disclosure; Page 77; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC or absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antifusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents one of the DP178-like/DP107-like peptides  
 CC of the invention.  
 CC  
 SQ Sequence 36 AA;  
 XX  
 XX

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESONQOEKNEELLELDKMANLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLLEESONQOEKNEELLELDKMANLWNMF 36

RESULT 12  
 AAU14013  
 ID AAU14013 standard; peptide; 36 AA.  
 AC AAU14013;  
 XX  
 XX 21-NOV-2001 (first entry)  
 DT  
 XX DP178 homologue derived from HIV-1 isolate RF.  
 DE  
 XX

KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
 KM antifusogenic; antiviral; HIV transmission.  
 XX  
 OS Human immunodeficiency virus 1 isolate RF.  
 XX  
 XX WO200151673-A2.  
 XX  
 XX 19-JUL-2001.  
 PD  
 XX 05-JUL-2000; 2000WO-US35727.  
 PF  
 XX 09-JUL-1999; 99US-0350841.  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 PI WPI: 2001-442157/47.  
 DR  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DP107/DP178 complex -  
 PS Disclosure; Fig 1; 259pp; English.  
 XX  
 XX The present invention relates to peptides which exhibit anti-retroviral  
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds  
 CC to amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence  
 CC or absence of a test compound, in a reaction mixture containing DP107  
 CC and DP178 peptides. The method is useful for identifying compounds,  
 CC including small molecule compounds, which may themselves exhibit  
 CC antifusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-like/DP107-like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents a DP178 homologue derived from  
 CC HIV-1 isolate RF.  
 CC  
 SQ Sequence 36 AA;  
 XX  
 XX

Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESONQOEKNEELLELDKMANLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLLEESONQOEKNEELLELDKMANLWNMF 36

RESULT 13  
 AAB92246  
 ID AAB92246 standard; Peptide; 36 AA.  
 AC AAB92246;  
 XX  
 XX 22-JUN-2001 (first entry)  
 DT  
 XX Virus related peptide SEQ ID NO:1422.  
 DE  
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KM blood component; modification; succinimideyl; maleimido group; amino;  
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO200069900-A2.  
 PN



XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 XX  
 PS Disclosure: Page 58; 587pp; English.  
 XX  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 RESULT 7  
 ABB01247  
 ID ABB01247 standard; Peptide; 36 AA.  
 XX  
 AC ABB01247;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 XX Viral DP178/107-like region peptide T1408.  
 KM Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KM virucide; heptad repeat region; transmembrane protein; gp41; HR1, HR2;  
 KM infection.  
 XX  
 OS Viridiae.  
 XX  
 OS WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 PT

XX Disclosure: Page 58; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 Query Match 100.0%; Score 200; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLELDKMANIMNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 RESULT 8  
 ABB02831  
 ID ABB02831 standard; Peptide; 36 AA.  
 XX  
 AC ABB02831;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral core polypeptide, SEQ ID NO: 1358.  
 XX  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KM virucide; heptad repeat region; transmembrane protein; gp41; HR1, HR2;  
 KM infection.  
 XX  
 OS Viridiae.  
 XX  
 OS WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US03988.  
 PF  
 XX 29-FEB-2000; 2000US-0515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI: 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -  
 PT  
 PS Disclosure: Page 524-525; 587pp; English.  
 XX  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.  
 CC

XX	HIV viral envelope protein stabilising peptide #3.
DE	
XX	Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;
KW	anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;
XX	alpha-helical region; ectodomain.
XV	
OS	Homo sapiens.
XX	
PN	WO200170262-A2.
PD	
XX	27-SEP-2001.
XX	
PF	15-MAR-2001; 2001WO-US08108.
XX	
PR	17-MAR-2000; 2000US-189981P.
XX	
PA	(PANANA-) PANACOS PHARM INC.
XX	
●	Wild CT, Allaway GP.
●	WPI; 2001-626098/72.
XX	
PT	Immunogenic composition for inhibiting HIV infection, comprises viral
PT	envelope protein or its fragment exterior to viral membrane, a
PT	stabilising peptide, and optionally, viral cell surface receptor or
PT	its fragment -
PS	
XX	Claim 6; Page 45; 84pp; English.
CC	The invention relates to methods of generating immunogens that elicit
CC	neutralising antibodies which target regions of viral envelope proteins
CC	such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of
CC	HIV-1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and
CC	AAU70677-AAU70743 represent stabilising peptides modelling the
CC	alpha-helical regions of the ectodomain of the HIV-1 transmembrane
CC	protein to stabilise fusion-active intermediate structures, which can be
CC	used as vaccine immunogens. Immunogenic compositions comprise a viral
CC	envelope protein or its fragment exterior to the viral membrane, a
CC	stabilising peptide to disrupt formation of structural intermediates
CC	necessary for viral fusion and entry, and optionally, a viral cell
CC	surface receptor or its fragment. The stabilising peptide is capable of
CC	associating with the envelope protein or its fragment to form a
CC	stabilised, fusion active structure. Antibody binding assays are used to
CC	determine the ability of immunogen vaccines to generate an immune
CC	response to various forms of envelope. Virus neutralisation assays can be
CC	used to characterise the antibody response raised against HIV-1 gp41
CC	domains. The sequences and methods are useful for inhibiting HIV
CC	infection, for inducing an immune response in an animal and for raising
●	antibodies.
XX	
SQ	Sequence 36 AA:
Query Match	100.0%; Score 200; DB 22; Length 36;
Best Local Similarity	100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;
OY	1 YTGIIYNLLEESONOENKCELLDKRANLMNMF 36 
Db	1 YTGIIYNLLEESONOENKCELLDKRANLMNMF 36
RESULT 5	
AAAG67041	
ID	AA67041 standard; Peptide; 36 AA.
XX	
AC	AA67041;
AC	
XX	
DT	03-JAN-2002 (first entry)
XX	
DE	HIV-1 gp41 peptide DP178 homologue DP-185.
XX	
TW	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

KW	virucide heptad repeat region; transmembrane protein; gp41; HRI; HR2;
KW	infection; DP185.
XX	
XX	Human immunodeficiency virus type 1.
OS	
XX	
PN	MO200164013-A2.
XX	
PD	07-SEP-2001.
XX	
PF	07-FEB-2001; 2001WO-US03988.
XX	
PR	29-FEB-2000; 2000US-0515965.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX	
DR	WPI; 2001-514829/56.
XX	
PT	Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX	
PT	fusion, useful for treating HIV and Respiratory Syncytial Virus
PT	infection -
XX	
PS	Example; Fig 1; 587pp; English.
XX	
CC	The invention relates to isolated analogues of the heptad-repeat region
CC	peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
CC	638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
CC	HRI) respectively, of HIV-1/IIAI transmembrane protein gp41. The HRI
CC	and HR2 regions of proteins interact non-covalently with each other
CC	and/or with peptides derived from them. This interaction is required for
CC	normal infectivity of viruses such as RSV and HIV. The heptad
CC	repeat region peptide analogues may be used to inhibit respiratory
CC	syncytial virus (RSV) infection in a cell. They may also be used to
CC	inhibit HIV infection. The present sequence is a peptide provided in
CC	the specification.
XX	
SQ	Sequence 36 AA:
	Query Match 100.0%; Score 200; DB 22; Length 36;
	Best Local Similarity 100.0%; Pred. No. 5.5e-18;
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 YTGIIYNLLEESQNOEKNEQFLFLDKRANLMMNF 36
DB	1 YTGIIYNLLEESQNOEKNEQFLFLDKRANLMMNF 36
RESULT 6	
ABBO1246	
ID	ABBO1246 standard; Peptide; 36 AA.
XX	
AC	ABBO1246;
XX	
DT	03-JAN-2002 (first entry)
XX	
DE	Viral DP178/107-like region peptide T1407.
XX	
XX	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW	virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
KW	infection.
XX	
OS	Virididae.
XX	
XX	
FH	Key
FT	1 Location/Qualifiers
FT	Modified-site
FT	/note= "N-terminal is substituted by Ac"
FT	36
FT	Modified-site
FT	/note= "C-terminal amide"
XX	
XX	MO200164013-A2.
XX	
XX	07-SEP-2001.

XX Example: Fig 1; 182pp; English.  
 PS This peptide is isolated from HIV-1 isolate RF, and is a homologue of  
 CC the peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the  
 CC HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha  
 CC helix at the C-terminal end of the gp41 ectodomain, and complexes with  
 CC DP-107 (corresponds to amino acids 558-595) which contains a leucine  
 CC zipper motif. The peptides complex via non-covalent protein-protein  
 CC interactions, and possess anti-viral activity. The peptide inhibits  
 CC transmission to uninfected cells, and can also be used as type and/or  
 CC subtype specific diagnostic tools.  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 16; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36  
 1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36

RESULT 2  
 AAR98400  
 ID AAR98400 standard; peptide; 36 AA.  
 AC AAR98400;  
 DT 17-FEB-1997 (first entry)  
 DE Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.  
 DE  
 DE Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM Influenza virus; hepatitis B virus.  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN W09619495-A1.  
 PD 27-JUN-1996.  
 PF 20-DEC-1995; 95WO-US16733.  
 PR 06-JUN-1995; 95US-0470896.  
 PR 20-DEC-1994; 94US-0360107.  
 PA (TRIM-) TRIMERIS INC.  
 PA (UIDU-) UNIT DUKE.  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Petteway SR, Wild CT;  
 DR WPI: 1996-309517/31.  
 XX  
 PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure; Fig 1; 471pp; English.  
 CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 17; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36

RESULT 3  
 AAW17013  
 ID AAW17013 standard; peptide; 36 AA.  
 AC AAW17013;  
 DT 01-JUL-1997 (first entry)  
 DE DP-178-like peptide useful for treatment of HIV infection.  
 DE  
 DE HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 KM  
 OS Human immunodeficiency virus type 1 RF isolate.  
 XX  
 PN W09640191-A1.  
 PD 19-DEC-1996.  
 PF 06-JUN-1996; 96WO-US09499.  
 PR 07-JUN-1995; 95US-0481957.  
 PA (TRIM-) TRIMERIS INC.  
 PI Johnson RM, Lambert DM;  
 DR WPI: 1997-099886/09.  
 XX  
 PT Compens. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Disclosure; Figure 1; 84pp; English.

CC AAW17012-W17016 are DP-178 homologues that are useful in the  
 CC treatment of HIV infection. DP-178 is a peptide corresponding to  
 CC residues 638-673 of HIV type 1 glycoprotein 41 (gp41) transmembrane  
 CC protein. DP-178 and its derivatives/homologues are used in combination  
 CC with a therapeutic agent, e.g. a reverse transcriptase, viral protease,  
 CC cytokine, glycosylation or viral mRNA processing inhibitor or a  
 CC nucleoside inhibitor. The peptides work by inhibiting viral replication  
 CC or inhibiting transmission. They may also be used in vaccines for  
 CC protecting against HIV infection.  
 CC  
 XX  
 SQ Sequence 36 AA:

Query Match 100.0%; Score 200; DB 18; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEDELLEDKWANLMMNF 36

RESULT 4  
 AAU70181  
 ID AAU70181 standard; Peptide; 36 AA.  
 AC AAU70181;  
 DT 14-FEB-2002 (first entry)

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-4

Perfect score: 200  
Sequence: 1 YTGIIYLNLEESQNOQEKNEQELLEDKWMLMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 segs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

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- 23: /SIDS2/gcgdata/geneseq/genesqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	16	AA67699
2	200	100.0	36	17	AA67699
3	200	100.0	36	18	AA67699
4	200	100.0	36	22	AAU70181
5	200	100.0	36	22	AA67041
6	200	100.0	36	22	ABBO1246
7	200	100.0	36	22	ABBO1247
8	200	100.0	36	22	ABBO2831
9	200	100.0	36	22	ABBO2832
10	200	100.0	36	22	AAU13792

11	200	100.0	36	22	AAU13793
12	200	100.0	36	22	AAU14013
13	200	100.0	36	22	AA67699
14	200	100.0	36	22	AA67699
15	200	100.0	36	22	AA67699
16	200	100.0	36	22	AA67699
17	200	100.0	36	22	AA67699
18	200	100.0	36	22	AA67699
19	200	100.0	36	22	AA67699
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25	200	100.0	36	22	AA67699
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27	200	100.0	36	22	AA67699
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38	200	100.0	36	22	AA67699
39	200	100.0	36	22	AA67699
40	200	100.0	36	22	AA67699
41	200	100.0	36	22	AA67699
42	200	100.0	36	22	AA67699
43	200	100.0	36	22	AA67699
44	200	100.0	36	22	AA67699
45	200	100.0	36	22	AA67699

#### ALIGNMENTS

RESULT 1	AA67699	standard; peptide: 36 AA.
XX	AA67699	
AC	AA67699	
XX	AA67699	
DT	24-AUG-1995 (first entry)	
XX	24-AUG-1995 (first entry)	
DE	DP-178 homologue derived from HIV-1 RF has antiviral activity.	
KW	antiviral activity: DP-178; DP-107; diagnostic; HIV-11A1;	
KW	human immunodeficiency virus; transmembrane protein; gp141;	
KW	alpha helix; leucine zipper; DP-185.	
XX		
OS	Human immunodeficiency virus (RF isolate).	
XX		
PN	WO9428920-A.	
XX		
PD	22-DEC-1994.	
XX		
PF	07-JUN-1994; 94WO-US05739.	
XX		
PR	07-JUN-1993; 93US-0073028.	
PA	(UYDU-) UNIV DUKE.	
XX		
PI	Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;	
XX	Peteway SR, Wild CT;	
DR	WPI; 1995-036105/05.	
XX		
PT	Computer search generated synthetic peptides - are inhibitors of HIV transmission	

DP178-like/DP107-1  
DP178 homologue de  
virus related pept  
Core polypeptide T  
Core polypeptide T  
HIV antiviral acti  
Seq ID NO. 33 from  
Envelope protein g  
HIV-1 gp120. protei  
Sequence encoded b  
HIV protein HT7  
Seq ID NO. 50 from  
Envelope protein g  
Seq ID NO. 38 from  
Envelope protein g  
Seq ID NO. 41 from  
Envelope protein g  
Sequence encoded b  
Ancestral HIV-1 gr  
DP185 corresponds  
DP-178-like peptid  
HIV-1 gp41 peptide  
DP178 homologue, p  
Seq ID NO. 43 from  
Envelope protein g  
Seq ID NO. 110 fro  
HIV envelope prote  
Seq ID NO. 13 from  
Envelope protein g  
Seq ID NO. 48 from  
Envelope protein g  
Seq ID NO. 67 from  
Consensus sequence  
HIV-1 BA-L clone-e

Job time : 16.759 secs

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STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-854-816-12

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Best Local Similarity 91.7%; Pred. No. 9.6e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YTNFTYTLLESQNOQEKNEQELLEDKWSLWNMF 36
Db 169 YTSLYTLLESQNOQEKNEQELLEDKWSLWNMF 204

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RESULT 15
US-10-032-162-15
Sequence 15, Application US/10032162
Publication No. US20030052839A1
GENERAL INFORMATION:
APPLICANT: BINLEY, JAMES M
APPLICANT: SCHUELTE, NORBERT
APPLICANT: OLSON, WILLIAM C
APPLICANT: PAUL, MADDON J
APPLICANT: JOHN, MOORE P
TITLE OF INVENTION: STABILIZED VIRAL ENVELOPE PROTEINS AND USES THEREOF
FILE REFERENCE: 2048/59331a2
CURRENT APPLICATION NUMBER: US/10/032,162
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/602,864
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 579
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-10-032-162-15

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Query Match          93.4%; Score 185; DB 9; Length 579;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 536 YPSEIYTLLESQNOQEKNEQELLEDKWSLWNMF 571

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Search completed: May 16, 2003, 12:10:22

LENGTH: 46  
 TYPE: PRF  
 ORGANISM: Human immunodeficiency virus type 1  
 US-09-779-451-45

Query Match 93.4% Score 185; DB 10; Length 46;  
 Best Local Similarity 91.7%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNITYTLLESQNOQEKNEQELLELDKWSLWNNF 36  
 DB 11 YTSYITLLESQNOQEKNEQELLELDKWSLWNNF 46

RESULT 12  
 US-09-854-816-8  
 Sequence 8, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice  
 Robert S. McDowell  
 J. Christopher Phelan  
 Melissa A. Starovasnik

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854, 816

FILING DATE: 15-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965, 056

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Phd., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Query Match 93.4% Score 185; DB 10; Length 268;  
 Best Local Similarity 91.7%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNITYTLLESQNOQEKNEQELLELDKWSLWNNF 36  
 DB 168 YTSYITLLESQNOQEKNEQELLELDKWSLWNNF 203

RESULT 13  
 US-09-854-816-9

Sequence 9, Application US/09854816  
 Patent No. US20020151473A1  
 GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice  
 Robert S. McDowell  
 J. Christopher Phelan  
 Melissa A. Starovasnik

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854, 816

FILING DATE: 15-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965, 056

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Phd., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 93.4% Score 185; DB 10; Length 268;  
 Best Local Similarity 91.7%; Pred. No. 9.6e-15;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNITYTLLESQNOQEKNEQELLELDKWSLWNNF 36  
 DB 168 YTSYITLLESQNOQEKNEQELLELDKWSLWNNF 203

RESULT 14  
 US-09-854-816-12  
 Sequence 12, Application US/09854816  
 Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESS: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

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; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: HIV-JRCSE
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-854-816-7

Query Match          94.4%; Score 187; DB 10; Length 268;
Best Local Similarity 94.4%; Pred. No. 5.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 168 YTNITVTLLEESONQOEKNEDELLELDKWSLWNMF 203

RESULT 9
US-09-854-816-28
; Sequence 28, Application US/09654816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovashnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; FILING DATE: 15-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:

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; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-854-816-28

Query Match          94.4%; Score 187; DB 10; Length 269;
Best Local Similarity 94.4%; Pred. No. 5.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 169 YTSIIVTLLEESONQOEKNEDELLELDKWSLWNMF 204

RESULT 10
US-09-779-451-47
; Sequence 47, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-47

Query Match          93.4%; Score 185; DB 10; Length 36;
Best Local Similarity 91.7%; Pred. No. 1.2e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 YTSIIVTLLEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 11
US-09-779-451-45
; Sequence 45, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-854-816-26

Query Match          96.0%; Score 190; DB 10; Length 268;
Best Local Similarity 94.4%; Pred. No. 2,4e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 168 YTNLTITLLEESONOQEKNEQELLELDKWSLWNMF 203

RESULT 5
US-09-891-609-4
; Sequence 4, Application US/09891609
; Patent No. US20020127238A1
; GENERAL INFORMATION:
; APPLICANT: Stamatiatos, Leonidas
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
; FILE REFERENCE: 2570-1-002N
; CURRENT APPLICATION NUMBER: US/09/891,609
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,608
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-4

Query Match          96.0%; Score 190; DB 10; Length 619;
Best Local Similarity 94.4%; Pred. No. 5,8e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 574 YTNLTITLLEESONOQEKNEQELLELDKWSLWNMF 609

RESULT 6
US-09-891-609-2
; Sequence 2, Application US/09891609
; Patent No. US20020127238A1
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; GENERAL INFORMATION:
; APPLICANT: Stamatiatos, Leonidas
; TITLE OF INVENTION: HIV-1 VACCINES AND SCREENING METHODS THEREFOR
; FILE REFERENCE: 2570-1-002N
; CURRENT APPLICATION NUMBER: US/09/891,609
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,608
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-891-609-2

Query Match          96.0%; Score 190; DB 10; Length 646;
Best Local Similarity 94.4%; Pred. No. 6,1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTTYITLLEESONOQEKNEQELLELDKWSLWNMF 36
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Db 601 YTNLTITLLEESONOQEKNEQELLELDKWSLWNMF 636

RESULT 7
US-09-476-242-2
; Sequence 2, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: HARTOG, Karin
; APPLICANT: MARTIN, Eric
; TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
; FILE REFERENCE: 1605,002
; CURRENT APPLICATION NUMBER: US/09/476,242
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-476-242-2

Query Match          96.0%; Score 190; DB 10; Length 847;
Best Local Similarity 94.4%; Pred. No. 8,1e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTTYITLLEESONOQEKNEQELLELDKWSLWNMF 36
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Db 629 YTNLTITLLEESONOQEKNEQELLELDKWSLWNMF 664

RESULT 8
US-09-854-816-7
; Sequence 7, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Pheasant
; Melissa A. Starovastnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
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TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-000-321-11

Query Match 100.0%; Score 198; DB 12; Length 145;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
Db 106 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 141

RESULT 2  
US-09-854-816-30  
Sequence 30, Application US/09854816  
Patent No. US20020151473A1

## GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-854-816-30

Query Match 100.0%; Score 198; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
Db 169 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 204

RESULT 3

US-09-854-816-31  
Sequence 31, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 269 amino acids

TYPE: Amino Acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-854-816-31

Query Match 100.0%; Score 198; DB 10; Length 269;  
Best Local Similarity 100.0%; Pred. No. 2.7e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
Db 169 YTNNTYTLLESQNOQEKNEQELLELDKWSLWNMF 204

RESULT 4  
US-09-854-816-26

Sequence 26, Application US/09854816

Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Computen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-3  
Perfect score: 198  
Sequence: 1 YTWITLLEESONQOEKNEQELLEDKWASLNNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues  
Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/PCYUS\_PUBCOMB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	198	100.0	269	10	US-09-854-816-30
3	198	100.0	269	10	US-09-854-816-31
4	190	96.0	268	10	US-09-854-816-26
5	190	96.0	619	10	US-09-891-609-4
6	190	96.0	646	10	US-09-891-609-2
7	190	96.0	847	10	US-09-476-242-2
8	187	94.4	268	10	US-09-854-816-7
9	187	94.4	269	10	US-09-854-816-28
10	185	93.4	36	10	US-09-779-451-47
11	185	93.4	46	10	US-09-779-451-45
12	185	93.4	268	10	US-09-854-816-8
13	185	93.4	268	10	US-09-854-816-9
14	185	93.4	269	10	US-09-854-816-12
15	185	93.4	579	9	US-10-032-162-15
16	185	93.4	625	9	US-10-032-162-17
17	185	93.4	643	9	US-10-032-162-13
18	184	92.9	267	10	US-09-854-816-38
19	184	92.9	268	10	US-09-854-816-41

20	183	92.4	46	10	US-09-854-816-109	Sequence 109, App
21	183	92.4	269	10	US-09-854-816-6	Sequence 6, Appl
22	181	91.4	268	10	US-09-854-816-13	Sequence 13, Appl
23	181	91.4	269	10	US-09-854-816-42	Sequence 42, Appl
24	180	90.9	233	10	US-09-854-816-50	Sequence 50, Appl
25	179	90.4	268	10	US-09-854-816-39	Sequence 39, Appl
26	178	89.9	267	10	US-09-854-816-11	Sequence 11, Appl
27	178	89.9	269	10	US-09-854-816-33	Sequence 33, Appl
28	177	89.4	269	10	US-09-854-816-20	Sequence 20, Appl
29	177	89.4	269	10	US-09-854-816-43	Sequence 37, Appl
30	177	89.4	269	10	US-09-854-816-46	Sequence 43, Appl
31	177	89.4	269	9	US-09-874-475-16	Sequence 46, Appl
32	176	88.9	36	9	US-10-116-797-1	Sequence 16, Appl
33	176	88.9	36	9	US-09-493-346-1	Sequence 1, Appl
34	176	88.9	36	9	US-09-796-202-10	Sequence 10, Appl
35	176	88.9	36	10	US-09-779-451-5	Sequence 5, Appl
36	176	88.9	36	10	US-09-834-628-1	Sequence 1, Appl
37	176	88.9	36	10	US-09-854-816-108	Sequence 108, App
38	176	88.9	36	10	US-09-854-816-176	Sequence 176, App
39	176	88.9	37	9	US-09-848-616-176	Sequence 41, Appl
40	176	88.9	46	10	US-09-779-451-41	Sequence 4, Appl
41	176	88.9	56	10	US-10-040-3498-2	Sequence 84, Appl
42	176	88.9	177	9	US-10-059-271-84	Sequence 81, Appl
43	176	88.9	221	9	US-10-059-271-81	
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ALIGNMENTS

RESULT 1  
US-10-000-321-11  
; Sequence 11, Application US/10000321  
; Patent No. US20020123039A1

GENERAL INFORMATION:  
APPLICANT: BRUST, Stefan  
KNAPP, Stefan  
GERKEN, Manfred  
GUERTLER, Lutz

TITLE OF INVENTION: Peptides derived from a retrovirus of the HIV group, and their use

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/000.321  
FILING DATE: 04-Dec-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/131,551  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 58315/106/BEAK

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids

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Fri May 16 13:45:12 2003

us-09-623-533a-3.rai

Page 7

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Oy  1 YNTYTYTTLLEESQNOOEKNEOETLEDDKASJLWNMF 36
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Db  169 YNTYTYTTLLEESQNOOEKNEOETLEDDKASJLWNMF 204

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Search completed: May 16, 2003, 11:22:10  
 Job time : 11.1928 secs

STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/394,021  
FILING DATE: 23-FEB-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 05 810.1  
FILING DATE: 23-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 58315/106/BEAK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-394-021-11

Query Match 100.0%; Score 198; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 6e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOOEKNEQELLELDKMASLWNMF 36  
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DB 106 YNTNTYTLLEESQNOOEKNEQELLELDKMASLWNMF 141

RESULT 14  
US-09-131-551-11  
Sequence 11, Application US/09131551  
Patent No. 6335158  
GENERAL INFORMATION:  
APPLICANT: BRUST, Stefan  
APPLICANT: KNAPP, Stefan  
APPLICANT: GUERTLER, Manfred  
TITLE OF INVENTION: Peptides derived from a retrovirus of  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/131,551  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/394,021  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: SANDERCOCK, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 58315/106/BEAK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-131-551-11

Query Match 100.0%; Score 198; DB 4; Length 145;  
Best Local Similarity 100.0%; Pred. No. 6e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOOEKNEQELLELDKMASLWNMF 36  
|||||  
DB 106 YNTNTYTLLEESQNOOEKNEQELLELDKMASLWNMF 141

RESULT 15  
US-08-965-056-30  
Sequence 30, Application US/08965056  
Patent No. 6271198  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
APPLICANT: J. Kevin Judice  
APPLICANT: Robert S. McDowell  
APPLICANT: J. Christopher Phelan  
APPLICANT: Melissa A. Starovastnik  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/965,056  
FILING DATE: 05-NO. 6271198-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: PI005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: linear  
US-08-965-056-30

Query Match 100.0%; Score 198; DB 4; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36  
|||||

DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36

RESULT 10

US-09-315-304B-1357  
Sequence 1357, Application US/09315304B

Patent No. 6348368

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M. D.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1357

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-1357

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36  
|||||

DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36

RESULT 11

US-08-255-208A-3  
Sequence 3, Application US/08255208A

Patent No. 6440656

GENERAL INFORMATION:

APPLICANT: Bolognesi, Daniel P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelleway, Jr., Stephen R.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

NUMBER OF SEQUENCES: 111

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-255-208A-3

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36  
|||||

DB 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36

RESULT 12

US-09-570-921-16  
Sequence 16, Application US/09570921

Patent No. 6453265

GENERAL INFORMATION:

APPLICANT: SERRES, PIERRE-FRANCOIS

TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE

FILE REFERENCE: 106213

CURRENT APPLICATION NUMBER: US/09/570,921

PRIOR FILING DATE: 2000-05-15

PRIOR APPLICATION NUMBER: PCT/FR98/02447

PRIOR FILING DATE: 1998-11-17

PRIOR APPLICATION NUMBER: FR/97/14387

PRIOR FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 144

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 138

TYPE: PRT

ORGANISM: Human

US-09-570-921-16

Query Match 100.0%; Score 198; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 5.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 36  
|||||

DB 99 YNTTYTTLLEESONOQEKNEQELLELDKWSLWNNF 134

RESULT 13

US-08-394-021-11  
Sequence 11, Application US/08394021

Patent No. 5830634

GENERAL INFORMATION:

APPLICANT: BRUST, Stefan

APPLICANT: KNAPP, Stefan

APPLICANT: GERKEN, Manfred

APPLICANT: GUERTLER, Lutz

TITLE OF INVENTION: Peptides derived from a retrovirus of

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESONOQEKNEQELLEIDKWSLWNMF 36  
DB 1 YNTYITLLEESONOQEKNEQELLEIDKWSLWNMF 36

RESULT 5  
US-08-485-551A-3  
Sequence 3, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESONOQEKNEQELLEIDKWSLWNMF 36  
DB 1 YNTYITLLEESONOQEKNEQELLEIDKWSLWNMF 36

RESULT 6  
US-08-471-913A-3  
Sequence 3, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-3

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36  
Db 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36

## RESULT 2

US-08-484-223B-3  
; Sequence 3, Application US/08484223B  
; Patent No. 6020459  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Pellew, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 245  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,223B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-484-223B-3

Query Match 100.0%; Score 198; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36  
Db 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36

## RESULT 3

US-08-919-597-3  
; Sequence 3, Application US/08919597  
; Patent No. 6054265  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-919-597-3

Query Match 100.0%; Score 198; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36  
Db 1 YTNNTYTLLEESONQOEKNEDELLELDKWSLWMMF 36

RESULT 4  
US-08-475-668A-3  
; Sequence 3, Application US/08475668A  
; Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pellew, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
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103.919 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198  
Sequence: 1 YTNFTYTLLEESONQOEKNEQLELDKWSLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Issued\_Patents\_AA:\*  
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4: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	36	3	US-08-486-099-3
2	198	100.0	36	3	US-08-484-223B-3
3	198	100.0	36	3	US-08-919-597-3
4	198	100.0	36	3	US-08-475-668A-3
5	198	100.0	36	3	US-08-485-551A-3
6	198	100.0	36	3	US-08-471-913A-3
7	198	100.0	36	4	US-08-485-264A-3
8	198	100.0	36	4	US-09-082-279B-1357
9	198	100.0	36	4	US-08-474-349A-3
10	198	100.0	36	4	US-09-315-304B-1357
11	198	100.0	36	4	US-08-255-208A-3
12	198	100.0	138	4	US-09-570-921-16
13	198	100.0	145	2	US-08-394-021-11
14	198	100.0	145	4	US-09-131-551-11
15	198	100.0	269	4	US-08-965-056-30
16	198	100.0	269	4	US-08-965-056-31
17	198	100.0	610	4	US-09-257-490-12
18	198	100.0	855	4	US-07-956-483-15
19	198	100.0	887	4	US-08-472-240A-6
20	193	97.5	36	1	US-08-073-028-3
21	193	97.5	36	3	US-08-360-107A-3
22	193	97.5	36	4	US-08-554-616-3
23	190	96.0	138	4	US-09-570-921-8
24	190	96.0	268	4	US-08-965-056-26
25	187	94.4	36	4	US-09-082-279B-1051
26	187	94.4	36	4	US-09-315-304B-1051
27	187	94.4	138	4	US-09-570-921-10

28	187	94.4	138	4	US-09-570-921-19	Sequence 19, Appl
29	187	94.4	268	4	US-08-965-056-7	Sequence 7, Appl
30	187	94.4	269	4	US-08-965-056-28	Sequence 28, Appl
31	185	93.4	36	4	US-09-082-279B-856	Sequence 856, App
32	185	93.4	36	4	US-09-315-304B-856	Sequence 856, App
33	185	93.4	138	4	US-09-570-921-12	Sequence 12, App
34	185	93.4	268	4	US-08-965-056-8	Sequence 8, Appl
35	185	93.4	268	4	US-08-965-056-9	Sequence 9, Appl
36	185	93.4	269	4	US-08-965-056-12	Sequence 12, Appl
37	185	93.4	855	4	US-07-956-483-14	Sequence 14, Appl
38	185	93.4	887	4	US-08-472-240A-5	Sequence 5, Appl
39	184	92.9	267	4	US-08-965-056-38	Sequence 38, Appl
40	184	92.9	268	4	US-08-965-056-41	Sequence 41, Appl
41	183	92.4	46	4	US-08-965-056-109	Sequence 109, App
42	183	92.4	269	4	US-08-965-056-6	Sequence 6, Appl
43	181	91.4	36	4	US-09-082-279B-642	Sequence 642, App
44	181	91.4	36	4	US-09-315-304B-642	Sequence 642, App
45	181	91.4	268	4	US-08-965-056-13	Sequence 13, Appl

#### ALIGNMENTS

RESULT 1  
US-08-486-099-3  
; Sequence 3, Application US/08486099  
; Patent No. 6013263  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Paul P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Pellew, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penrite & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-031  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-486-099-3  
Query Match 100.0%; Score 198; DB 3; Length 36;

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DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
SQ SEQUENCE 866 AA; 98423 MW; E42C8BA2509B056 CRC64;

Query Match
Best Local Similarity 94.4%; Score 189; DB 15; Length 866;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 36
DB 648 YTNLTITLLEESONQOEKNEDELLDKWASLWNMF 683

RESULT 10
O9YXN4 PRELIMINARY: PRT; 122 AA.
AC O9YXN4
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENV Envelope glycoprotein immunodominant region (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RJ7BRP116;
RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savcira A.,
RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
RA Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL EMBL: AF034069; AAC79321.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14811 MW; F154B211B9D456D5 CRC64;

Query Match
Best Local Similarity 94.9%; Score 188; DB 15; Length 122;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 36
DB 78 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 113

RESULT 11
O9EAA2 PRELIMINARY: PRT; 122 AA.
AC O9EAA2
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BX161;
RA MEDLINE=20134570; PubMed=10669328;
RA Weidie P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Ollivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475(2000).
DR EMBL: AF190950; AAG02312.1;

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DR InterPro: IPR000328; Env_GP41.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14751 MW; 302E5D7E45ED007D CRC64;

Query Match
Best Local Similarity 91.7%; Score 188; DB 15; Length 122;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 36
DB 78 YTNVTYTLLEESONQOEKNEDELLDKWASLWNMF 113

RESULT 12
O11944 PRELIMINARY: PRT; 849 AA.
AC O11944
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein gp160.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB8.C1;
RA MEDLINE=96100812; PubMed=7483788;
RA Vella C., Smith M.H., Farrar G.H., Jones D.H., Daniels R.S.;
RT "A molecular and serologic study of the envelope gene of the British
RT isolate: HIV-IGB8.";
RL Vaccine 13:735-741(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB8.C1;
RX MEDLINE=98035047; PubMed=9367752;
RA Douglas N.W., Munro G.H., Daniels R.S.;
RT "HIV/SIV glycoproteins: Structure-Function Relationships.";
RL J. Mol. Biol. 273:122-149(1997).
DR EMBL: Y13716; CAA74044.1;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 849 AA; 96612 MW; 3026E908267F63 CRC64;

Query Match
Best Local Similarity 94.9%; Score 188; DB 15; Length 849;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 36
DB 631 YNTVTYTLLEESONQOEKNEDELLDKWASLWNMF 666

RESULT 13
O9YXM9 PRELIMINARY: PRT; 122 AA.
AC O9YXM9
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]

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GenCore version 5.1.4-p5-A578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198

Sequence: 1 YTNNTYTLLESQNOQEKNEQELLELDKWSIWMWF 36

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Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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Database : SPTREMBL.21.\*  
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2: sp\_bacteria:\*  
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4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
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16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	190	96.0	860	15	09YP43 human immun
6	190	96.0	860	15	09YP50 human immun
7	190	96.0	863	15	09WJ04 human immun
8	190	96.0	864	15	09YP48 human immun
9	189	95.5	866	15	09E1R5 human immun
10	188	94.9	122	15	09YXN4 human immun
11	188	94.9	122	15	09EAA2 human immun
12	188	94.9	849	15	011944 human immun
13	187	94.4	122	15	09YXW9 human immun
14	187	94.4	122	15	091J06 human immun
15	187	94.4	848	15	074999 human immun
16	187	94.4	855	15	09E1R7 human immun

17	187	94.4	858	15	080867 human immun
18	187	94.4	858	15	080865 human immun
19	187	94.4	864	15	09E610 human immun
20	186	93.9	122	15	09EA97 human immun
21	186	93.9	122	15	09EA82 human immun
22	186	93.9	122	15	091JN5 human immun
23	186	93.9	852	15	092761 human immun
24	186	93.9	852	15	073303 human immun
25	186	93.9	852	15	041546 human immun
26	185	93.4	42	15	069910 human immun
27	185	93.4	122	15	09YX08 human immun
28	185	93.4	123	15	09YXR3 human immun
29	185	93.4	684	15	091K06 human immun
30	185	93.4	841	15	041556 human immun
31	185	93.4	847	15	075760 human immun
32	185	93.4	849	15	077368 human immun
33	185	93.4	849	15	080851 human immun
34	185	93.4	851	15	056110 human immun
35	185	93.4	851	15	080852 human immun
36	185	93.4	855	15	091K00 human immun
37	185	93.4	856	15	09E1S5 human immun
38	185	93.4	856	15	072993 human immun
39	185	93.4	856	15	041539 human immun
40	185	93.4	857	15	073288 human immun
41	185	93.4	857	15	073289 human immun
42	185	93.4	857	15	08U170 human immun
43	185	93.4	859	15	08U185 human immun
44	185	93.4	859	15	08U180 human immun
45	185	93.4	859	15	08U179 human immun

## ALIGNMENTS

RESULT 1  
ID 080161 PRELIMINARY: PRT: 853 AA.  
AC 080161;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope polypeptide.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92046357; PubMed=1658383;  
RA Cheng-Mayer C., Shioda T., Levy J.A.;  
RT "Host range, replicative, and cytopathic properties of human immunodeficiency virus type 1 are determined by very few amino acid changes in tat and gp120".  
RL J. Virol. 65:6931-6941(1991).  
DR EMBL: L07422; AAA80324.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00516; GP120: 1.  
DR Pfam: PF00517; GP41: 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 853 AA: 97056 MW: 2181503CFLD14789 CRC64;

Query Match 100.0%; Score 198; DB 15; Length 853;  
Best Local Similarity 100.0%; Pred. No. 1.3e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNNTYTLLESQNOQEKNEQELLELDKWSIWMWF 36  
DB 635 YTNNTYTLLESQNOQEKNEQELLELDKWSIWMWF 670

RESULT 2  
O91BN3

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[illegible]





[illegible]

Query Match	Best local Similarity	88.9%	Score 176;	DB 1;	Length 855;
Matches	31;	Conservative	86.1%;	Pred. No. 9,2e-14;	Mismatches 3; Indels 0; Gaps 0;
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DB	637	YTHLYTLLEESQNOEKNEQELLELDKWSLNMF	672		
RESULT 11					
ENV_HV1B1					
ID	ENV_HV1B1	STANDARD:	PRT:	856 AA.	
AC	P03375:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
DE	ENV.				
OS	Human immunodeficiency virus type 1 (BHD isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11678;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615;				
RA	Ratner L., Hesselstine W., Patarca R., Liyak K.J., Starich B.R., Josephs S.F., Dotan E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Pelletway S.R. Jr., Pearson M.L., Laltenberger J., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";				
RL	Nature 313:277-284(1985).				
RL	[2]				
RP	DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.				
RX	MEDLINE=90285159; PubMed=235306;				
RA	Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;				
RT	"Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells.";				
RT	J. Biol. Chem. 265:10373-10382(1990).				
CC	----				

Query Match	Best Local Similarity	Matches	Score 178:	DB 1:	Length 867:
1 YNTYTYLLEESQNOQEKNEOELLELDKASLWNF 36	89.9%	32	Pred. No. 5.4e-14:	2	Mismatches 2: Indels 0: Gaps 0:

ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11684;			
RN	11			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Hesselton W., Patarca R., Litvak K.J., Starcich B.R., Josephs S.F., Dorian E.R., Rafalski J.A., Whitehorn E.A., Baumesler K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Latenberger J.A., Pappas T.S., Ghrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RT	Nature 313:277-284(1985).			
RL	-----			
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CC	-----			
DR	EMBL; K02011; AAA44661.1; -			
DR	HIV; K02011; ENV5BH8.			
DR	GlycoSuiteDB; P04582; -			
DR	InterPro; IPR000328; Env_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KM	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal.			
KW	Signal.			
FT	1	30		
FT	CHAIN	506		
FT	CHAIN	507	851	
FT	DISULFID	54	74	
FT	DISULFID	119	205	
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FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
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FT	CARBOHYD	141	141	
FT	CARBOHYD	156	156	
FT	CARBOHYD	160	160	
FT	CARBOHYD	186	186	
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FT	CARBOHYD	234	234	
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FT	CARBOHYD	262	262	
FT	CARBOHYD	276	276	
FT	CARBOHYD	295	295	
FT	CARBOHYD	301	301	
FT	CARBOHYD	332	332	
FT	CARBOHYD	339	339	
FT	CARBOHYD	356	356	

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SO SEQUENCE 856 AA; 97526 MW; DB68D1E49C404DE9 CRC64;

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Query Match 90.9%; Score 180; DB 1; Length 856;

Best Local Similarity 88.9%; Pred. No. 3e-14; Mismatches 0; Gaps 0;

Matches 32; Conservative 2; Indels 0; Gaps 0;

Db 638 YTSLYNLIIESONQOEKNEQLELDKWSLWNF 673

ENV\_HV1RH STANDARD; PRT; 865 AA.

AC P04579;  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).  
 OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11701;

RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,  
 RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.,  
 RT "Identification and characterization of conserved and variable  
 RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of  
 RT AIDS.";  
 RT Cell 45:637-648(1986).

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 CC or send an email to license@isb-sib.ch).

DR EMBL; M17451; AAA45057.1; -  
 DR HIV; M17451; ENVSF.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.

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DR Pfam: PF00517; GP41. 1.  

KW AIDS; Coat protein; Glycoprotein; Transmembrane;  

KW Signal.  

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FT CHAIN 30 519  

FT CHAIN 520 865  

FT DISULFD 53 73  

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FT DISULFD 125 209  

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FT CARBOHD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).  

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FT CARBOHD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).  

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SO SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

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Query Match 89.9%; Score 178; DB 1; Length 865;

Best Local Similarity 88.9%; Pred. No. 5.4e-14; Mismatches 3; Indels 0; Gaps 0;

Matches 32; Conservative 1; Indels 0; Gaps 0;

Db 647 YTGIIYNLIIESONQOEKNEQLELDKWSLWNF 682

ENV\_HV1J3 STANDARD; PRT; 867 AA.

AC P12489;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).  
 OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11694;  
 RN [1]

MEDLINE=68219542; Pubmed=3369091;  
Gargio C., Guo H.-G., Franchini G., Aldrovini A., Collalti E.,  
Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.,  
"Envelope sequences of two new United States HIV-1 isolates.",  
Virology 164:551-556(1988).  
1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
1984 IN SOUTHERN CALIFORNIA.

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EMBL; M17450; -; NOT\_ANNOTATED\_CDS.

PIR; B28922; VCLJSC.

HIV; MI7450; ENV\$SC;  
Inst: Pro: TP000328-

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InterPro: IPR000777: GP120,
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Pfam; PF00516; GP120; 1.

Pfam; PF00517; GP41; 1.

AIDS; Coat protein; Poly

SIGNAL. 1 29

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CHAIN	511	856
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DISOEL ID	110	200
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DISULFID	219	247
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FT	CARBONHD	457	457	N-LINKED <th>(GLCNAC . . .)</th> <th>(POTENTIAL)</th>	(GLCNAC . . .)	(POTENTIAL)
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FT	CARBONHD	816	816	N-LINKED <th>(GLCNAC . . .)</th> <th>(POTENTIAL)</th>	(GLCNAC . . .)	(POTENTIAL)
SEQ	SEQUENCE	856 AA;	97055 MW;	DATA4DA600DBEA7A08	CRR64;	

Query Match	93.4%	Score 185;	DB 1;	Length 856;
Best Local Similarity	91.7%;	Pred. No. 7.5e-15;		
Matches 33;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0;

Oy 1 YTNTIYTLLEESQNOEKNEQELLELDKWSLWNMF 36  
||:|||||  
Db 638 YTSLIYTLLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 6	
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ID	ENV_HV1W1
STANDARD:	PRT;
	856 AA.

DT 01-JUL-1993 (Rel. 26, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (WU1 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=31678;

RN  
 123  
 RP  
 SEQUENCE FROM N.A.  
 RX  
 MEDLINE=86218077; PubMed=2423250;  
 RA  
 Starch B. R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,  
 RA  
 Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;  
 RT  
 Identification and characterization of conserved and variable  
 RT  
 regions in the envelope gene of HTLV-III/LAV, the retrovirus of

RE Cell 42:037-04013067.  
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
CC WAS PERINATALLY INFECTED BY HER MOTHER.

DR InterPro: IPR000328; Env GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW ARDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;

FT	SIGNAL	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	30	510	TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	511	856	BY SIMILARITY
FT	DISULFID	53	73	

DISULEID	125	196	BY SIMILARITY.
FT	130	152	BY SIMILARITY.
DISULEID	218	247	BY SIMILARITY.

FT	DISULEID	376	444	BY SIMILARITY.
FT	DISULFID	383	417	BY SIMILARITY.

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: M38429; AAB03749.1; -

DR HIV: M38429; ENV5JRCSE.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 32

FT CHAIN 504 848

FT DISULFID 53 73

FT DISULFID 118 203

FT DISULFID 125 194

FT DISULFID 130 154

FT DISULFID 216 245

FT DISULFID 226 237

FT DISULFID 294 328

FT DISULFID 374 437

FT DISULFID 381 410

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 137 137

FT CARBOHYD 153 153

FT CARBOHYD 157 157

FT CARBOHYD 185 185

FT CARBOHYD 195 195

FT CARBOHYD 228 228

FT CARBOHYD 239 239

FT CARBOHYD 260 260

FT CARBOHYD 274 274

FT CARBOHYD 287 287

FT CARBOHYD 293 293

FT CARBOHYD 299 299

FT CARBOHYD 329 329

FT CARBOHYD 336 336

FT CARBOHYD 352 352

FT CARBOHYD 382 382

FT CARBOHYD 388 388

FT CARBOHYD 392 392

FT CARBOHYD 403 403

FT CARBOHYD 440 440

FT CARBOHYD 453 453

FT CARBOHYD 603 603

FT CARBOHYD 608 608

FT CARBOHYD 617 617

FT CARBOHYD 629 629

FT CARBOHYD 808 808

SO SEQUENCE 848 AA; 96475 MW; 207675F51227ECF3 CRC64;

Query Match

Best Local Similarity 94.4%; Score 187; DB 1; Length 848;

Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNFTITLLEESQOQKNEQELLELDKWSLWMTF 36

DB 630 YTNFTITLLEESQOQKNEQELLELDKWSLWMTF 665

ENV\_HV153

ENV\_HV153 STANDARD; PRT; 852 AA.

AC P19549;

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 40, Last annotation update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

OC Viruses; Retrovirus; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90317906; PubMed=2370688;

RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";

RT J. Virol. 64:4016-4020(1990).

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CC EMBL: M38427; AAA5067.1; -

DR HIV: M38427; ENV5SEF3.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 31

FT CHAIN 507 852

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 156

FT DISULFID 219 248

FT DISULFID 228 240

FT DISULFID 297 331

FT DISULFID 377 439

FT DISULFID 384 412

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 136 136

FT CARBOHYD 141 141

FT CARBOHYD 142 142

FT CARBOHYD 155 155

FT CARBOHYD 159 159

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 242 242

FT CARBOHYD 263 263

FT CARBOHYD 277 277

FT CARBOHYD 290 290

FT CARBOHYD 296 296

FT CARBOHYD 332 332

FT CARBOHYD 339 339

FT CARBOHYD 355 355

FT CARBOHYD 385 385

FT CARBOHYD 391 391

FT CARBOHYD 397 397

FT CARBOHYD 401 401

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 607 607

FT CARBOHYD 612 612

FT CARBOHYD 621 621

FT CARBOHYD 633 633

FT CARBOHYD 812 812

SO SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

Query Match

Best Local Similarity 94.4%; Score 187; DB 1; Length 852;

Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

	Query March	100.0%	Score 198:	DB 1,	length 855;
	Best Local Similarity	100.0%;	Pred.	No. 2e-16;	
	Matches 36;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.
OY	1 YTNITYTLLEBSQNOOEKNEDELLDLKWASIAMNF	36			
db	637 YTNITYTLLEBSQNOOEKNEDELLDLKWASIAMNF	672			

RP SEQUENCE FROM N.A.  
 RX MEDLINE=90347835. PubMed=23849520:  
 RA Cheng-Mayer C., Unitroga M., Tung J.W., Dina D., Levy J.,  
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or  
 RL macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";  
 J. Virol. 64:4390-4398(1990).  
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 DR EMBL: M65024; AAA45072.1; -  
 DR HIV; M38428; ENVSSF162.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR

Query Match 96.0%; Score 190; DB 1; Length 847;  
 Best Local Similarity 94.4%; Pred. 1.8e-15;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC	ENV_HV1J3	ENV_HV1JR	STANDARD:	PRT:	848 AA.
AC	P20871:				
AD	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
CN	ENV.				
OS	Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).				
OC	Viruses; Retroid vltruses; Retroviridae; Lentiviruts.				
OX	NCBI_TaxID=11688;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Koyanagi S., Chen I.S.Y.;				
RL	Submitted (DEC-1988) to the HIV data bank.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way used for commercial purposes and for commercial use by and for commercial				
CC	modified and that statement is not removed.				



Query Match	88.9%	Score 176;	DB 2;	Length 350;
Best Local Similarity	86.1%;	Pred. No. 1.3e-13;		
Matches 31; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0

RESULT 13  
S22000  
envelope protein gp120/gp41 - human immunodeficiency virus type 1

Cross-references: EMBL:X61351  
Superfamily: type E retrovirus env polypeptide

Query Match	88.98;	Score 176;	DB 2;	Length 358;
Best Local Similarity	86.18;	Pred. No. 1.3e-13;		
Matches 31; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0

```
OY      1 YTNVTYTTLTLEESQNOQEKNQEELLELDKMWASLWNWF 36  
       . || : |||||:|||||:|||||:||||| |||||  
Db     140 YTSLTYTLTLESQNOQEKNQEDLLLEDKWDLSLNWVF 175
```

## RESULT 14

a;Status: preliminary  
 a;Molecule type: DNA

```
QY      1 YTNITVLTLEESQNOQEKNEQELLELDKWSLWNMF 36
          ||:||||:|||||||:||||||| |||||
Db     140 YTSIIYLTLEESQNOQEKNEQDLELDKWSLWNMF 175
```

RESULT 15  
S33985

Query Match	88.9%;	Score 176;	DB 2;	Length 85;
Best Local Similarity	86.1%;	Pred. No. 3.4e-13;		
Matches	31;	Conservative	4;	Mismatches 1;
				Indels 0;
				Gaps 0

```
QY      1 YNTNITYLTLEESQNQGEKNEQEELLELDKWASLNNWF   36  
        ||::|:||||| | | | | | | | | | | | |  
Db    633 YTSLIHSLSLEESQNQGEKNEQEELLELDKWASLNNWF   66
```

```
Search completed: May 16, 2003, 11:25:05
Job time : 12.1446 secs
```

A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match 92.4%; Score 183; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 1.8e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 36  
DB 139 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 174

RESULT 8  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
A:Variety: isolate 28  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
C:Accession: S21998; S70425  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by phylogenetic analysis  
A:Reference number: S21990  
A:Accession: S21998  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1136940  
A:Accession: S70425  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-222, 'X', 224-358 <STE2>  
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
C:Superfamily: type E retrovirus env polyprotein

Query Match 91.9%; Score 182; DB 2; Length 358;  
Best Local Similarity 88.9%; Pred. No. 2.4e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 36  
DB 140 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 175

RESULT 9

S21998  
polyprotein P - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polyprotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Guille, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015  
A>Note: this virus was isolated from the mother's sexual partner

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Product: transmembrane #status predicted <TMN>

F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: CA

Query Match 90.9%; Score 180; DB 2; Length 443;  
Best Local Similarity 88.9%; Pred. No. 5.3e-14;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 36  
DB 378 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 413

RESULT 10  
VCLJ3W

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WM01)

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997

C:Accession: A24774

R:Starck, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,

Cell 45, 637-648, 1986

A:Title: Identification and characterization of conserved and variable regions in the

A:Reference number: A24774; MUID:86218077; PMID:2423250

A:Accession: A24774

A:Molecule type: DNA

A:Residues: 1-856 <STA>

A:Cross-references: GB:K03455; GB:M38432; NID:91906382

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-501/Product: coat protein gp120 #status predicted <GP1>

F:502-847/Product: coat protein gp41 #status predicted <GP2>

F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,

Query Match 90.9%; Score 180; DB 1; Length 856;  
Best Local Similarity 88.9%; Pred. No. 1.1e-13;  
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 36  
DB 638 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 673

RESULT 11  
S22006

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: S70420; S22006

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70420

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191

A:Experimental source: patient 1

A>Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 88.9%; Score 176; DB 2; Length 357;  
Best Local Similarity 86.1%; Pred. No. 1.3e-13;  
Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 36  
DB 139 YTNNTYTLLEESONQOEKNEDELLEDKWASLWNNF 174

RESULT 12  
S22002



GenCore version 5.1.4-p5\_4578  
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# OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-3

Perfect score: 198

Sequence: 1 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	855	1 VCLJA2	env polypeptide pr
2	185	93.4	847	2 T09448	env polypeptide pr
3	185	93.4	847	2 S13289	env polypeptide pr
4	185	93.4	861	1 VCLJSC	env polypeptide pr
5	184	92.9	357	2 S21994	env polypeptide pr
6	184	92.9	357	2 S21996	env polypeptide pr
7	183	92.4	357	2 S21992	env polypeptide pr
8	180	91.9	358	2 S21998	env polypeptide pr
9	180	90.9	443	2 C41621	env polypeptide pr
10	180	90.9	856	1 VCLJ3W	env polypeptide pr
11	176	88.9	357	2 S22006	env polypeptide pr
12	176	88.9	358	2 S22002	env polypeptide pr
13	176	88.9	358	2 S22000	env polypeptide pr
14	176	88.9	358	2 S70417	env polypeptide pr
15	176	88.9	851	2 S33985	env polypeptide pr
16	176	88.9	854	2 S13288	env polypeptide pr
17	176	88.9	856	1 VCLJ3J	env polypeptide pr
18	176	88.9	861	1 VCLJ3I	env polypeptide pr
19	173	87.4	859	1 VCLJ3N	env polypeptide pr
20	172	86.9	357	2 S22004	env polypeptide pr
21	172	86.9	445	2 A41621	env polypeptide pr
22	172	86.9	853	1 H44001	env polypeptide pr
23	172	86.9	853	1 S54384	env polypeptide pr
24	172	86.9	855	1 VCLJ3R	env polypeptide pr
25	170	85.9	454	2 B41621	env polypeptide pr
26	170	85.9	729	1 VCLJ3X	env polypeptide pr
27	170	85.9	852	1 VCLJ3B	env polypeptide pr
28	170	85.9	861	1 VCLJ3B	env polypeptide pr
29	169	85.4	852	2 T12016	env polypeptide pr

30	167	84.3	846	1 VCLJND	env polypeptide pr
31	167	84.3	856	1 VCLJVL	env polypeptide pr
32	167	84.3	868	1 VCLJHL	env polypeptide pr
33	166	83.8	859	2 T01672	env polypeptide pr
34	162	81.8	136	2 J00266	env polypeptide pr
35	162	81.8	136	2 J00954	env polypeptide pr
36	156	78.8	854	1 VCLJST	env polypeptide pr
37	150	75.8	856	1 A44963	env polypeptide pr
38	146	73.7	357	2 S21990	env polypeptide pr
39	133	67.2	877	2 S49197	env polypeptide pr
40	124	62.6	863	2 A53034	env polypeptide pr
41	87	43.9	881	1 VCLJG3	env polypeptide pr
42	87	43.9	881	2 S03068	env polypeptide pr
43	87	43.9	889	1 VCLJG5	env polypeptide pr
44	86	43.4	151	2 S30448	env polypeptide pr
45	86	43.4	151	2 S30452	env polypeptide pr

## ALIGNMENTS

RESULT 1  
VCLJA2  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
N:Alternate names: coat polypeptide  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <S>  
A:Cross-references: GB:K02007; NID:G328658; PIDN:AA59882.1; PID:G328666  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,  
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0% Score 198; DB 1; Length 855;  
Best Local Similarity 100.0%; Pred. No. 7.9e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 36  
DB 637 YTNITITLLEESQNOEKNEDELLELDKWSLMMNF 672  
RESULT 2  
T09448  
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z16673  
A:Accession: T09448  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:G1465777; PID:G1465781  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide

AC AAY89136;

XX 23-MAY-2000 (first entry)

DT Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA;

XX Query Match 97.0%; Score 191; DB 21; Length 36;

XX Best Local Similarity 97.2%; Pred. No. 3e-17;  
 XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLDKWASLWNF 36  
 II |  
 DB 1 YTSLSHSLEESONQOEKNEDELLDKWASLWNF 36

Search completed: May 16, 2003, 11:12:04  
 Job time : 32.4578 secs

XX Sequence 36 AA;  
SQ  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 13  
AAV8729  
ID AAV8729 standard; peptide; 36 AA.  
XX  
AC AAV8729;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
OS Core polypeptide fragment T No. 84.  
XX  
PN Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN WO9595615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
DR WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
PS Disclosure; Page 22; 124pp; English.  
XX  
CC The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAV8651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.  
XX  
SQ Sequence 36 AA;  
QY  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLSILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 14  
AAV89135  
ID AAV89135 standard; peptide; 36 AA.  
XX  
AC AAV89135;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 573.  
XX  
DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN WO9595615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
DR WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
PS Disclosure; Page 30; 124pp; English.  
XX  
CC The invention relates to hybrid polypeptides comprising enhancer peptide  
CC sequence linked to core polypeptides. The enhancer polypeptides are  
CC derived from various retroviral envelope (gp41) protein sequences,  
CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
CC pharmacokinetic properties such as increasing the half-life of any core  
CC polypeptide that they are linked to. The core polypeptides are any  
CC polypeptide that may be introduced into a living system and that can  
CC function as a pharmacologically useful peptide for the treatment or  
CC prevention of a disease. The core polypeptides are bioactive peptides  
CC selected from a growth factor, cytokine, differentiation factor,  
CC interleukin, interferon, colony stimulating factor, hormone or  
CC angiogenic factor. The peptides of the invention can be used for  
CC inhibiting viral infection and can be used in anti-viral and  
CC anti-fusogenic treatments. Sequences AAV8651-Y90055 represent core  
CC polypeptide fragments that can be used in the invention. Some sequences  
CC among those indicated also comprise enhancer fragments at terminal ends  
CC and form hybrid polypeptides.  
XX  
SQ Sequence 36 AA;  
QY  
Query Match 97.0%; Score 191; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSLSILHSILIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 15  
AAV89136  
ID AAV89136 standard; peptide; 36 AA.  
XX

XX SQ Sequence 36 AA: 97.0%; Score 191; DB 21; Length 36;  
 Query Match Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNNF 36  
 |||  
 DB 1 YTSILHSLEESQNOQEKNEDELLELDKWSLWNNF 36

RESULT 11  
 AAB14533 standard; peptide: 36 AA.  
 AC AAB14533;  
 XX  
 DT 24-NOV-2000 (first entry)

XX HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).  
 KM HIV-1; gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KM envelope glycoprotein; prophylaxis; therapy.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200040616-A1.  
 PD 13-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000WO-US00456.  
 PR 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 PA (WILD/) WILD C T.  
 PA (WEISS/) WEISS C D.  
 PI Wild CT, Weiss CD;  
 DR WPI; 2000-465959/40.  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -  
 PS Claim 13; Page 12; 97pp; English.

XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralising antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp4 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.

XX Sequence 36 AA: 97.0%; Score 191; DB 21; Length 36;  
 Query Match Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNNF 36  
 |||  
 DB 1 YTSILHSLEESQNOQEKNEDELLELDKWSLWNNF 36

RESULT 12  
 AAY88665 standard; peptide: 36 AA.  
 ID AAY88665;  
 AC AAY88665;  
 XX  
 DT 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 20.  
 DE  
 XX  
 KM Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9959615-A1.  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 PR 20-MAY-1998; 98US-0082279.  
 PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI; 2000-136792/12.  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure: Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-V90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 24; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 97.0%; Score 191; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWNF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide: 36 AA.  
XX AAB52688;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #66.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX PI formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX KM chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PN partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 12; Page 25; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 97.0%; Score 191; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLWNF 36  
DB 1 YTSLSHSLEESQNOQEKNEQELLELDKWSLWNF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide: 36 AA.  
XX AAB52818;  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #97.  
XX PA Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX PI formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX KM chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO20006622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM.  
XX DR WPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 14; Page 40; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

## RESULT 6

AAV31955

ID AAV31955 standard; Peptide: 36 AA.

XX AAV31955;

XX 21-DEC-1999 (first entry)

XX Synthetic peptide T-20 (DP-178).

XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.

XX Synthetic.

XX Human immunodeficiency virus type 1.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

XX Modified-site 36 /note= "C-terminal amide"

XX WO9948513-A1.

XX 30-SEP-1999.

XX 22-MAR-1999; 99WO-US06230.

XX 23-MAR-1998; 98US-0045920.

XX 01-MAY-1998; 98US-0071877.

XX (TRIM-) TRIMERIS INC.

XX Kang M, Bray B, Lichty M, Mader C, Merutka G;

XX WPI: 1999-591038/50.

XX Methods of peptide synthesis, particularly used to produce T-20 or

XX T-20 like peptides

XX Claim 1; Page 102; 120pp; English.

XX The present sequence represents an N- and C-terminal modified

XX peptide, designated T-20 (or DP-178), corresponding to amino acids

XX 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.

XX The invention relates to methods for the synthesis of peptides,

XX in particular T-20 and T-20-like peptides. The method involves

XX synthesizing specific side-chain protected peptide fragment

XX intermediates of T-20 or a T-20-like peptide on a solid support,

XX coupling the protected fragments in solution to form a protected

XX T-20 or T-20-like peptide, followed by deprotection of the side

XX chains to yield the final T-20 or T-20-like peptide. The invention

XX also relates to individual peptide fragments (see AAV31956-73) which

XX act as intermediates in the synthesis of peptides of interest (e.g.

XX T-20), and to particular groups of peptide fragments which act as

XX intermediates in the synthesis of the peptide of interest. The

XX method allows for the large scale, economical production of high

XX purity peptides.

XX Sequence 36 AA:

XX Query Match 97.0%; Score 191; DB 20; Length 36;

XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;

XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 YTGILHSILIESQNOQEKNEQLELIDKWSLWNMF 36

XX 1 YTSLSHSILIESQNOQEKNEQLELIDKWSLWNMF 36

## RESULT 7

AAV31974

ID AAV31974 standard; Peptide: 36 AA.

XX AAV31974;

XX 21-DEC-1999 (first entry)

XX HIV-1 LAI gp41 T-20 peptide.

XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.

XX Human immunodeficiency virus type 1.

XX WO9948513-A1.

XX 30-SEP-1999.

XX 22-MAR-1999; 99WO-US06230.

XX 23-MAR-1998; 98US-0045920.

XX 01-MAY-1998; 98US-0071877.

XX (TRIM-) TRIMERIS INC.

XX Kang M, Bray B, Lichty M, Mader C, Merutka G;

XX WPI: 1999-591038/50.

XX Methods of peptide synthesis, particularly used to produce T-20 or

XX T-20 like peptides

XX Disclosure; Page 9; 120pp; English.

XX The present sequence represents a peptide, designated T-20 (or

XX DP-178), that corresponds to amino acids 638-673 of the

XX transmembrane protein gp41 of HIV-1 LAI isolate. The invention

XX relates to methods for the synthesis of peptides, in particular

XX C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.

XX The method involves synthesizing specific side-chain protected

XX peptide fragment intermediates (see AAV31956-73) of T-20 or a

XX T-20-like peptide on a solid support, coupling the protected

XX fragments in solution to form a protected T-20 or T-20-like peptide,

XX followed by deprotection of the side chains to yield the final T-20

XX or T-20-like peptide. The invention also relates to individual

XX peptide fragments which act as intermediates in the synthesis of

XX peptides of interest (e.g. T-20), and to particular groups of

XX peptide fragments which act as intermediates in the synthesis of

XX the peptide of interest. The method allows for the large scale,

XX economical production of high purity peptides.

XX Sequence 36 AA:

XX Query Match 97.0%; Score 191; DB 20; Length 36;

XX Best Local Similarity 97.2%; Pred. No. 3e-17; 1; Indels 0; Gaps 0;

XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 1 YTGILHSILIESQNOQEKNEQLELIDKWSLWNMF 36

XX 1 YTSLSHSILIESQNOQEKNEQLELIDKWSLWNMF 36

## RESULT 8

AAB52655

ID AAB52655 standard; Peptide: 36 AA.

XX AAB52655;

XX 23-FEB-2001 (first entry)

XX T20/DP178 peptide fragment #33.

XX Antiinflammatory: T20/DP178; gp41 ectodomain; HIV-1 fusion;

XX formyl peptide receptor family; FPR; inflammatory response up-regulation;

XX Chemotractant.

RESULT 4  
AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
AC AAV22912;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
KM HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F WO9820036-A1.  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI; 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 233-234; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA;  
XX  
Query Match 97.0%; Score 191; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5  
AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
AC AAV22805;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
KM HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F WO9820036-A1.  
PD 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
XX  
DR WPI; 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure; Page 143-144; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA;  
XX  
Query Match 97.0%; Score 191; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PA (UYDU-) UNIV DUKE.  
 XX  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Pellewey SR, Wild CT;  
 XX  
 XX WPI: 1995-036105/05.  
 DR  
 XX  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PI HIV transmission  
 XX  
 XX Claim 11; Page 132; 182pp; English.  
 PS  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibits transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX Sequence 36 AA;  
 SQ

Query Match 97.0%; Score 191; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YTSLHSLEESQNOEKNEDELLELDKWSLWNMF 36

# RESULT 2

AAR98398  
 ID AAR98398 standard; peptide; 36 AA.  
 XX  
 XX AAR98398;  
 AC  
 XX  
 XX 17-FEB-1997 (first entry)  
 DT  
 XX  
 XX DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
 DE  
 XX  
 XX Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALLMORT5; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM influenza virus; hepatitis B virus.  
 XX  
 XX Human immunodeficiency virus type 1.

XX W09619495-A1.  
 PN  
 XX  
 XX 27-JUN-1996.  
 PD  
 XX  
 XX 20-DEC-1995; 95WO-US16733.  
 PF  
 XX  
 XX 06-JUN-1995; 95US-0470896.  
 PR  
 XX 20-DEC-1994; 94US-0360107.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PA (UYDU-) UNIV DUKE.  
 PI  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Pellewey SR, Wild CT;  
 XX  
 XX WPI: 1996-309517/31.  
 DR  
 XX  
 XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMORT5, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 XX Disclosure; Fig 1; 471pp; English.  
 XX

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMORT5,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.

XX Sequence 36 AA;  
 SQ

Query Match 97.0%; Score 191; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YTSLHSLEESQNOEKNEDELLELDKWSLWNMF 36

# RESULT 3

AAW17011  
 ID AAW17011 standard; peptide; 36 AA.  
 XX  
 XX AAW17011;  
 AC  
 XX  
 XX 30-JUN-1997 (first entry)  
 DT  
 XX  
 XX HIV-1 derived peptide useful for treatment of HIV infection.  
 DE  
 XX  
 XX HIV, STV: human; simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 XX  
 XX Human immunodeficiency virus type 1 LAI isolate.  
 OS  
 XX  
 XX W09640191-A1.  
 PN  
 XX  
 XX 19-DEC-1996.  
 PD  
 XX  
 XX 06-JUN-1996; 96WO-US09499.  
 PF  
 XX  
 XX 07-JUN-1995; 95US-0481957.  
 PR  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Johnson RM, Lambert DM;  
 PI  
 XX WPI: 1997-099886/09.  
 DR  
 XX  
 XX Compns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 PT  
 XX  
 XX Claim 2; Figure 1; 84pp; English.  
 PS  
 XX  
 XX AAW17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.

XX Sequence 36 AA;  
 SQ

Query Match 97.0%; Score 191; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 3e-17;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEDELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 1 YTSLHSLEESQNOEKNEDELLELDKWSLWNMF 36

GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197  
Sequence: 1 YTGILHSLEESNQOEKNEDELIDKASLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	191	97.0	36	DP-178 derived firo
2	191	97.0	36	DP178 corresponds
3	191	97.0	36	HIV-1 derived pept
4	191	97.0	36	SEQ ID NO. 108 firo
5	191	97.0	36	SEQ ID NO. 1 from
6	191	97.0	36	Synthetic peptide
7	191	97.0	36	HIV-1 LAI gp41 T-2
8	191	97.0	36	T20/DP178 peptide
9	191	97.0	36	T20/DP178 peptide
10	191	97.0	36	T20/DP178 peptide

11	191	97.0	36	AA14533	HIV-1 isolate LAI
12	191	97.0	36	AA18865	Core polypeptide f
13	191	97.0	36	AA188729	Core polypeptide f
14	191	97.0	36	AA189135	Core polypeptide f
15	191	97.0	36	AA189136	Core polypeptide f
16	191	97.0	36	AA189242	Core polypeptide f
17	191	97.0	36	AA189424	Core polypeptide f
18	191	97.0	36	AA189692	Core polypeptide f
19	191	97.0	36	AA189735	Core polypeptide f
20	191	97.0	36	AA189777	Core polypeptide f
21	191	97.0	36	AA189982	Core polypeptide f
22	191	97.0	36	AA189983	Core polypeptide f
23	191	97.0	36	AA189999	Core polypeptide f
24	191	97.0	36	AA190033	Core polypeptide f
25	191	97.0	36	AA190179	HIV viral envelope
26	191	97.0	36	AA190741	HXB2 transmembrane
27	191	97.0	36	AA192961	Anti-HIV peptide T
28	191	97.0	36	AA192961	HIV-1 gp41 peptide
29	191	97.0	36	AA192961	HIV-1 gp41 peptide
30	191	97.0	36	AA192961	Biotin-labeled HI
31	191	97.0	36	AA192961	Viral DP178/107-11
32	191	97.0	36	AA192961	Viral DP178/107-11
33	191	97.0	36	AA192961	Viral DP178/107-11
34	191	97.0	36	AA192961	Viral DP178/107-11
35	191	97.0	36	AA192961	RSV F1 protein DPL
36	191	97.0	36	AA192961	Viral DP178/107-11
37	191	97.0	36	AA192961	Viral DP178/107-11
38	191	97.0	36	AA192961	Viral DP178/107-11
39	191	97.0	36	AA192961	Viral DP178/107-11
40	191	97.0	36	AA192961	Viral DP178/107-11
41	191	97.0	36	AA192961	Fluorescein-labeled
42	191	97.0	36	AA192961	Viral DP178/107-11
43	191	97.0	36	AA192961	Viral DP178/107-11
44	191	97.0	36	AA192961	Viral DP178/107-11
45	191	97.0	36	AA192961	HIV-1 gp41 DP178 p

#### ALIGNMENTS

RESULT 1	
ID	AA14533
XX	AA14533 standard: Peptide: 36 AA.
AC	AA14533:
AC	24-AUG-1995 (first entry)
DT	DP-178 derived from HIV-1 isolate LAI has antiviral activity.
XX	
DE	antiviral activity: DP-178; DP-107; diagnostic; HIV-1LAI;
KW	human immunodeficiency virus; transmembrane protein; gp41;
KW	alpha helix; leucine zipper; DP-185.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site
FT	Location/Qualifiers
FT	1 /note="optionally has an amino, acetyl,
FT	9-Fluorenylmethoxy-carbonyl, hydrophobic or,
FT	macromolecular carrier gp. attached"
FT	Modified-site
FT	38 /note="optionally has a carboxyl, amido, hydrophobic
FT	or macromolecular carrier gp. attached"
XX	
XX	MO9428920-A.
PN	22-DEC-1994.
XX	
PD	07-JUN-1994;
XX	94MO-US05739.
PF	07-JUN-1994;
XX	93US-0073028.
PR	
XX	

; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 100.0%; Score 179; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. NO. 3.8e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHSLIEESQKQKNEQELLELDKWSLWNWF 33  
|||||  
Db 147 LIHSLIEESQKQKNEQELLELDKWSLWNWF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPKE, HEINRICH  
; APPLICANT: BUDDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

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Best Local Similarity 100.0%; Pred. NO. 4.2e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHSLIEESQKQKNEQELLELDKWSLWNWF 33  
|||||  
Db 169 LIHSLIEESQKQKNEQELLELDKWSLWNWF 201

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Job time : 15.4458 secs

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env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Burger, H.; Weiss, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:9328631; PIDN:AB03792.1; PID:9555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
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Best Local Similarity 97.2%; Pred. No. 3,3e-15;
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YQ 1 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 36
|||||
VCLJIV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hodson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
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C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
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Best Local Similarity 97.2%; Pred. No. 3,4e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 643 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 678
YQ 1 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 36
|||||
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
```

```
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiss, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:9328631; PIDN:AB03792.1; PID:9555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
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F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
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F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
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Best Local Similarity 91.7%; Pred. No. 1,9e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
DB 378 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 413
YQ 1 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 36
|||||
VCLJVL
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Wuesting, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
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A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
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F:31-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
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F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 94.4%; Score 184; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 4e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 638 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 672
YQ 1 YTSIHSLSIESONQOEKNEDELLEDKWASLNMWF 35
|||||
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
```

C:Accession: A24774  
 R:Starch, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M3432; NID:g1906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GPI>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 94.4%; Score 184; DB 1; Length 856;  
 Best local similarity 91.7%; Pred. No. 4e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||:::|||||  
 Db 638 YTSILYTLIEESONQOEKNEDELLELDKWSLWNMF 673

RESULT 8  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #extl\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 94.4%; Score 184; DB 1; Length 861;  
 Best local similarity 91.7%; Pred. No. 4e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||:::|||||  
 Db 643 YTSILYTLIEESONQOEKNEDELLELDKWSLWNMF 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.8%; Score 181; DB 2; Length 357;  
 Best local similarity 88.9%; Pred. No. 3.4e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||:::|||||  
 Db 139 YTSILYTLIEESONQOEKNEDELLELDKWSLWNMF 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222, 'X', 224-358 <STE2>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.8%; Score 181; DB 2; Length 358;  
 Best local similarity 88.9%; Pred. No. 3.4e-14;  
 Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||:::|||||  
 Db 140 YTSILYTLIEESONQOEKNEDELLELDKWSLWNMF 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #extl\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: Submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypotein

Query Match 92.3%; Score 180; DB 2; Length 357;  
Best Local Similarity 88.9%; Pred. No. 4.5e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
|||:::|||||  
DB 139 YTGILYTLIEESONQOEKNEQELLELDKWSLWNMF 174

#### RESULT 12

env polypotein glycoprotein - human immunodeficiency virus type 1 (strain JFL)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Paro, S.; Vinters, H.V.; Akash, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,  
submitted to the EMBL Data Library, July 1996  
Reference number: Z16673  
Accession: T09448  
Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.8%; Score 179; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 1.6e-13;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
|||:::|||||  
DB 629 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 664

#### RESULT 13

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
Accession: S13289  
Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 91.8%; Score 179; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 1.6e-13;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
|||:::|||||  
DB 629 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 664

#### RESULT 14

A41621

env polypotein M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: A41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621  
A:Molecule type: DNA  
A:Residues: 1-445 <BUR>  
A:Cross-references: GB:M77228; NID:g328627; PIDN:AAB03790.1; PID:g555013  
A:Note: this virus was isolated from the mother  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-253/Product: coat protein gp120 (fragment) #status predicted <GPI>  
F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:426-445/Dominant: transmembrane #status predicted <TMN>  
F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 90.3%; Score 176; DB 2; Length 445;  
Best Local Similarity 86.1%; Pred. No. 1.7e-13;  
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
|||:::|||||  
DB 380 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 415

#### RESULT 15

VCLJAZ

env polypotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:g328658; PIDN:AAB59882.1; PID:g328666  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Dominant: signal sequence #status predicted <SIG>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TMN>  
F:87,129,140,158,184,190,200,244,265,297,298,304,334,341,358,364,388,394,400,408,445,  
F:610,624,636,815/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 90.3%; Score 176; DB 1; Length 855;  
Best Local Similarity 86.1%; Pred. No. 3.6e-13;  
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
|||:::|||||  
DB 637 YTSIYTLIEESONQOEKNEQELLELDKWSLWNMF 672

Search completed: May 16, 2003, 11:25:10  
Job time: 13.1446 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match          99.0%; Score 193; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSIHSLSIESONOQKNEQLELDKWSLWNMF 36
Db 633 YTSIHSLSIESONOQKNEQLELDKWSLWNMF 668

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RESULT 2
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_Taxid=11678;
NCBI_Taxid=11678;
RN (1)
  RP MEDLINE=8511123; PubMed=2578615;
  RA Rafter L., Haseltine R., Pataraia R., Livak K.J., Starcich B.R.,
  RA Josephs S.F., Dorian E.R., Rafalski J.A., Whitehorn E.A.,
  RA Baumeister K., Ivanoff L., Peteway S.R., Jr., Pearson M.L.,
  RA Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C.,
  RA Wong-Staal F.;
  RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
  RL Nature 313:277-284(1985).
RN (2)
  RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
  RX MEDLINE=90285159; PubMed=2355006;
  RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
  RA Gregory T.J.;
  RT "Assignment of intrachain disulfide bonds and characterization of
  potential glycosylation sites of the type 1 recombinant human
  immunodeficiency virus envelope glycoprotein (gp120) expressed in
  Chinese hamster ovary cells."
  RL J. Biol. Chem. 265:10373-10382(1990).
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CC EMBL: M15654; AAA44205.1;
CC PIR: A03973; VCLH13.
CC HIV: M15654; ENV5BH102.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
  Signal.
KW SIGNAL.
FT 1 30
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
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FT CARBOHYD 230 230
FT CARBOHYD 241 241
FT CARBOHYD 262 262
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FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
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FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BF61A18931BB27 CRC64;

```

```

Query Match          99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSIHSLSIESONOQKNEQLELDKWSLWNMF 36
Db 638 YTSIHSLSIESONOQKNEQLELDKWSLWNMF 673

```

```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; O09779;

```



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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
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FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SO SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

```

```

Query Match          99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSIHSLSIESQNOEKNEDELLEDKWASLWMP 36
    |||:|||||:|||||:|||||:|||||:|||||
Db 638 YSLHSLSIESQNOEKNEDELLEDKWASLWMP 673

```

```

RESULT 5
ENV_HV1LM STANDARD: PRT: 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
US Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC -----
CC EMBL: 012055; AAA76690.1;
CC DR GAYCSUITEB; Q70626;
CC DR Interpro; IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 266 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SO SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match          99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTSIHSLSIESQNOEKNEDELLEDKWASLWMP 36
    |||:|||||:|||||:|||||:|||||:|||||
Db 638 YSLHSLSIESQNOEKNEDELLEDKWASLWMP 673

```

```

RESULT 6
ENV_HV1BR STANDARD: PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

```





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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

DR EMBL: M17450; V: NOT\_ANNOTATED\_CDS.

DR PIR: B28922; V: VCLJ3C.

DR HIV: M17450; ENV:SC.

DR InterPro: IPR000328; Env.GP41.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL. 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 87

FT CARBOHYD 129 129

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

FT CARBOHYD 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

SO SEQUENCE

Query Match 94.4%; Score 184; DB 1; Length 856; Best Local Similarity 91.7%; Pred. No. 6.3e-15; Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQKNEQELLELDKWSILMNF 36  
||||:|||||

Db 638 YTSIHSLSIESQNOQKNEQELLELDKWSILMNF 673

RESULT 10  
ENV\_HV1M1 STANDARD; PRT: 856 AA.  
ID P31872;  
AC 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

DE ENV.

OS Human immunodeficiency virus type 1 (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OC NCBI\_TaxID=31678;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=66218077; PubMed=2423250.

RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS";

RL Cell 45:637-648(1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

CC PIR: A24774; V: VCLJ3W.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW SIGNAL. 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 856 AA; 97526 MW; DB68DLE49C404D93 CRC64;

SO SEQUENCE

Query Match 94.4%; Score 184; DB 1; Length 856; Best Local Similarity 91.7%; Pred. No. 6.3e-15; Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQKNEQELLELDKWSILMNF 36  
||||:|||||

```

Db      638 YTSIYNLIEESQNOGKNEOELLELDKWSLWMP 673
RESULT 11
ENV_HV1W2 STANDARD: PRT; 847 AA.
AC      POS5880;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-NOV-1988 (Rel. 09, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE      glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN      ENV.
OS      Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC      Viruses: Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11705;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86235450; PubMed=3012778;
       Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
       Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks W.P.:
       "Genetic variation in HIV-1/HIV/LAV over time in patients with AIDS or
       at risk for AIDS."
       Science 232:1548-1553(1986).
CC      -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
       BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
       WAS PERINATALLY INFECTED BY HER MOTHER.
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CC      or send an email to license@sib-sib.ch).
-----
CC      EMBL: M12507; AAB12990.1; -.
DR      HIV; M12507; ENV5WJM2.
DR      InterPro: IPR000328; Env_GP41.
DR      InterPro: IPR000777; GP120.
DR      Pfam: PF00516; GP120; 1.
DR      Pfam: PF00517; GP41; 1.
KM      AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
       Signal.
FT      SIGNAL 1 29
FT      CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT      CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.
FT      DISULFID 53 73
FT      DISULFID 118 202 BY SIMILARITY.
FT      DISULFID 125 193 BY SIMILARITY.
FT      DISULFID 130 152 BY SIMILARITY.
FT      DISULFID 215 244 BY SIMILARITY.
FT      DISULFID 225 236 BY SIMILARITY.
FT      DISULFID 293 326 BY SIMILARITY.
FT      DISULFID 372 435 BY SIMILARITY.
FT      DISULFID 379 408 BY SIMILARITY.
FT      CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT      CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE 847 AA; 96466 MW; CDIE33D73AA5BCAE CRC64.

Query Match      93.3%; Score 182; DB 1; Length 847;
Best Local Similarity 94.4%; Pred. No. 1,Je-14;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSIYNLIEESQNOGKNEOELLELDKWSLWMP 36
Db      629 YTSIYNLIEESQNOGKNEOELLELDKWSLWMP 664
RESULT 12
ENV_HV1W3 STANDARD: PRT; 852 AA.
AC      P19549;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE      glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN      ENV.
OS      Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC      Viruses: Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11690;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90317906; PubMed=2370688;
       RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
       "Human immunodeficiency virus type 1 cellular host range,
       replication, and cyclophaticity are linked to the envelope region of
       the viral genome."
       J. Virol. 64:4016-4020(1990).
CC      -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC      BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC      WAS PERINATALLY INFECTED BY HER MOTHER.
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CC      or send an email to license@sib-sib.ch).
-----
CC      EMBL: M38427; AAA45067.1; -.
DR      HIV; M38427; ENV5SF33.
DR      InterPro: IPR000328; Env_GP41.
DR      InterPro: IPR000777; GP120.
DR      Pfam: PF00516; GP120; 1.
DR      Pfam: PF00517; GP41; 1.
KM      AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
       Signal.
FT      SIGNAL 1 31
FT      CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT      CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT      DISULFID 53 73
FT      DISULFID 118 206 BY SIMILARITY.
FT      DISULFID 125 197 BY SIMILARITY.
FT      DISULFID 130 156 BY SIMILARITY.
FT      DISULFID 219 248 BY SIMILARITY.
FT      DISULFID 229 240 BY SIMILARITY.
FT      DISULFID 292 331 BY SIMILARITY.
FT      DISULFID 327 439 BY SIMILARITY.
FT      DISULFID 384 412 BY SIMILARITY.
FT      CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

```



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 -----

DR EMBL: M17451; AAA5057.1; -  
 DR HIV; M17451; ENV58RF.  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL. 1 29  
 FT CHAIN 30 519  
 FT CHAIN 520 865  
 FT DISULFID 53 73  
 FT DISULFID 118 218  
 FT DISULFID 125 209  
 FT DISULFID 130 157  
 FT DISULFID 231 252  
 FT DISULFID 241 252  
 FT DISULFID 309 343  
 FT DISULFID 389 452  
 FT DISULFID 396 425  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 136 136  
 FT CARBOHYD 139 139  
 FT CARBOHYD 156 156  
 FT CARBOHYD 193 193  
 FT CARBOHYD 194 194  
 FT CARBOHYD 197 197  
 FT CARBOHYD 198 198  
 FT CARBOHYD 203 203  
 FT CARBOHYD 210 210  
 FT CARBOHYD 247 247  
 FT CARBOHYD 254 254  
 FT CARBOHYD 275 275  
 FT CARBOHYD 289 289  
 FT CARBOHYD 302 302  
 FT CARBOHYD 308 308  
 FT CARBOHYD 314 314  
 FT CARBOHYD 344 344  
 FT CARBOHYD 351 351  
 FT CARBOHYD 367 367  
 FT CARBOHYD 397 397  
 FT CARBOHYD 403 403  
 FT CARBOHYD 407 407  
 FT CARBOHYD 413 413  
 FT CARBOHYD 418 418  
 FT CARBOHYD 455 455  
 FT CARBOHYD 471 471  
 FT CARBOHYD 620 620  
 FT CARBOHYD 625 625  
 FT CARBOHYD 634 634  
 FT CARBOHYD 646 646  
 FT CARBOHYD 825 825  
 SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADAC CRC64;

Query Match 90.8%; Score 177; DB 1; Length 865;  
 Best Local Similarity 86.1%; Pred. No. 4.6e-14;  
 Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSIHSLEESONQOEKNEQELLEDKVASTLWNP 36  
 DB 647 YTGIIYNLLEESONQOEKNEQELLEDKVASTLWNP 682

RESULT 15  
 ID ENV\_HVJ3 STANDARD; PRT; 867 AA.  
 AC P12489;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (H3 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11694;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352108; Pubmed=2669897;  
 RA Komiya N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.,  
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of  
 RT HIV-1 and their expression in bacteria."  
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).  
 CC -----  
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 -----  
 DR EMBL: M21138; AAB03526.1; -  
 DR HIV; M21138; ENV58J3.  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KM Signal.  
 FT SIGNAL. 1 30  
 FT CHAIN 31 516  
 FT CHAIN 517 867  
 FT DISULFID 53 73  
 FT DISULFID 118 217  
 FT DISULFID 125 208  
 FT DISULFID 130 160  
 FT DISULFID 230 259  
 FT DISULFID 240 251  
 FT DISULFID 308 342  
 FT DISULFID 388 457  
 FT DISULFID 395 430  
 FT CARBOHYD 87 87  
 FT CARBOHYD 135 135  
 FT CARBOHYD 140 140  
 FT CARBOHYD 143 143  
 FT CARBOHYD 159 159  
 FT CARBOHYD 163 163  
 FT CARBOHYD 168 168  
 FT CARBOHYD 189 189  
 FT CARBOHYD 199 199  
 FT CARBOHYD 209 209  
 FT CARBOHYD 246 246  
 FT CARBOHYD 253 253  
 FT CARBOHYD 274 274  
 FT CARBOHYD 288 288  
 FT CARBOHYD 307 307  
 FT CARBOHYD 350 350  
 FT CARBOHYD 366 366  
 FT CARBOHYD 372 372  
 FT CARBOHYD 396 396  
 FT CARBOHYD 402 402  
 FT CARBOHYD 408 408  
 FT CARBOHYD 412 412  
 FT CARBOHYD 418 418  
 FT CARBOHYD 423 423

FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA: 98399 MW; 5F2310146B8E8680 CRC64;

Query Match 90.8%; Score 177; DB 1; Length 867;  
 Best Local Similarity 88.9%; Pred. No. 4,6e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSIHSLIESQNOQEKNEQELLDDKWSLWNF 36  
 |||:|:||||| ||||| ||||| |||||  
 Db 649 YTSIYTLIESQNOQEKNEQELLGLDKWASLWNF 684

Search completed: May 16, 2003, 11:13:36  
 Job time : 7.07229 secs



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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-536  
Perfect score: 195  
Sequence: 1 YTSIHSLIEESONQOEKNEDELLEDKWASLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	645	15	09933A6 human immun
2	193	99.0	747	15	070607 human immun
3	193	99.0	748	15	070606 human immun
4	193	99.0	752	15	070604 human immun
5	193	99.0	752	15	070605 human immun
6	193	99.0	752	15	070608 human immun
7	193	99.0	851	15	078243 human immun
8	193	99.0	852	15	089797 human immun
9	193	99.0	854	15	085582 human immun
10	193	99.0	856	15	072502 human immun
11	193	99.0	856	15	092877 simian-huma
12	193	99.0	856	15	074599 human immun
13	193	99.0	856	15	074090 human immun
14	189	96.9	838	15	003806 human immun
15	189	96.9	854	15	090178 human immun
16	189	96.9	854	15	078705 human immun

17	189	96.9	854	15	078225 human immun
18	189	96.9	855	15	003805 human immun
19	188	96.4	856	15	0905M7 human immun
20	187	95.9	616	15	0993B0 human immun
21	187	95.9	618	15	0993B2 human immun
22	187	95.9	757	15	090722 human immun
23	187	95.9	848	15	069990 human immun
24	186	95.4	123	15	09YXR3 human immun
25	185	94.9	122	15	0901W0 human immun
26	184	94.4	42	15	069910 human immun
27	184	94.4	443	15	080023 human immun
28	184	94.4	841	15	041556 human immun
29	184	94.4	849	15	077368 human immun
30	184	94.4	849	15	080851 human immun
31	184	94.4	851	15	056110 human immun
32	184	94.4	851	15	080852 human immun
33	184	94.4	856	15	072993 human immun
34	184	94.4	856	15	041539 human immun
35	184	94.4	857	15	080170 human immun
36	184	94.4	858	15	080190 human immun
37	184	94.4	858	15	080188 human immun
38	184	94.4	859	15	080185 human immun
39	184	94.4	859	15	080180 human immun
40	184	94.4	859	15	080179 human immun
41	184	94.4	859	15	080177 human immun
42	184	94.4	859	15	080173 human immun
43	184	94.4	859	15	080850 human immun
44	184	94.4	862	15	080184 human immun
45	184	94.4	862	15	080183 human immun

## ALIGNMENTS

## RESULT 1

09933A6 PRELIMINARY; PRT; 645 AA.  
ID 09933A6;  
AC 09933A6;  
DT 01-JUN-2001 (TREMREL. 17, Created)  
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M., White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4 T cell epitope hotspots to exposed strands of HIV envelope glycoprotein suggests structural influences on antigen processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env\_GPA1.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide; Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 99.0%; Score 193; DB 15; Length 645;

Best Local Similarity 97.2%; Pred. No. 4e-15; Mismatches 0; Indels 0; Gaps 0;

09 1 YTSIHSLIEESONQOEKNEDELLEDKWASLWMP 36  
DB 607 YTSIHSLIEESONQOEKNEDELLEDKWASLWMP 642

```
RESULT 2
ID 070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
EN Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12034; AAA76669.1;
  InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64:

Query Match 99.0%; Score 193; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESONOEKNEQELLEDKWASLWNMF 36
DB 633 YTSLSHSLSIESONOEKNEQELLEDKWASLWNMF 668

RESULT 3
ID 070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
EN Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12032; AAA76668.1;
  InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64:
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DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C676948 CRC64:

Query Match 99.0%; Score 193; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESONOEKNEQELLEDKWASLWNMF 36
DB 634 YTSLSHSLSIESONOEKNEQELLEDKWASLWNMF 669

RESULT 4
ID 070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
EN Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE-95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HTLV type IIIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
  Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA76665.1;
  InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64:

Query Match 99.0%; Score 193; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 4.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESONOEKNEQELLEDKWASLWNMF 36
DB 638 YTSLSHSLSIESONOEKNEQELLEDKWASLWNMF 673

RESULT 5
ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
EN Envelope glycoprotein (Fragment).
CN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 SQ NON\_TER 752 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 36  
 DB 638 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT: 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 SQ NON\_TER 752 752  
 SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 36  
 DB 638 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 673

DB 638 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT: 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CAAT7628.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B97E98027 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 5.3e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 36  
 DB 633 YTSIIHSLIESONOQEKNEQELLELDKWSLWNF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT: 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

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RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW90-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12053; AAA76685.1; -
DR EMBL: U12036; AAA76671.1; -
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;
KW Transmembrane.
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;

Query Match          99.0%; Score 193; DB 15; Length 852;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 36
|||||
634 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 669

RESULT 9
ID 085582; PRELIMINARY; PRT; 854 AA.
AC 085582;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RT J. Virol. 59:284-291(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Buckler C.E.;
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92219406; PubMed=1373204;
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T
RT lymphocytes.";
RT J. Virol. 66:3151-3154(1992).
DR EMBL: M19921; AAA44992.1; -
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match          99.0%; Score 193; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 36
|||||
DB 636 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 671

RESULT 10
ID 072502; PRELIMINARY; PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ENV polypotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
RT from primary virus cultures using the polymerase chain reaction.";
RT J. Virol. 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
RT retrovirus in human and nonhuman cells transfected with an infectious
RT molecular clone.";
RT J. Virol. 59:284-291(1986).
DR EMBL: U26942; AAB60578.1; -
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match          99.0%; Score 193; DB 15; Length 854;
Best Local Similarity 97.2%; Pred. No. 5.3e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 36
|||||
DB 636 YTSIIHSLIEESONOEKNEQELLELDKWSLWNMF 671

RESULT 11
ID 092877; PRELIMINARY; PRT; 856 AA.
AC 092877;
DT 01-NOV-1996 (TREMBLrel. 08, Created)
DT 01-NOV-1996 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99098984; PubMed=9882298;

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RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodiroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodiroski J.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SO SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;  
 Query Match 99.0%; Score 193; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 5.3e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNF 673  
 RESULT 12  
 ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates";  
 RL Virology 174:103-116(1990).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RA Iwatai Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SO SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;  
 Query Match 99.0%; Score 193; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 5.3e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNF 673  
 RESULT 13  
 074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates";  
 RL Virology 174:103-116(1990).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatai Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SO SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;  
 Query Match 99.0%; Score 193; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 5.3e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTSIHSLSIESQNOEKNEDELLELDKWSLWNF 36  
 Db 638 YTSLSHSLSIESQNOEKNEDELLELDKWSLWNF 673  
 RESULT 14  
 ID 003806 PRELIMINARY; PRT; 838 AA.  
 AC 003806;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Reitz M., Popovic M., Gartner S., Gallo R., Reed-Connole E.,  
 RA Beaver B.;  
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: M68894; AAA44196.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
 SO SIGNAL 1  
 FT CHAIN ? 493 EXTERIOR MEMBRANE GLYCOPROTEIN (GP120)  
 FT (BY SIMILARITY).  
 FT CHAIN 494 838 (BY SIMILARITY).  
 FT TRANSMEMBRANE GLYCOPROTEIN (GP41)  
 FT (BY SIMILARITY).  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 216 BY SIMILARITY.  
 FT DISULFID 125 184 BY SIMILARITY.  
 FT DISULFID 130 145 BY SIMILARITY.  
 FT DISULFID 206 235 BY SIMILARITY.

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FT DISULFID 216 227 BY SIMILARITY.
FT DISULFID 284 318 BY SIMILARITY.
FT DISULFID 364 427 BY SIMILARITY.
FT DISULFID 371 400 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 619 619 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 798 798 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 838 AA; 95328 MW; 1104B1CA10CFB4D CRC64;
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Query Match 96.9%; Score 189; DB 15; Length 838;
Best Local Similarity 97.2%; Pred. No. 1.6e-14;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 620 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 655
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OS 090178 PRELIMINARY; PRT; 854 AA.
AC 090178;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
ENVELOPE glycoprotein.
ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95074930; PubMed=7983770;
RA Fang H., Pincus S.H.;
RT "Unique insertion sequence and pattern of CD4 expression in variants
RT selected with immunotoxins from human immunodeficiency virus type 1-
RT infected T cells";
RT J. Virol. 69:75-81(1995).
RL [2]
RN SEQUENCE FROM N.A.
RP Fang H., Pincus S.H.;
RT "Spontaneous activation of human immunodeficiency virus type 1 in an
RT immunotoxin-resistant variant T cell line";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070521; AAC28452.1;
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
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KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;
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Query Match 96.9%; Score 189; DB 15; Length 854;
Best Local Similarity 94.4%; Pred. No. 1.6e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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DB 636 YTSIHSLSIESQNOEKNQELLEDKWSLWNP 671
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Job time: 27.3124 secs
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GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-536  
Perfect score: 195  
Sequence: 1 YTSIHSLIESQNOQEKNEQELLELDKASIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 10%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	1 US-08-073-028-1	Sequence 1, Appli
2	193	99.0	36	3 US-08-486-099-1	Sequence 1, Appli
3	193	99.0	36	3 US-09-071-877-1	Sequence 1, Appli
4	193	99.0	36	3 US-08-360-107A-1	Sequence 1, Appli
5	193	99.0	36	3 US-08-484-223B-1	Sequence 1, Appli
6	193	99.0	36	3 US-08-919-597-1	Sequence 1, Appli
7	193	99.0	36	3 US-08-475-668A-1	Sequence 1, Appli
8	193	99.0	36	3 US-08-485-551A-1	Sequence 1, Appli
9	193	99.0	36	3 US-08-471-913A-1	Sequence 1, Appli
10	193	99.0	36	4 US-08-554-616-1	Sequence 1, Appli
11	193	99.0	36	4 US-08-485-264A-1	Sequence 1, Appli
12	193	99.0	36	4 US-09-082-279B-15	Sequence 15, Appli
13	193	99.0	36	4 US-09-082-279B-497	Sequence 497, App
14	193	99.0	36	4 US-09-082-279B-498	Sequence 498, App
15	193	99.0	36	4 US-09-082-279B-603	Sequence 603, App
16	193	99.0	36	4 US-09-082-279B-630	Sequence 630, App
17	193	99.0	36	4 US-09-082-279B-631	Sequence 631, App
18	193	99.0	36	4 US-09-082-279B-705	Sequence 705, App
19	193	99.0	36	4 US-09-082-279B-834	Sequence 834, App
20	193	99.0	36	4 US-09-082-279B-1076	Sequence 1076, Ap
21	193	99.0	36	4 US-09-082-279B-1121	Sequence 1121, Ap
22	193	99.0	36	4 US-08-965-056-1	Sequence 1161, Ap
23	193	99.0	36	4 US-08-965-056-108	Sequence 108, App
24	193	99.0	36	4 US-09-045-920-1	Sequence 1, Appli
25	193	99.0	36	4 US-08-474-349A-1	Sequence 399, App
26	193	99.0	36	4 US-08-474-349A-399	Sequence 399, App
27	193	99.0	36	4 US-08-474-349A-399	Sequence 399, App

28	193	99.0	36	4 US-08-474-349A-413	Sequence 413, App
29	193	99.0	36	4 US-09-315-304B-15	Sequence 15, Appl
30	193	99.0	36	4 US-09-315-304B-497	Sequence 497, App
31	193	99.0	36	4 US-09-315-304B-498	Sequence 498, App
32	193	99.0	36	4 US-09-315-304B-603	Sequence 603, App
33	193	99.0	36	4 US-09-315-304B-630	Sequence 631, App
34	193	99.0	36	4 US-09-315-304B-705	Sequence 705, App
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36	193	99.0	36	4 US-09-315-304B-1076	Sequence 1076, Ap
37	193	99.0	36	4 US-09-315-304B-1121	Sequence 1121, Ap
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39	193	99.0	36	4 US-09-315-304B-1469	Sequence 1469, Ap
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42	193	99.0	36	4 US-08-255-208A-1	Sequence 1, Appli
43	193	99.0	37	4 US-08-082-279B-771	Sequence 771, App
44	193	99.0	37	4 US-09-082-279B-775	Sequence 775, App
45	193	99.0	37	4 US-09-082-279B-775	Sequence 775, App

ALIGNMENTS

RESULT 1  
US-08-073-028-1  
Sequence 1, Application US/08073028  
Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennle & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1  
Query Match 99.0%; Score 193; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 YTSIHSLIESQNOQEKNEQELLELDKASIMNMF 36  
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Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Mathews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Choi

APPLICANT: Bray, Brian

APPLICANT: Lichey, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Marutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

US-09-071-877-1

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Mathews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 7,1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTSIHSLIESQNOEKNEDELLELDKWSLWNF 36

RESULT 5  
US-08-484-223B-1

Sequence 1, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIESQNOEKNEDELLELDKWSLWNF 36  
Db 1 YTSIHSLIESQNOEKNEDELLELDKWSLWNF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIESQNOEKNEDELLELDKWSLWNF 36  
Db 1 YTSIHSLIESQNOEKNEDELLELDKWSLWNF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6080065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475.668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
98-475-668A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelletway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485.551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelletway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471.913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.1e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36  
DB 1 YTSIHSLIEESQNOQEKNEQELLELDKWSLWNNF 36

```
RESULT 10
US-08-554-616-1
: Sequence 1, Application US/08554616
: Patent No. 6133418
: GENERAL INFORMATION:
: APPLICANT: Bolognesi, Dani P.
: APPLICANT: Matthews, Thomas J.
: APPLICANT: Wild, Carl T.
: TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
: TITLE OF INVENTION: TRANSMISSION
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/554,616
: FILING DATE: 06-NOV-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/073,028
: FILING DATE: 07-JUN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7872-004-999
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-8864/9741
: TELETYPE: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
US-08-554-616-1
: Query Match 99.0%; Score 193; DB 4; Length 36;
: Best Local Similarity 97.2%; Pred. No. 7.1e-18;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOQEKNEQELLEDKWASLWNF 36
Db 1 YTSLSHSLSIESQNOQEKNEQELLEDKWASLWNF 36

RESULT 11
US-08-485-264A-1
: Sequence 1, Application US/08485264A
: Patent No. 6228983
: GENERAL INFORMATION:
: APPLICANT: Bolognesi, Dani P.
: APPLICANT: Matthews, Thomas J.
: APPLICANT: Wild, Carl T.
: APPLICANT: Barney, Shawn O.
: APPLICANT: Lambert, Dennis M.
: APPLICANT: Pellew, Stephen R.
: APPLICANT: Langlois, Alphonse J.
: TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
: TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
: TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
: NUMBER OF SEQUENCES: 232
```

```
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036-2711.
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,264A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7872-021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELETYPE: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 36 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
US-08-485-264A-1
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```
Query Match 99.0%; Score 193; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 7.1e-18;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOQEKNEQELLEDKWASLWNF 36
Db 1 YTSLSHSLSIESQNOQEKNEQELLEDKWASLWNF 36
```

```
RESULT 12
US-09-082-279B-15
: Sequence 15, Application US/09082279B
: Patent No. 6258782
: GENERAL INFORMATION:
: APPLICANT: Barney, Shawn
: APPLICANT: Guthrie, Kelly
: APPLICANT: Merutka, Gene
: APPLICANT: Anwer, Mohamed
: APPLICANT: Lambert, Dennis
: TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
: TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
: FILE REFERENCE: 7872-043
: CURRENT APPLICATION NUMBER: US/09/082,279B
: CURRENT FILING DATE: 1998-05-20
: NUMBER OF SEQ ID NOS: 1515
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 36
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Core polypeptide
US-09-082-279B-15
```

```
Query Match 99.0%; Score 193; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 7.1e-18;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSIHSLSIESQNOQEKNEQELLEDKWASLWNF 36
|||||
```

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNMF 36

## RESULT 13

Sequence 497, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNMF 36

RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNMF 36

RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 99.0%; Score 193; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 7.1e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHSLSIESQNOOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:13

Job time: 11.1928 secs



NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||:|||||  
DB 1 YTSLSHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1

Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||:|||||  
DB 1 YTSLSHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

LT 4  
9-796-202-10

Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||:|||||  
DB 1 YTSLSHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||:|||||  
DB 1 YTSLSHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 6

US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON-GUN  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||:|||||  
DB 1 YTSLSHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

```

RESULT 7
US-09-854-816-1
; Sequence 1, Application US/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 99.0%; Score 193; DB 10; Length 36;
Best Local Similarity 97.2%; Pred. No. 1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-09-854-816-108
; Sequence 108, Application US/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-09-854-816-108
Query Match 99.0%; Score 193; DB 10; Length 36;
Best Local Similarity 97.2%; Pred. No. 1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-09-848-616-176
; Sequence 176, Application US/09848616
; Publication No. US20030054010A1
GENERAL INFORMATION:
APPLICANT: Sebbel, Peter
Dunant, Nicolas
APPLICANT: Bachmann, Martin
Tissot, Alain
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700, 0180002
CURRENT APPLICATION NUMBER: US/09/848,616
CURRENT FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 176
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DP176c peptide
US-09-848-616-176
Query Match 99.0%; Score 193; DB 9; Length 37;
Best Local Similarity 97.2%; Pred. No. 1.1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

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```
Db      2 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 37
RESULT 10
US-09-779-451-41
: Sequence 41, Application US/09779451
: Patent No. US20020094521A1
: GENERAL INFORMATION:
: APPLICANT: Wild, Carl T.
: APPLICANT: Allaway, Graham P.
: TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
: FILE REFERENCE: 1900.0300003
: CURRENT FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 60/235,901
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/181,543
: PRIOR FILING DATE: 2000-02-10
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: PatentIn version 3.0
: ID NO 41
: LENGTH: 46
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-41
Query Match          99.0%; Score 193; DB 10; Length 46;
Best Local Similarity 97.2%; Pred. No. 1.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YTSIHSLSIESQNOQEKNEQELLELDKWSIWMNF 36
Db      11 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 46
RESULT 11
US-09-779-451-4
: Sequence 4, Application US/09779451
: Patent No. US20020094521A1
: GENERAL INFORMATION:
: APPLICANT: Wild, Carl T.
: APPLICANT: Allaway, Graham P.
: TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
: FILE REFERENCE: 1900.0300003
: CURRENT APPLICATION NUMBER: US/09/779,451
: CURRENT FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 60/235,901
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/181,543
: PRIOR FILING DATE: 2000-02-10
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 4
: LENGTH: 56
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4
Query Match          99.0%; Score 193; DB 10; Length 56;
Best Local Similarity 97.2%; Pred. No. 1.6e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YTSIHSLSIESQNOQEKNEQELLELDKWSIWMNF 36
Db      16 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 51
RESULT 12
US-10-040-349B-2
: Sequence 2, Application US/10040349B
: Publication No. US20030082521A1
: GENERAL INFORMATION:
: APPLICANT: Brasseur, Robert

Db      2 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 37
: APPLICANT: Charlotiaux, Benoit
: APPLICANT: Chevalier, Michel
: APPLICANT: El Habib, Raphaelle
: APPLICANT: Krell, Tino
: TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
: FILE REFERENCE: 01-078-A
: CURRENT APPLICATION NUMBER: US/10/040,349B
: CURRENT FILING DATE: 2002-07-09
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 177
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: (1)..(177)
: OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2
Query Match          99.0%; Score 193; DB 9; Length 177;
Best Local Similarity 97.2%; Pred. No. 5.5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YTSIHSLSIESQNOQEKNEQELLELDKWSIWMNF 36
Db      104 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 139
RESULT 13
US-10-059-271-84
: Sequence 84, Application US/10059271
: Publication No. US20030082208A1
: GENERAL INFORMATION:
: APPLICANT: REPKE, HEINRICH
: APPLICANT: BUDDÉ, ECKHARD
: APPLICANT: NICOLAUS, STEFAN
: TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
: FILE REFERENCE: ALBRE-22
: CURRENT APPLICATION NUMBER: US/10/059,271
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: DE 101 06 295
: PRIOR FILING DATE: 2001-02-02
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 84
: LENGTH: 221
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-10-059-271-84
Query Match          99.0%; Score 193; DB 9; Length 221;
Best Local Similarity 97.2%; Pred. No. 7e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YTSIHSLSIESQNOQEKNEQELLELDKWSIWMNF 36
Db      131 YTSLIHSLIESQNOQEKNEQELLELDKWSIWMNF 166
RESULT 14
US-10-059-271-81
: Sequence 81, Application US/10059271
: Publication No. US20030082208A1
: GENERAL INFORMATION:
: APPLICANT: REPKE, HEINRICH
: APPLICANT: BUDDÉ, ECKHARD
: APPLICANT: NICOLAUS, STEFAN
: TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
```

; TITLE OF INVENTION: BEING IMMOBILIZED  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 81  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 99.0%; Score 193; DB 9; Length 232;  
Best Local Similarity 97.2%; Pred. No. 7.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIIHSLIEESONQOEKNEQELLELDKASLWNMF 36  
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Db 144 YTSIIHSLIEESONQOEKNEQELLELDKASLWNMF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPEKE, HEINRICH  
; APPLICANT: BUDD, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 99.0%; Score 193; DB 9; Length 254;  
Best Local Similarity 97.2%; Pred. No. 8.1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSIIHSLIEESONQOEKNEQELLELDKASLWNMF 36  
|||:|||||  
Db 166 YTSIIHSLIEESONQOEKNEQELLELDKASLWNMF 201

Search completed: May 16, 2003, 12:10:25  
Job time : 16.759 secs



GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLYSLIESQNOQEKNEQLRLDKWASLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A.GeneSeq.101002.\*
- 1: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT.\*
  - 2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT.\*
  - 3: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT.\*
  - 4: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT.\*
  - 5: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT.\*
  - 6: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT.\*
  - 7: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT.\*
  - 8: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT.\*
  - 9: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT.\*
  - 10: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT.\*
  - 11: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT.\*
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  - 15: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT.\*
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  - 22: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*
  - 23: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	100.0	36	22	ABR00638
2	194	100.0	36	22	ABR02115
3	194	100.0	36	22	AAU13186
4	194	100.0	36	22	AAU13186
5	194	100.0	36	22	AAU13186
6	194	100.0	36	22	AAU13186
7	192	99.0	268	23	AAU13186
8	192	99.0	268	23	AAU13186
9	192	99.0	268	23	AAU13186
10	192	99.0	268	23	AAU13186

11	191	98.5	233	19	AAV22854	SEQ ID NO. 50 from
12	191	98.5	233	23	ABG68325	Envelope protein g
13	191	98.5	268	19	AAV22813	SEQ ID NO. 9 from
14	191	98.5	268	23	ABG68284	Envelope protein g
15	191	98.5	269	19	AAV22816	SEQ ID NO. 12 from
16	191	98.5	269	23	ABG68287	Envelope protein g
17	191	98.5	284	10	AAU94507	Sequence encoded b
18	191	98.5	855	19	AAU43069	HIV-1 gp120 protei
19	190	97.9	269	19	AAV22850	SEQ ID NO. 46 from
20	190	97.9	269	23	ABG68321	Envelope protein g
21	189	97.4	36	16	AAU64364	DP-178 derived fro
22	189	97.4	36	17	AAU98398	DP178 corresponds
23	189	97.4	36	18	AAU17011	HIV-1 derived pept
24	189	97.4	36	19	AAV22912	SEQ ID NO. 108 fro
25	189	97.4	36	19	AAV22805	SEQ ID NO. 1 from
26	189	97.4	36	20	AAV31974	Synthetic peptide
27	189	97.4	36	20	AAV31974	HIV-1 LAI gp11 T-2
28	189	97.4	36	21	AAU52655	T20/DP178 peptide
29	189	97.4	36	21	AAU52658	T20/DP178 peptide
30	189	97.4	36	21	AAU52618	HIV-1 isolate LAI
31	189	97.4	36	21	AAU14533	Core polypeptide f
32	189	97.4	36	21	AAU86655	Core polypeptide f
33	189	97.4	36	21	AAU86729	Core polypeptide f
34	189	97.4	36	21	AAU89135	Core polypeptide f
35	189	97.4	36	21	AAU89136	Core polypeptide f
36	189	97.4	36	21	AAU89242	Core polypeptide f
37	189	97.4	36	21	AAU89424	Core polypeptide f
38	189	97.4	36	21	AAU89692	Core polypeptide f
39	189	97.4	36	21	AAU89735	Core polypeptide f
40	189	97.4	36	21	AAU89777	Core polypeptide f
41	189	97.4	36	21	AAU89882	Core polypeptide f
42	189	97.4	36	21	AAU89983	Core polypeptide f
43	189	97.4	36	21	AAU89983	Core polypeptide f
44	189	97.4	36	22	AAU70179	HIV viral envelope
45	189	97.4	36	22	AAU70741	HX2 transmembrane

ALIGNMENTS

RESULT 1	ABR00638	standard; Peptide; 36 AA.
ID	ABR00638	
AC	ABR00638	
DT	03-JAN-2002	(first entry)
DE	Viral DP178/107-like region peptide T720.	
XX	Human immunodeficiency virus: HIV; respiratory syncytial virus: RSV;	
KW	virulence: heptad repeat region; transmembrane protein; gp11; HRL; HR2;	
KW	infection.	
XX	Viridiae.	
OS		
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	1
FT	Modified-site	/note="N-terminal is substituted by ac"
FT	Modified-site	/note="C-terminal amide"
PN	WO200164013-A2.	
PD	07-SEP-2001.	
XX		
XX	07-FEB-2001; 2001WO-US03988.	
XX		
XX	29-FEB-2000; 2000US-0515965.	
XX		
XX	(TRIM-) TRIMERIS INC.	
XX		
XX	Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;	



CC anti-fusogenic, antiviral or intracellular modulatory activity. The  
 CC DP178-1like/DP107-1like peptides are useful to inhibit human and non-human  
 CC retroviral, particularly HIV, transmission to uninfected cells. The  
 CC present sequence represents one of the DP178-1like/DP107-1like peptides  
 CC of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 194; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||  
 DB 1 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 4  
 AAB77633

AAB77633 standard; Peptide; 36 AA.

XX AAB77633;

DT 19-APR-2001 (first entry)

XX Core polypeptide T720.

XX Core polypeptide; enhancer; antiviral; anti-HIV;  
 KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 KM coiled-coil peptide interaction; fusion-related disorder;  
 KM bacterial infection; viral infection.

XX Unidentified.

OS WO200103723-A1.

XX 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US18772.

XX 09-JUL-1999; 99US-0350641.

XX (TRIM-) TRIMERIS INC.

PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

PI WPI: 2001-147136/15.

DR New hybrid polypeptide, useful for preventing, treating and diagnosing  
 XX e.g. viral infections, comprises an enhancer peptide linked to a core  
 XX polypeptide -  
 XX Disclosure: Page 44; 151pp; English.

XX The present sequence is a core polypeptide which may be linked to  
 CC an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of  
 CC the core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving  
 CC treated-coil peptide interactions. Other uses include preventing,  
 CC treating and/or diagnosing disorders involving fusion events (e.g.  
 CC modulation of neurotransmitter exchange and sperm-egg fusion),  
 CC intracellular processes involving coiled-coil peptides (e.g. bacterial  
 CC infections) and viral infections that involve cell-cell and/or  
 CC virus-cell fusion (e.g. viral infections caused by human  
 CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 CC The enhancer peptide sequence increases the half-life and reduces the  
 CC clearance rate of therapeutic peptides, which increases their efficacy  
 CC and minimises the incidence and severity of adverse side effects.  
 CC In addition, this increases the sensitivity of the diagnostic procedure

CC In which they are used.

XX Sequence 36 AA;

Query Match 100.0%; Score 194; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||  
 DB 1 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 5  
 AAR67724

ID AAR67724 standard; Protein; 850 AA.

XX AAR67724;

DT 07-SEP-1995 (first entry)

XX gp120 from the HIV GNE8 isolate.

XX HIV; human immunodeficiency virus; gp120; glycoprotein;

XX GNE clone; GNE8 isolate.

XX Human immunodeficiency virus type 1.

PN WO9428929-A.

XX 22-DEC-1994.

XX 07-JUN-1994; 94WO-US06036.

XX 07-JUN-1993; 93US-0072833.

XX (GETH ) GENENTECH INC.

XX Berman PW, Nakamura GR;

XX WPI: 1995-036112/05.

XX N-PSDB; AAO76018.

PT Use of HIV gp 120 polypeptide(s) - for developing probes for the  
 PT analysis, prevention and therapy of HIV infection  
 XX Claim 23; Page 27-30; 108pp; English.

XX This protein is the gp120 (envelope glycoprotein) from the GNE8 isolate  
 CC of HIV-1 (human immunodeficiency virus type 1). There are neutralising  
 CC epitopes in the V2 and C4 domains of gp120, in addition to the  
 CC neutralising epitopes in the V3 domain. Although the amino acid sequences  
 CC of the neutralising epitopes in the V2, V4 and C4 domains are variable,  
 CC the amount of variation is highly constrained. This facilitates the  
 CC design of HIV subunit vaccines that can induce antibodies that neutralise  
 CC the most common HIV strains for a given geographic region. This invention  
 CC provides a multivalent gp120 subunit vaccine where the gp120 present in  
 CC the vaccine is from at least two HIV isolates which have different amino  
 CC acid sequences for a neutralising epitope in these regions.

XX Sequence 850 AA;

Query Match 100.0%; Score 194; DB 16; Length 850;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 36  
 |||  
 DB 632 YTSLSYSLIEESONQOEKNEDELLELDKWSLWNMF 667

RESULT 6  
 AAT22817

ID AAY22817 standard; Protein: 268 AA.  
 XX AAY22817;  
 AC  
 XX  
 DT 19-AUG-1999 (first entry)  
 DE  
 XX SEQ ID NO. 13 from W09820036.  
 XX  
 DE HIV; gp41 protein: constrained helical peptide; HIV infection;  
 XX vaccine; antibody: viral membrane fusion; viral infectivity;  
 XX ligand affinity purification; protein A replacement;  
 KM immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PN W09820036-A1.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 05-NOV-1997: 97WO-US20069.  
 XX  
 PR 16-JUN-1997: 97US-0876698.  
 XX 06-NOV-1996: 96US-0743698.  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovassnik MA;  
 PI Wells JA;  
 XX  
 DR WPI: 1998-286866/25.  
 XX  
 XX Production of constrained helical peptide(s) by linking side chains  
 PT on termi of octa:peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 PS  
 PS Claim 11; Page 152-153; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the invention. The constrained helical  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 XX  
 SQ Sequence 268 AA:  
 XX  
 Query Match 99.0%; Score 192; DB 19; Length 268;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSIYSLIESGNOOEKNEQELLEDKQASLWNNF 36  
 DB 168 YTSLSIYSLIESGNOOEKNEQELLEDKQASLWNNF 203  
 RESULT 7  
 ABG68288

ID ABG68288 standard; Protein: 268 AA.  
 XX ABG68288;  
 AC  
 XX  
 DT 07-OCT-2002 (first entry)  
 DE  
 XX Envelope protein gp41 from HIV clade B strain #7.  
 XX  
 DE HIV; glycoprotein: gp41; antigen; helical conformation;  
 XX virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 XX viral envelope protein; vaccine; virucide; anti-HIV.  
 XX  
 OS Human immunodeficiency virus type 1 clade B.  
 XX  
 PN US6271198-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 05-NOV-1997: 97US-0965056.  
 XX  
 PR 16-JUN-1997: 97US-049787P.  
 XX 06-NOV-1996: 96US-0743698.  
 PR 16-JUN-1997: 97US-0876698.  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovassnik MA;  
 PI Wells JA;  
 XX  
 DR WPI: 2002-487624/52.  
 XX  
 XX New cyclic peptides from human immune deficiency virus gp41, useful for  
 PT treatment or prevention of HIV infection, are constrained to have  
 PT alpha-helical conformation  
 PT  
 PS  
 PS Disclosure: Column 147-150; 175pp; English.  
 XX  
 CC The invention relates to cyclic peptides (A) with a constrained helical  
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope  
 CC protein) of human immunodeficiency virus (HIV). The cyclic  
 CC peptides have formulas given in the specification part of which are  
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
 CC C, D, E or O. The peptides are used to cause induction of a specific  
 CC immune response, resulting in antibodies that prevent virus-induced  
 CC membrane fusion. The peptides are used to treat subjects with, or at risk  
 CC of, HIV infection, either as antilution/anti-infection agents or,  
 CC preferably where associated with a carrier, as an immunogen (including as  
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
 CC cases of health care accidents. The peptides can be based on specific HIV  
 CC strains, e.g. breakthrough isolates of HIV that have developed during  
 CC vaccine trials, so a combination of them should cover a wide range of  
 CC protection. The present sequence is gp41 protein from a particular  
 CC HIV clade used to derive a consensus sequence of gp41.  
 CC  
 XX  
 SQ Sequence 268 AA:  
 XX  
 Query Match 99.0%; Score 192; DB 23; Length 268;  
 Best Local Similarity 97.2%; Pred. No. 4.7e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSIYSLIESGNOOEKNEQELLEDKQASLWNNF 36  
 DB 168 YTSLSIYSLIESGNOOEKNEQELLEDKQASLWNNF 203  
 RESULT 8  
 AAR14905  
 ID AAR14905 standard; Protein: 855 AA.  
 XX  
 AC AAR14905;  
 XX

DT 17-DEC-2001 (updated)  
 DT 05-FEB-1992 (first entry)  
 XX  
 DE HIV-1 BA-L clone-encoded env protein.  
 XX  
 KW human immunodeficiency virus; United States; MN isolate; AIDS;  
 KW viral envelope protein.  
 XX  
 OS Human immunodeficiency virus-1;  
 XX  
 PN USN7599491-N.  
 XX  
 PD 15-OCT-1991.  
 XX  
 PF 17-OCT-1990; 90US-0183830.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 XX  
 PA (USSH ) NAT INST OF HEALTH.  
 XX  
 PS Reitz M;  
 XX  
 DR WPI: 1991-346752/47.  
 DR N-PSDB; AAQ14753.  
 XX  
 PT US HIV-1 isolates MN-ST1 and BA-L, ENV protein and DNA - are  
 PT useful in therapeutics, vaccines and diagnostic tests  
 XX  
 PS Example 3; Fig 9; 61pp; English.  
 XX  
 CC A HindIII fragment of unintegrated viral DNA representing the HIV-1  
 CC (BA-L) genome was cloned by standard techniques into lambda phage  
 CC Charon 28 DNA from total DNA of peripheral blood macrophages  
 CC infected with and producing HIV-1 (BA-L). A positive clone was  
 CC selected by hybridisation using a HIV-1 envelope probe. This clone,  
 CC designated BA-L1, contained the entire env gene. The insert was  
 CC subcloned and sequenced and the amino acid sequence deduced from  
 CC it.  
 CC (Note: Revised entry submitted to correct the patent number format of  
 CC US Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpl/updates/ntis-us.html](http://www.derwent.com/dwpl/updates/ntis-us.html).)  
 CC  
 SQ Sequence 855 AA;  
 XX  
 Query Match 99.0%; Score 192; DB 12; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 YTSIYSLIESQNOEKNEQELLEDKWSLWMP 36  
 |||:|||||  
 636 YTSIYSLIESQNOEKNEQELLEDKWSLWMP 671  
 XX  
 RESULT 9  
 AAW11581  
 ID AAW11581 standard; Protein; 855 AA.  
 XX  
 AC AAW11581;  
 XX  
 DT 25-MAR-1997 (first entry)  
 XX  
 DE Human Immunodeficiency Virus-1 strain BA-L envelope protein.  
 XX  
 KW Acquired immune deficiency syndrome; AIDS; envelope protein;  
 KW env gene; vaccine.  
 XX  
 OS Human immunodeficiency virus type 1 (strain BA-L).  
 XX  
 PN US5576000-A.  
 XX  
 PD 19-NOV-1996.  
 XX

PF 17-OCT-1990; 90US-0599491.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 PR 25-FEB-1993; 93US-0022835.  
 PR 15-FEB-1993; 95US-0388809.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX  
 DR WPI: 1997-011206/01.  
 DR N-PSDB; AAT58551.  
 XX  
 PT New isolated envelope protein of HIV-1 strain BA-L and recombinant  
 PT equivalents - useful as immunogens for vaccines and antibody prodn.,  
 PT typical of US clinical isolates  
 XX  
 PS Claim 1; Fig 9; 86pp; English.  
 XX  
 CC A HindIII fragment of unintegrated viral DNA representing the BA-L  
 CC genome was cloned into lambda phage Charon 28 DNA from total DNA of  
 CC peripheral blood lymphocytes infected with and producing HIV-1(BA-L).  
 CC A positive clone was selected by hybridisation using a HIV-1 env  
 CC probe. This clone, designated BA-L1, was found to contain the  
 CC entire gene for the envelope protein on a 2.8 kb HindIII-XbaI  
 CC fragment and a 0.4 kb EcoRI-HindIII fragment. When cloned together  
 CC these fragments comprise the env gene, as well as the coding regions  
 CC for rev and the rev-responsive element of env, both necessary for  
 CC efficient expression in eukaryotic cells. The claimed recombinantly  
 CC produced envelope protein can be used as an immunogen for raising  
 CC antibodies against HIV.  
 CC  
 SQ Sequence 855 AA;  
 XX  
 Query Match 99.0%; Score 192; DB 18; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 YTSIYSLIESQNOEKNEQELLEDKWSLWMP 36  
 |||:|||||  
 636 YTSIYSLIESQNOEKNEQELLEDKWSLWMP 671  
 XX  
 RESULT 10  
 AAW88113  
 ID AAW88113 standard; Protein; 855 AA.  
 XX  
 AC AAW88113;  
 XX  
 DT 09-APR-1999 (first entry)  
 XX  
 DE Env protein of the BA-L strain of Human immunodeficiency virus type 1.  
 XX  
 KW HIV-1; HIV-1 strain BA-L; env protein; vaccine;  
 KW immunotherapy; HIV infection; immunogen; HIV-1 diagnosis.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 11  
 FT /note= "Gln encoded by CG"  
 XX  
 PD 09-FEB-1999.  
 XX  
 PF 14-MAY-1996; 96US-0647714.  
 XX  
 PR 17-OCT-1990; 90US-0599491.  
 PR 25-FEB-1993; 93US-0022835.  
 PR 15-FEB-1995; 95US-0388809.  
 PR 14-MAY-1996; 96US-0647714.  
 XX

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA Franchini G, Gallo RC, Gartner S, Lori FC, Markham PD;  
 PI Popovic M, Reitz MS;  
 XX WPI: 1999-152779/13.  
 DR N-PSDB; AAX04767.  
 PT DNA encoding env protein of the human immune deficiency virus  
 PT isolate BA-L - useful for producing protein for use in vaccines, as  
 PT assay reagent and to generate antibodies  
 PS Example 1; Fig 9A-C; 87pp; English.  
 CC The present sequence represents the envelope protein of the BA-L  
 CC (ATCC 40880) strain of Human immunodeficiency virus type 1 (HIV-1)  
 CC strain MN-ST1. BA-L is more typical of United States isolates of  
 CC HIV-1 than previously known strains. Recombinant, complete env protein  
 CC of the BA-L strain is used as a vaccine component and for immunotherapy  
 CC of existing HIV infections, to detect HIV-specific antibodies, e.g. in  
 CC donated blood, and as an immunogen to raise specific antibodies, for  
 CC HIV-1 diagnosis.  
 SQ Sequence 855 AA;  
 SQ  
 Query Match 99.0%; Score 192; DB 20; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 1.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLIYSLIEESQNOEKNEOELELDKWSLWMPF 36  
 DB 636 YTSLIYSLIEESQNOEKNEOELELDKWSLWMPF 671  
 RESULT 11  
 AAY22854  
 ID AAY22854 standard; Protein; 233 AA.  
 AC AAY22854;  
 XX  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 50 from WO9820036.  
 KW HIV: gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 OS Human immunodeficiency virus.  
 PN WO9820036-A1.  
 PD 14-MAY-1998.  
 PF 05-NOV-1997; 97WO-US20069.  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 PA (GETH ) GENENTECH INC.  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI: 1998-286866/25.  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection

PS Claim 11; Page 192-193; 279pp; English.  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 SQ Sequence 233 AA;  
 SQ  
 Query Match 98.5%; Score 191; DB 19; Length 233;  
 Best Local Similarity 97.2%; Pred. No. 5.4e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLIYSLIEESQNOEKNEOELELDKWSLWMPF 36  
 DB 168 YTSLIYNLIEESQNOEKNEOELELDKWSLWMPF 203  
 RESULT 12  
 ABG68325  
 ID ABG68325 standard; Protein; 233 AA.  
 AC ABG68325;  
 XX  
 DT 07-OCT-2002 (first entry)  
 DE Envelope protein gp41 from HIV clade B strain #44.  
 KW HIV: glycoprotein; gp41; antigen; helical conformation;  
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 KW viral envelope protein; vaccine; virucide; anti-HIV.  
 OS Human immunodeficiency virus type 1 clade B.  
 PN US6271198-B1.  
 PD 07-AUG-2001.  
 PF 05-NOV-1997; 97US-0965056.  
 PR 16-JUN-1997; 97US-049787P.  
 PR 06-NOV-1996; 96US-0743698.  
 PR 16-JUN-1997; 97US-0876698.  
 PA (GETH ) GENENTECH INC.  
 PI Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI: 2002-487624/52.  
 PT New cyclic peptides from human immune deficiency virus gp41, useful for  
 PT treatment or prevention of HIV infection, are constrained to have  
 PT alpha-helical conformation  
 PS Disclosure; Column 207-208; 175pp; English.

XX The invention relates to cyclic peptides (A) with a constrained helical  
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope  
CC protein) of human immunodeficiency virus (HIV). The cyclic  
CC peptides have formulas given in the specification part of which are  
CC derived from a consensus sequence of gp41 derived from HIV clades A, B,  
CC C, D, E or O. The peptides are used to cause induction of a specific  
CC immune response, resulting in antibodies that prevent virus-induced  
CC membrane fusion. The peptides are used to treat subjects with, or at risk  
CC of, HIV infection, either as antifusion/anti-infection agents or,  
CC preferably where associated with a carrier, as an immunogen (including as  
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or  
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency  
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in  
CC cases of health care accidents. The peptides can be based on specific HIV  
CC strains, e.g. breakthrough isolates of HIV that have developed during  
CC vaccine trials, or a combination of them should cover a wide range of  
CC protection. The present sequence is gp41 protein from a particular  
CC HIV clade used to derive a consensus sequence of gp41.

## Sequence 233 AA:

Query Match 98.5%; Score 191; DB 23; Length 233;  
Best Local Similarity 97.2%; Pred. No. 5.4e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLYSLEESQNOEKNEQELLELDKWSLIMNF 36  
168 YTSLSLYSLEESQNOEKNEQELLELDKWSLIMNF 203

## RESULT 13

AAV22813  
ID AAV22813 standard; Protein; 268 AA.

XX AC AAY22813;

XX DT 19-AUG-1999 (first entry)

XX DE SEQ ID NO. 9 from WO9820036.

XX KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
XX vaccine; antibody; viral membrane fusion; viral infectivity;

XX KM ligand affinity purification; protein A replacement;

XX KW immunoglobulin purification; epitope mimic.

XX OS Human immunodeficiency virus.

XX WO9820036-A1.

XX PD 14-MAY-1998.

XX PE 05-NOV-1997; 97WO-US20069.

XX PR 16-JUN-1997; 97US-0876698.

XX PR 06-NOV-1996; 96US-0743698.

XX PA (GETH ) GENENTECH INC.

XX PI Braisted A, Judice JK, McDowell RS, Phelean JC, Starovasanik MA;  
XX PI Wells JA;

XX DR WPI; 1998-286866/25.

XX PT Production of constrained helical peptide(s) by linking side chains  
XX PT on termini of octa-peptide - derived from human immunodeficiency  
XX PT virus gp41 protein, useful in vaccines for treatment and prevention  
XX PT of infection

XX PS Claim 11; Page 148-149; 279pp; English.

XX CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
XX CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins

CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.

## SQ Sequence 268 AA:

Query Match 98.5%; Score 191; DB 19; Length 268;  
Best Local Similarity 97.2%; Pred. No. 6.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLYSLEESQNOEKNEQELLELDKWSLIMNF 36  
168 YTSLSLYSLEESQNOEKNEQELLELDKWSLIMNF 203

## RESULT 14

ABG68284  
ID ABG68284 standard; Protein; 268 AA.

XX AC ABG68284;

XX DT 07-OCT-2002 (first entry)

XX DE Envelope protein gp41 from HIV clade B strain #3.

XX KW HIV; glycoprotein; gp41; antigen; helical conformation;  
XX virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;

XX KM viral envelope protein; vaccine; virucide; anti-HIV.

XX OS Human immunodeficiency virus type 1 clade B.

XX PN US6271198-B1.

XX PD 07-AUG-2001.

XX PE 05-NOV-1997; 97US-0965056.

XX PR 16-JUN-1997; 97US-049787P.

XX PR 06-NOV-1996; 96US-0743698.

XX PR 16-JUN-1997; 97US-0876698.

XX PA (GETH ) GENENTECH INC.

XX PI Braisted AC, Judice JK, McDowell RS, Phelean JC, Starovasanik MA;  
XX PI Wells JA;

XX DR WPI; 2002-487624/52.

XX PT New cyclic peptides from human immune deficiency virus gp41, useful for  
XX PT treatment or prevention of HIV infection, are constrained to have  
XX PT alpha-helical conformation

XX PS Disclosure; Column 141-142; 175pp; English.

XX CC The invention relates to cyclic peptides (A) with a constrained helical  
XX CC conformation, derived from gp41 (glycoprotein 41, a viral envelope  
XX CC protein) of human immunodeficiency virus (HIV). The cyclic



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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLIYSLIEESONQOEKNEOELLELDKWASLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	98.5	443	2 C41621	env polypeptide p
2	191	98.5	856	1 VCLJ3W	env polypeptide pr
3	191	98.5	861	1 VCLJSC	env polypeptide pr
4	189	97.4	851	2 S33985	env polypeptide -
5	189	97.4	854	2 S13288	env protein - huma
6	189	97.4	856	1 VCLJH3	env polypeptide pr
7	189	97.4	861	1 VCLJLV	env polypeptide pr
8	188	96.9	357	2 S21994	envelope protein g
9	188	96.9	358	2 S21998	envelope protein g
10	187	96.4	357	2 S21996	envelope protein g
11	184	94.8	847	2 T09448	envelope glycoprote
12	184	94.8	847	2 S13289	env protein - huma
13	183	94.3	445	2 A41621	env polypeptide M
14	182	93.8	358	2 S22002	envelope protein g
15	182	93.8	358	2 S22000	envelope protein g
16	182	93.8	358	2 S70417	envelope protein g
17	182	93.8	852	2 T12016	envelope glycoprote
18	181	93.8	859	1 VCLJMN	env polypeptide pr
19	181	93.3	357	2 S22004	envelope protein g
20	181	93.3	855	1 VCLJAL	env polypeptide pr
21	180	92.8	856	1 VCLJVL	env polypeptide pr
22	179	92.3	853	2 S34384	envelope polypepte
23	179	92.3	855	1 VCLJZR	env polypeptide pr
24	178	91.8	357	2 S22006	envelope protein g
25	178	91.8	843	1 H44001	env polypeptide pr
26	177	91.2	846	1 VCLJND	env polypeptide pr
27	175	90.2	357	2 S21992	envelope protein g
28	175	90.2	852	1 VCLJBR	env polypeptide pr
29	173	89.2	729	1 VCLJKB	env polypeptide pr

30	173	89.2	861	1 VCLJKB	env polypeptide pr
31	172	88.7	859	2 T01672	envelope polypepte
32	169	87.1	454	2 B41621	env polypeptide D
33	168	86.6	868	1 VCLJH4	env polypeptide -
34	165	85.1	136	2 J00266	envelope polypepte
35	165	85.1	136	2 J00266	envelope polypepte
36	155	79.9	854	1 VCLJST	env polypeptide pr
37	154	79.4	856	1 A44963	env polypeptide pr
38	152	78.4	357	2 S21990	envelope protein g
39	141	72.7	877	2 S49197	envelope protein p
40	124	63.9	863	2 A53034	gag polypeptide -
41	86	44.3	881	1 VCLJG3	env polypeptide -
42	86	44.3	881	2 S03068	env protein - huma
43	86	44.3	889	1 VCLJG5	env polypeptide -
44	85	43.8	151	2 S30448	env protein - huma
45	85	43.8	151	2 S30452	env protein - huma

## ALIGNMENTS

RESULT 1  
C41621  
env polypeptide p - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polypeptide  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #extl\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Guila, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi  
A:Reference number: M41621; M01D:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AA803792.1; PID:955015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polypeptide  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP2>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:423-443/Domain: transmembrane #status predicted <TMN>  
F:123,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 98.5% Score 191; DB 2; Length 443;  
Best Local Similarity 97.2%; Pred. No. 1,9e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIYSLIEESONQOEKNEOELLELDKWASLWNMF 36  
DB 378 YTSLIYSLIEESONQOEKNEOELLELDKWASLWNMF 413  
RESULT 2  
VCLJ3W  
env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #extl\_change 07-Nov-1997  
C:Accession: A24774  
R:Starckel, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the  
A:Reference number: A24774; M01D:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:91906382  
C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 98.5%; Score 191; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 3,9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 36  
 Db 638 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 673

RESULT 3  
 VCLJSC  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guirgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Staal, Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics: env  
 A:Gene: env

C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-861/Product: env polyprotein #status predicted <EP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,366,396

Query Match 98.5%; Score 191; DB 1; Length 861;  
 Best Local Similarity 97.2%; Pred. No. 3,9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 36  
 Db 643 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 678

ULT 4  
 S33985  
 env polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
 C:Accession: S33985  
 R:Carlini, F.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S33985  
 A:Accession: S33985  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-851 <CAR>  
 A:Cross-References: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 97.4%; Score 189; DB 2; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 6,8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 36  
 Db 633 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 668

RESULT 5  
 S13288  
 env protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C:Accession: S13288  
 R:O'Brien, W.A.; Koyanagi, Y.; Nemasle, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
 A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
 A:Reference number: S13288; MUID:91043044; PMID:2172833  
 A:Accession: S13288  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-854 <OBR>  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 97.4%; Score 189; DB 2; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6,8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 36  
 Db 636 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 671

RESULT 6  
 VCLJH3  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03973  
 R:Ratner, L.; Hesselink, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; D  
 nberger, J.A.; Pappas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
 Nature 313, 277-284, 1985  
 A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
 A:Reference number: A93353; MUID:85111123; PMID:2578615  
 A:Accession: A03973  
 A:Molecule type: DNA  
 A:Residues: 1-856 <RAT>  
 A:Cross-References: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA  
 C:Genetics: env  
 A:Gene: env

C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
 F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,  
 F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status pre

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 6,8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 36  
 Db 638 YTSLSLIEESONQOEKNEDELLELDKMSLWNMF 673

RESULT 7  
 VCLJLV  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03975  
 R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allison, M.  
 Cell 40, 9-17, 1985  
 A:Title: Nucleotide sequence of the AIDS virus, LAV.

1 YTSLIYSLIEESQNOQEKNEQELLELDKWSIWNWF 36  
 |||||:|||||  
 643 YTSLIHSLIEESQNOQEKNEQELLELDKWSIWNWF 678

Query Match	96.9%	Score 188;	DB 2;	Length 357;
Best Local Similarity	94.4%	Pred. No. 33e15;		
Matches	34;	Conservative	2;	Mismatches 0;
				Indels 0;
				Gaps 0;
OY	1	YTSLSYSLIESQNOEKNEQELLELDKWKASIMNMF	36	
		:    :		
Db	139	YTTLLYTLIESQNOEKNEQELLELDKWKASIMNMF	174	

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R:Cross-references: EMBL:X61359; NID:960182; PIDN:CAAA3630.1; PID:960183
R:Steuiler, H.: Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
C:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:11736940
A:Accession: S70425
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
C:Cross-references: EMBL:X61359; NID:960182; PIDN:CAAA3630.1; PID:960183
C:Superfamily: type E retrovirus env polyprotein

Query Match      96.9%: Score 188; DB 2; Length 358;
Best Local Similarity 94.4%: Pred. No. 3,3e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLIYSLEESNQOEKNEDELLELDKWASLMWNF 36
|||||:|||||:|||||:|||||:|||||:|||||:
Db      140 YTSLIYTLIEFSNQOEKNEDELLELDKWASLMWNF 175

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuiler, H.: Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:11736940
A:Accession: S70422
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STR2>
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAAA3624.1; PID:q1067129
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match      96.4%: Score 187; DB 2; Length 357;
Best Local Similarity 94.4%: Pred. No. 4.4e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSLIYSLEESNQOEKNEDELLELDKWASLMWNF 36
|||:|||||:|||||:|||||:|||||:|||||:
Db      139 YTGIIYTLIEFSNQOEKNEDELLELDKWASLMWNF 174

RESULT 11
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.: Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16573
A:Accession: T09448
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match      94.8%: Score 184; DB 2; Length 847;
Best Local Similarity 94.4%: Pred. No. 2.7e-14;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSLIYSLEESNQOEKNEDELLELDKWASLMWNF 36
|||||:|||||:|||||:|||||:|||||:|||||:

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FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAFA6008BA7A08 CRC64;

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Query Match          98.5%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIYSLIEESONOEKNEQELLEDKWASLWNMF 36
DB 638 YTSLIYSLIEESONOEKNEQELLEDKWASLWNMF 673

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RESULT 2
ENV_HV1W1          STANDARD;      PRT;      856 AA.
AC P31672;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=31678;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86218077; PubMed=2423250;
RA Starich B.R., Ham B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
RA Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT Identification and characterization of conserved and variable
RT regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS.
RT Aids.
RL Cell 45:637-648(1986).
CC -I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
DR PIR: A24774; VCLJ3W.
DR InterPro: IPR000328; Env GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
FT SIGNAL 1 29

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FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 205 BY SIMILARITY.
FT DISULFID 125 196 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 444 BY SIMILARITY.
FT DISULFID 383 417 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97526 MW; DB6BD1E49C40ADE9 CRC64;

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Query Match          98.5%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,5e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIYSLIEESONOEKNEQELLEDKWASLWNMF 36
DB 638 YTSLIYSLIEESONOEKNEQELLEDKWASLWNMF 673
RESULT 3
ENV_HV1B8          STANDARD;      PRT;      851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R.,
RA Josephs S.F., Doran E.R., Ratski J.A., Whitehorn E.A.,
RA Bauleister K., Ivanoff L., Peteway S.R., Jr., Pearson M.L.,
RA Laubenderger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RT Nature 313:277-284(1985).
RL Nature 313:277-284(1985).
CC -----
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CC -----  
 DR EMBL: K02011; AAA44661.1; -  
 DR HIV: K02011; ENVSIB8.  
 DR GlycosultedB: P04582; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 30  
 FT CHAIN 31 506  
 FT DISULFID 507 851  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 236 331  
 FT DISULFID 378 440  
 FT DISULFID 385 413  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
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 FT CARBOHYD 366 366  
 FT CARBOHYD 392 392  
 FT CARBOHYD 401 401  
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 FT CARBOHYD 468 468  
 FT CARBOHYD 606 606  
 FT CARBOHYD 611 611  
 FT CARBOHYD 620 620  
 FT CARBOHYD 632 632  
 FT CARBOHYD 669 669  
 FT CARBOHYD 745 745  
 FT CARBOHYD 811 811  
 FT CARBOHYD 851 AA; 96644 MW; D16A3C90857785F1 CRC64;  
 SO SEQUENCE

Query Match 97.4%; Score 189; DB 1; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 1.1e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSEESNOOEKNEDELLEDKWASLWNF 36  
 DB 633 YTSLSLSEESNOOEKNEDELLEDKWASLWNF 668

ENV\_HV1S3 STANDARD: PRT: 852 AA.  
 AC P19549: 01-FEB-1991 (rel. 17, Created)

DT 01-FEB-1991 (rel. 17, last sequence update)  
 DT 16-OCT-2001 (rel. 40, last annotation)  
 DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane  
 DE glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].  
 DE ENV.  
 GN Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).  
 OS Viruses; Retrod viruses; Retroviridae; Lentivirus.  
 OC NCBI\_Taxid=11690;  
 RX MEDLINE=90317906; PubMed=2370688;  
 RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
 RT "Human immunodeficiency virus type 1 cellular host range,  
 RT replication, and cytopathicity are linked to the envelope region of  
 RT the viral genome";  
 RL J. Virol. 64:4016-4020(1990).

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DR EMBL: M38427; AAA45067.1; -  
 DR HIV: M38427; ENVSSE33.  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.

KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 31  
 FT CHAIN 32 506  
 FT DISULFID 507 852  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 156  
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 FT DISULFID 229 240  
 FT DISULFID 297 331  
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 FT DISULFID 384 412  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 142 142  
 FT CARBOHYD 155 155  
 FT CARBOHYD 159 159  
 FT CARBOHYD 188 189  
 FT CARBOHYD 198 198  
 FT CARBOHYD 242 242  
 FT CARBOHYD 263 263  
 FT CARBOHYD 277 277  
 FT CARBOHYD 290 290  
 FT CARBOHYD 296 296  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 355 355  
 FT CARBOHYD 385 385  
 FT CARBOHYD 391 391  
 FT CARBOHYD 397 397  
 FT CARBOHYD 401 401  
 FT CARBOHYD 405 405  
 FT CARBOHYD 442 442  
 FT CARBOHYD 457 457  
 FT CARBOHYD 607 607  
 FT CARBOHYD 612 612  
 FT CARBOHYD 621 621  
 FT CARBOHYD 633 633



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DR EMBL; K03455; AAB50262.1; -  
 DR EMBL; AF038399; AAB99976.1; -  
 DR EMBL; AF038319; AAC82596.1; -  
 DR HIV; K03455; ENVSHXB2.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 624 624  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.le-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLIEESONQOEKNEQELLELDKWSLNNWF 36  
 DB 638 YTSLSLIEESONQOEKNEQELLELDKWSLNNWF 673

RESULT 7  
 ENV\_HY1H3 STANDARD; PRT; 856 AA.

AC P04624;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxId=11707;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85228248; PubMed=2988795;  
 RA Crowl R., Ganquly K., Gordon M., Conroy R., Schaber M., Kramer R.,  
 RA Shaw G.M., Wong-Straal F., Reddy E.P.;  
 RT "HIV-1 env gene products synthesized in E. coli are recognized by  
 RT antibodies present in the sera of AIDS patients.";  
 RL Cell 41:979-986(1985).  
 CC -----  
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DR EMBL; M14100; AAA44679.1; -  
 DR HIV; M14100; ENVSHXB3.  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 DR Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
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 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 624 624

FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 97188 MW; 373C68B84C1AFC CRC64;

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1,le-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36  
 Db 638 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 8  
 ENV\_HVILM STANDARD; PRT; 856 AA.  
 AC 070626;  
 DE 15-JUL-1998 (Rel. 36, Created)  
 DE 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE ENV.  
 OS Human immunodeficiency virus type 1 (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=82834;

RA MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,  
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1153(1994).

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CC EMBL: U12055; AAAT6690.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.

FT SIGNAL 1 30  
 FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 54 74 BY SIMILARITY.  
 FT DISULFID 119 205 BY SIMILARITY.  
 FT DISULFID 126 196 BY SIMILARITY.  
 FT DISULFID 131 157 BY SIMILARITY.  
 FT DISULFID 218 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 331 BY SIMILARITY.  
 FT DISULFID 378 445 BY SIMILARITY.  
 FT DISULFID 385 418 BY SIMILARITY.  
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E687 CRC64;

Query Match 97.4%; Score 189; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1,le-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36  
 Db 638 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 9  
 ENV\_HVILM STANDARD; PRT; 861 AA.  
 AC P03377;  
 DE 21-JUL-1986 (Rel. 01, Created)  
 DE 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 DE ENV.  
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11686;

RA MEDLINE=8509333; PubMed=2981635;  
 RA Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;  
 RT "Nucleotide sequence of the AIDS virus, LAV."  
 RL Cell 40:9-17(1985).

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CC EMBL: K02013; AAB59751.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30

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FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 517 861 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 210 BY SIMILARITY.
FT DISULFID 126 201 BY SIMILARITY.
FT DISULFID 131 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 336 BY SIMILARITY.
FT DISULFID 383 450 BY SIMILARITY.
FT DISULFID 390 423 BY SIMILARITY.
FT CARBOHYD 88 428 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 755 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 821 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA: 97487 MW: 04DE2BAD4E4FD63A CRC64:

Query Match
Best Local Similarity 97.4% Score 189; DB 1; Length 861;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLYSLIEESQNOEKNEDELLELDKWSLIMNF 36
DB 643 YTSLYSLIEESQNOEKNEDELLELDKWSLIMNF 678

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RL J. Virol. 64:4390-4398(1990).
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CC -----
DR EMBL: M65024; AAA45072.1;
DR HIV: M38428; ENVSEF162.
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00516; Gp120; 1.
DR Pfam: PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KW Signal.
FT CHAIN 1 29
FT CHAIN 30 502
FT DISULFID 53 73
FT DISULFID 118 203
FT DISULFID 125 194
FT DISULFID 130 155
FT DISULFID 216 245
FT DISULFID 226 237
FT DISULFID 294 338
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87 87
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FT CARBOHYD 274 274
FT CARBOHYD 293 293
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FT CARBOHYD 454 454
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA: 96135 MW: 0A901317FD7FE2AB CRC64:

Query Match
Best Local Similarity 96.9% Score 188; DB 1; Length 847;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTSLYSLIEESQNOEKNEDELLELDKWSLIMNF 36
DB 629 YTNLYTLIEESQNOEKNEDELLELDKWSLIMNF 664

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RESULT 10
ENV_HV1SL1 STANDARD: PRT: 847 AA.
AC P19550:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane
DE glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., O'Riordan M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
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FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 847 AA; 96466 MW; CD1E33D73A5BCAE CRC64;

Query Match 95.4%; Score 185; DB 1; Length 847;
Best Local Similarity 94.4%; Pred. No. 3.5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLIESQNOEKNEQELLELDKWSLWME 36
Db 629 YTSLYSLIESQNOEKNEQELLELDKWSLWME 664

RESULT 13
ENV_HV1J3 STANDARD; PRT; 867 AA.
ID ENV_HV1J3
AC P12489;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11694;
RX NCBI_TaxID=11694;
RA SEQUENCE FROM N.A.
RA MEDLINE=89352108; PubMed=2669897;
RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
RA "Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
RA AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M21138; AAB03526.1; -
CC HIV: M21138; ENV5JH3.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
CC SIGNAL 1 30
CC CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
CC DISULFID 53 73 BY SIMILARITY.
CC DISULFID 118 217 BY SIMILARITY.
CC DISULFID 125 208 BY SIMILARITY.

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FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 388 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 867 AA; 98399 MW; 5F231014B8B8680 CRC64;

Query Match 94.8%; Score 184; DB 1; Length 867;
Best Local Similarity 94.4%; Pred. No. 4.8e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLYSLIESQNOEKNEQELLELDKWSLWME 36
Db 649 YTSLYSLIESQNOEKNEQELLELDKWSLWME 684

RESULT 14
ENV_HV1MN STANDARD; PRT; 856 AA.
ID ENV_HV1MN
AC P05877;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11696;
RX NCBI_TaxID=11696;
RA SEQUENCE FROM N.A.
RA MEDLINE=88219542; PubMed=3169091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.;
RA "Envelope sequences of two new United States HIV-1 isolates."
RA Virology 164:531-536(1988).
CC -i- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

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FT	CARBOHYD	610	610	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. . .)	(POTENTIAL)
SO	SEQUENCE	855 AA;	97438 MM;	A3BC20573AACAI2	CRC64;

FT	CARBOHYD	610	610	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .) <td>(POTENTIAL).</td>	(POTENTIAL).

FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	636	636	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	815	815	N-LINKED (GLCNAC. . .)	(POTENTIAL).

FT	CARBOHYD	815	815	N-LINKED (GLCNAC. . .)	(POTENTIAL) .
SQ	SEQUENCE	855 AA;	97438 MW;	A3BC20573AAC41A2	CRC64;

Query Match	93.3%	Score 181	DB 1	Length 855
...	...	...	...	...

Best Local Similarity 88.98; Pred. No. 1, 1e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0;

QY 1 YTSLIYSLIEESQNOQEKNEQELLELDKWSLWNWF 36

Db 637 YTNITYTLEESQNOQEKNEQELLELDKWSAIWNWF 672

[illegible]

Search completed: May 16, 2003, 11:13:36  
Job time : 6.07229 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-537  
Perfect score: 194  
Sequence: 1 YTSLLYSLIEESQNOEKNEDELLDKWASIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.rodent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriophage:\*
- 17: sp.archae:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194	100.0	848	15	069990 human immun
2	192	99.0	838	15	003806 human immun
3	192	99.0	854	15	078225 human immun
4	192	99.0	855	15	003805 human immun
5	191	98.5	42	15	069910 human immun
6	191	98.5	443	15	080023 human immun
7	191	98.5	841	15	041556 human immun
8	191	98.5	849	15	077368 human immun
9	191	98.5	849	15	080851 human immun
10	191	98.5	851	15	056110 human immun
11	191	98.5	851	15	080852 human immun
12	191	98.5	856	15	072993 human immun
13	191	98.5	856	15	041539 human immun
14	191	98.5	857	15	080170 human immun
15	191	98.5	858	15	080190 human immun
16	191	98.5	858	15	080188 human immun

## ALIGNMENTS

17	191	98.5	859	15	080185	080185 human immun
18	191	98.5	859	15	080180	080180 human immun
19	191	98.5	859	15	080179	080179 human immun
20	191	98.5	859	15	080177	080177 human immun
21	191	98.5	859	15	080173	080173 human immun
22	191	98.5	859	15	080850	080850 human immun
23	191	98.5	862	15	080184	080184 human immun
24	191	98.5	862	15	080183	080183 human immun
25	191	98.5	862	15	080182	080182 human immun
26	191	98.5	862	15	080178	080178 human immun
27	191	98.5	862	15	080174	080174 human immun
28	191	98.5	868	15	080186	080186 human immun
29	190	97.9	848	15	069988	069988 human immun
30	189	97.4	123	15	09YXR3	09YXR3 human immun
31	189	97.4	645	15	0993A6	0993A6 human immun
32	189	97.4	747	15	070607	070607 human immun
33	189	97.4	748	15	070608	070608 human immun
34	189	97.4	752	15	070604	070604 human immun
35	189	97.4	752	15	070605	070605 human immun
36	189	97.4	752	15	070608	070608 human immun
37	189	97.4	851	15	078243	078243 human immun
38	189	97.4	852	15	069992	069992 human immun
39	189	97.4	852	15	089797	089797 human immun
40	189	97.4	854	15	085582	085582 human immun
41	189	97.4	854	15	072502	072502 human immun
42	189	97.4	855	15	09E1R7	09E1R7 human immun
43	189	97.4	856	15	092877	092877 human immun
44	189	97.4	856	15	074599	074599 human immun
45	189	97.4	856	15	074090	074090 human immun

## RESULT 1

069990 PRELIMINARY; PRT; 848 AA.

AC 069990;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
EN Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=651;  
RX MEDLINE=96190564; PubMed=8627686;  
RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S., Karlsson G., Sodroski J., Morgado M., Galvao-Castro B., von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M., Hahn B.H.;  
RA Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. The WHO and NIAID Networks for HIV Isolation and Characterization.";  
RT J. Virol. 70:1651-1657(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=651;  
RX NIAID/NIH DAIDS Variation Program;  
RA Submitted (MAY-1994) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=651;  
RX MCEVILLY M.M.;  
RA Submitted (APR-1994) to the EMBL/Genbank/DBJ databases.  
DR EMBL; U08442; AA04065.1;  
DR InterPro; IPR000328; Env\_Gp41.  
DR InterPro; IPR000777; Gp120.  
DR Pfam; PF00516; Gp120; 1.  
DR Pfam; PF00517; Gp41; 1.

[illegible]

FT	CARBOHYD	598	598	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	619	619	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	798	798	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SO	SEQUENCE	838 AA;	95328 MW;	N1044B1CA10CFB4D	CRC64;
QY	Query Match		99.0%;	Score 192;	DB 15;
	Best Local Similarity	97.2%;	Pred. No. 2,7e-15;	Length 838;	
	Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Db	1 YTSIIYSLEESQNOEKNEQELLELDKWSIWMNF 36				
	620 YTSIIYSLEESQNOEKNEQELLELDKWSIWMNF 655				
RESULT 3					
078225					
ID	078225	PRELIMINARY;	PRT;	854 AA.	
AC	078225:				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Env protein.				
GN	ENV.				
OC	Human immunodeficiency virus type 1.				
OS	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RN	11				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BA-1;				
RX	MEDLINE=91289160; PubMed=1905842;				
RA	Hwang S.S., Boyle T.J., Lyerly H.K., Cullen B.R.;				
RT	"Identification of the envelope V3 loop as the primary determinant of				
RT	cell tropism in HIV-1";				
RL	Science 253:71-74(1991).				
DR	EMBL; M63929; AAA75116.1; "				
DR	InterPro; IPR000328; Env_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.				
SEQ	SEQUENCE 854 AA; 97186 MW; 005FC81B5C8BFD8 CRC64;				
Query Match		99.0%;	Score 192;	DB 15;	Length 854;
Best Local Similarity		97.2%;	Pred. No. 2,7e-15;		
Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 YTSIIYSLEESQNOEKNEQELLELDKWSIWMNF 36				
	636 YTSIIYSLEESQNOEKNEQELLELDKWSIWMNF 671				
RESULT 4					
003805					
ID	003805	PRELIMINARY;	PRT;	855 AA.	
AC	003805:				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	Envelope protein GP160 precursor [CONTAINS: GP120; GP41].				
GN	ENV.				
OS	Human immunodeficiency virus type 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
RN	11				
RP	SEQUENCE FROM N.A.				
RA	Reitz M., Popovic M., Gartner S., Gallo R., Reed-Connole E.,				
RA	Beaver B.;				
RL	Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; M68893; AAA44191.1; "				
DR	InterPro; IPR000328; Env_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				

DR Pfam: PF00517; GP41, 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.  
 FT SIGNAL 1 ? 509 ? EXTERIOR MEMBRANE GLYCOPROTEIN (GP120).  
 FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN (GP41).  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 209 BY SIMILARITY.  
 FT DISULFID 125 200 BY SIMILARITY.  
 FT DISULFID 130 160 BY SIMILARITY.  
 FT DISULFID 222 251 BY SIMILARITY.  
 FT DISULFID 232 243 BY SIMILARITY.  
 FT DISULFID 300 334 BY SIMILARITY.  
 FT DISULFID 380 443 BY SIMILARITY.  
 FT DISULFID 387 416 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 855 AA; 96988 MW; EC631A3B84180C8D CRC64;  
 Query Match 99.0%; Score 192; DB 15; Length 855;  
 Best Local Similarity 97.2%; Pred. No. 2,7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 636 YTSIYSLIEESONOEKNEQELLELDKASLWNMF 671  
 RESULT 5  
 ID 069910 PRELIMINARY: PRT: 42 AA.  
 AC 069910;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE GP41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9421161; PubMed=7512731;  
 RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human

RT monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
 DR EMBL: U06740; AAA19153.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41, 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 42 42  
 SQ SEQUENCE 42 AA; 5248 MW; 613EB1B2DBB31A722 CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 42;  
 Best Local Similarity 97.2%; Pred. No. 1.6e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 7 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 42  
 RESULT 6  
 ID 080023 PRELIMINARY: PRT: 443 AA.  
 AC 080023;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env protein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92107924; PubMed=1763038;  
 RA Burger H., Weiser B., Flaherty K., Gulla J., Nguyen P.N., Gibbs R.A.;  
 RT "Evolution of human immunodeficiency virus type 1 nucleotide sequence  
 RT diversity among close contacts.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11236-11240(1991).  
 DR EMBL: M77230; AAB03792.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120, 1.  
 DR Pfam: PF00517; GP41, 1.  
 KW Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 443 443  
 SQ SEQUENCE 443 AA; 50195 MW; 428E1A864E4D5BCD CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 443;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLYSLIEESONOEKNEQELLELDKASLWNMF 36  
 DB 378 YTSIYSLIEESONOEKNEQELLELDKASLWNMF 413  
 RESULT 7  
 ID 041556 PRELIMINARY: PRT: 841 AA.  
 AC 041556;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C17;  
 RX MEDLINE=98105804; PubMed=9445059;

RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,  
 RA Walker B.D., Neumann A.U., Vernund S.H., Mestecky J., Jackson S.,  
 RA Felmore E., Cao Y., Gao Y., Kalam S., Kunstman K.J., McDonald D.,  
 RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.,  
 RT Immunological and virological analyses of persons infected by human  
 RT immunodeficiency virus type 1 while participating in trials of  
 RT recombinant gp120 subunit vaccines.";  
 RL J. Virol. 72:1552-1576(1998).  
 DR EMBL: U84814; AAC58844.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDs; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 841 AA; 95802 MW; AAF0104893D91667 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 841;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 623 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 658  
 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 36

RESULT 8  
 ID 07368 PRELIMINARY; PRT; 849 AA.  
 AC 07368;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBITaxId=11676;  
 RX NCBITaxId=11676;  
 RP SEQUENCE FROM N.A.  
 RA Buckner-White A., Theodore T.;  
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: M8430; AAA44073.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDs; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 849 AA; 97166 MW; 8DBECBA86AA92467 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 849;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 36  
 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 666

RESULT 9  
 ID 080851 PRELIMINARY; PRT; 849 AA.  
 AC 080851;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GP160.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBITaxId=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-KR3026;  
 RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;  
 RA "Evidence for the spread of immune-escape HIV-1 subtype B in the  
 RT Korean population.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A417427; CAD10139.1; -;  
 SQ SEQUENCE 849 AA; 96428 MW; FD660E39D1895C27 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 849;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 36  
 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 666

RESULT 10  
 ID 056110 PRELIMINARY; PRT; 851 AA.  
 AC 056110;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NC NCBITaxId=11676;  
 RX NCBITaxId=11676;  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-SFMH58.1;  
 RA MEDLINE-98178716; PubMed-9519894;  
 RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,  
 RA Sheppard W.H.;  
 RT "Diversity of the human immunodeficiency virus type 1 envelope  
 RT glycoprotein in San Francisco Men's Health Study participants";  
 RL AIDs Res. Hum. Retroviruses 14:329-337(1998).  
 DR EMBL: AF025756; AAC40593.1; -;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000173; GAP\_dhrogenase.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR PROSITE: PS00071; GAPDH; UNKNOWN\_1.  
 KW AIDs; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96516 MW; 1CDAC83EE6464531 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 36  
 1 YTSLIYTLIEESONQOEKNEQELLELDKWSLWNMF 668

RESULT 11  
 ID 080852 PRELIMINARY; PRT; 851 AA.  
 AC 080852;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE GP160.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBITaxId=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-KR3026;  
 RA Daniels R.S., Patel D., Xiang Z., Zheng N.N., Kang C.;

RT "Evidence for the spread of immune-escape HIV-1 subtype B in the  
RT Korean population."  
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ417426; CAD10138.1; -  
SQ SEQUENCE 851 AA; 96667 MW; 2CAA47A865B9CFAD CRC64;

Query Match 98.5%; Score 191; DB 15; Length 851;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 36  
DB 633 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 668

RESULT 12

ID 072993 PRELIMINARY; PRT; 856 AA.  
AC 072993;  
01-NOV-1996 (TREMBlrel. 01, Created)  
01-NOV-1996 (TREMBlrel. 01, last sequence update)  
01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Env protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9628454; PubMed=8679299;  
RA Guillon C., Bedin F., Fouchier R.A., Schutemaker H., Gruters R.A.;  
RT "Completion of nucleotide sequences of non-synctium-inducing and  
RT syncytium-inducing HIV type 1 variants isolated from the same  
RT patient."  
RN AIDS Res. Hum. Retroviruses 11:1537-1541(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Guillon C., Bedin F., Fouchier R.A.M., Schutemaker H., Gruters R.A.;  
RT Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U34604; AAC54649.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
SQ SEQUENCE 856 AA; 96685 MW; BD1B19EE6B182DE0 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 36  
DB 638 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 673

RESULT 13

ID 041539 PRELIMINARY; PRT; 856 AA.  
AC 041539;  
01-JAN-1998 (TREMBlrel. 05, Created)  
01-JAN-1998 (TREMBlrel. 05, last sequence update)  
01-DEC-2001 (TREMBlrel. 19, last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C10;  
RX MEDLINE=98105804; PubMed=9445059;  
RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,

RA Walker B.D., Neumann A.U., Vermund S.H., Westlock J., Jackson S.,  
RA Fenamore E., Cao Y., Gao F., Kalam S., Kunstan K.J., McDonald D.,  
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;  
RT "Immunological and virological analyses of persons infected by human  
RT immunodeficiency virus type 1 while participating in trials of  
RT recombinant gp120 subunit vaccines."  
RT J. Virol. 72:1552-1576(1998).  
DR EMBL: U84800; AAC58827.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
FT NON\_TER 1  
SQ SEQUENCE 856 AA; 97545 MW; 7971B750E9ADFEA8 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 36  
DB 638 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 673

RESULT 14

ID 080L70 PRELIMINARY; PRT; 857 AA.  
AC 080L70;  
01-MAR-2002 (TREMBlrel. 20, Created)  
01-MAR-2002 (TREMBlrel. 20, last sequence update)  
01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE GP160 protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;  
RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells  
RT and Herpesvirus saimiri transformed T-cells is comparable."  
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ418516; CAD10926.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
SQ SEQUENCE 857 AA; 97590 MW; 3FE27F18D19DB31 CRC64;

Query Match 98.5%; Score 191; DB 15; Length 857;  
Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 36  
DB 639 YTSLYSLIEESONQOEKNEOELLELDKWSLWNMF 674

RESULT 15

ID 080L90 PRELIMINARY; PRT; 858 AA.  
AC 080L90;  
01-MAR-2002 (TREMBlrel. 20, Created)  
01-MAR-2002 (TREMBlrel. 20, last sequence update)  
01-JUN-2002 (TREMBlrel. 21, last annotation update)  
DE GP160 protein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Zheng N.N., Vella C., Easterbrook P.J., Daniels R.S.;  
 RT "Selection on isolation of HIV-1 in peripheral blood mononuclear cells  
 and Herpesvirus saimiri transformed T-cells is comparable."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ418496; CAD10906.1; -;  
 DR InterPro; IPR000328; Env\_Gp41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 SQ SEQUENCE 858 AA; 97600 MW; 444D6861F6C0355 CRC64;  
 Query Match 98.5%; Score 191; DB 15; Length 858;  
 Best Local Similarity 97.2%; Pred. No. 3.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 16, 2003, 11:19:48  
 Time : 26.3124 secs

AC AAY89136;

XX 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 XX anti-fusogenic; differentiation factor; interleukin; interferon;  
 XX colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX WO9959615-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX MPI; 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

XX Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SU Sequence 36 AA;

Query Match 98.0%; Score 192; DB 21; Length 36;

Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIESONQOEKNEOELLELDKWSLNNWF 36

Db 1 YTSLIHTLIESONQOEKNEOELLELDKWSLNNWF 36

Search completed: May 16, 2003, 11:12:06  
 Job time : 32.4578 secs



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XX      Sequence      36 AA:
SQ
Query Match      98.0%; Score 192; DB 21; Length 36;
Best Local Similarity 97.2%; Pred. No. 6,5e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36
        |||||:|||||:|||||:|||||:|||||:|||||:
DB      1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 11
AAB14533
ID      AAB14533 standard; peptide; 36 AA.
AC
AC      AAB14533:
DT      24-NOV-2000 (first entry)

XX      HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).
KW      HIV-1; gp41 C-helical domain;
KW      gp41 transmembrane-proximal amphipathic alpha-helical segment;
KW      core 6-helix bundle; viral entry inhibition; immunogenic;
KW      antibody; humoral response; broad spectrum vaccine; anti-HIV;
KW      envelope glycoprotein; prophylaxis; therapy.
XX
OS      Human immunodeficiency virus type 1.
XX
PN      WO2000040616-A1.
XX
PD      13-JUL-2000.
XX
PE      10-JAN-2000; 2000MO-US00456.
XX
PR      08-JAN-1999; 990S-0115404.
PR      07-JAN-2000; 2000US-0480336.
XX
PA      (WIID/) WIID C T.
PA      (WEIS/) WEISS C D.
XX
PI      Wild CT, Weiss CD;
XX
DR      WPI; 2000-465959/40.
XX
PT      Raising neutralizing antibody response to human immunodeficiency virus,
PT      comprises administering a polypeptide capable of forming a stable
PT      coiled-coil solution structure -
PS      Claim 13, Page 12; 97pp; English.
XX
XX      Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically
XX      claimed peptides derived from the C-helical domain of the gp41
XX      envelope glycoprotein from a variety of HIV-1 isolates. The invention
XX      relates to raising a neutralising antibody response to a broad spectrum
XX      of HIV (human immunodeficiency virus) strains and isolates, comprising
XX      the administration of a peptide which corresponds to or mimics highly
XX      conserved portions of gp41 which are important in mediating the process
XX      of viral entry into host cells. Such peptides can correspond to or
XX      mimic the coiled coil solution structure of the N-helical domain
XX      (the heptad repeat region), or can correspond or mimic the C-helical
XX      domain (the transmembrane-proximal amphipathic alpha-helical segment),
XX      or the gp41 core 6-helix bundle, which is formed by the interaction
XX      of the N- and C-helical domains of three gp41 proteins. The peptides
XX      can be administered either singly or as a combination (particularly a
XX      combination of N-helical and C-helical peptides), and can be
XX      multimerised. For example, N- and C-helical domain peptides can
XX      be alternately linked together to form a peptide which mimics the
XX      core 6-helix bundle. Administration of the peptide(s) generates a
XX      humoral response, with the production of antibodies against gp41
XX      structures involved in viral entry. As these portions of gp41 are well
XX      conserved, such antibodies may be effective against a broad range of

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CC      HIV strains and isolates. The peptide compositions may be administered
CC      as a prophylactic or therapeutic vaccine to generate antibodies which
CC      reduce or inhibit the ability of HIV to infect uninfected cells. A
CC      composition comprising polyclonal or monoclonal antibodies can be
CC      administered to reduce HIV infection of uninfected cells. Antibodies
CC      raised against entry-relevant gp41 structures may also be used
CC      therapeutically and as tools to further elucidate the mechanism of HIV
CC      cell entry.
XX
SQ      Sequence      36 AA:
XX
Query Match      98.0%; Score 192; DB 21; Length 36;
Best Local Similarity 97.2%; Pred. No. 6,5e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36
        |||||:|||||:|||||:|||||:|||||:|||||:
DB      1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 12
AA88665
ID      AA88665 standard; peptide; 36 AA.
XX
XX      AA88665:
AC
AC      23-MAY-2000 (first entry)
DT
XX
DE      Core polypeptide fragment T No. 20.
XX
XX      Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW      HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW      anti-fusogenic; differentiation factor; interleukin; interferon;
KW      colony stimulating factor; hormone; angiogenic factor.
XX
XX      Unidentified.
OS
XX
PN      WO95959615-A1.
XX
PD      25-NOV-1999.
XX
PE      20-MAY-1999; 99MO-US11219.
XX
PR      20-MAY-1998; 98US-0082279.
XX
PA      (TRIM-) TRIMERS INC.
XX
XX      Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
DR      WPI; 2000-136792/12.
XX
PT      A new hybrid polypeptide with enhanced pharmacokinetic properties
PT      comprises enhancer sequence -
PS      Disclosure; Page 21; 124pp; English.
XX
XX      The invention relates to hybrid polypeptides comprising enhancer peptide
XX      sequence linked to core polypeptides. The enhancer polypeptides are
XX      derived from various retroviral envelope (gp11) protein sequences,
XX      especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX      pharmacokinetic properties such as increasing the half-life of any core
XX      polypeptide that they are linked to. The core polypeptides are any
XX      polypeptide that may be introduced into a living system and that can
XX      function as a pharmacologically useful peptide for the treatment or
XX      prevention of a disease. The core polypeptides are bioactive peptides
XX      selected from a growth factor, cytokine, differentiation factor,
XX      interleukin, interferon, colony stimulating factor, hormone or
XX      angiogenic factor. The peptides of the invention can be used for
XX      inhibiting viral infection and can be used in anti-viral and
XX      anti-fusogenic treatments. Sequences AA88651-990055 represent core
XX      polypeptide fragments that can be used in the invention. Some sequences
XX      among those indicated also comprise enhancer fragments at terminal ends
XX      and form hybrid polypeptides.

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XX XX Human immunodeficiency virus type 1.
OS XX WO200066622-A1.
PN XX
PD XX 09-NOV-2000.
PE XX 05-MAY-2000; 2000WO-US12371.
PR XX 05-MAY-1999; 99US-0132686.
PA XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
DR XX WPI; 2000-656493/63.
PT XX
PP partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor
antagonist is used to modulate inflammation -
RD
RE Claim 12; Page 24; 148pp; English.
RW
RX The present sequence is a peptide fragment of T20/DPI78. T20/DPI78 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DPI78 is
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T20/DPI78
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemotactic and activator of human peripheral blood phagocytes
CC (but not T cells). The present peptide can be used to modulate an
CC inflammatory response in a subject.
SQ Sequence 36 AA:
SY
SZ
T1 Query Match 98.0%; Score 192; DB 21; Length 36;
Best Local Similarity 97.2%; Pred. No. 6.5e-17;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
T2
T3
T4
T5
T6
T7
T8
T9
TA 1 YTSLIHTLIESQNOEKNEQLLELDKWSLMNF 36
TB |||||||:|||||||:|||||||:|||||||
TC 1 YTSLIHSILIESQNOEKNEQLLELDKWSLMNF 36
TD
TE
TF
TG
TH
TI RESULT 9
TT AAB52688
ID AAB52688 standard; Peptide; 36 AA.
IS
IX AAB52688;
IY
IZ
JA 23-FEB-2001 (first entry)
JB XX
JC XX T20/DPI78 peptide fragment #66.
JD XX
JE XX Antinflammatory; T20/DPI78; gp41 ectodomain; HIV-1 fusion;
JF formyl peptide receptor family; FPR; Inflammatory response up-regulation;
JG Chemotractant.
JH XX
JI XX Human immunodeficiency virus type 1:
JJ OS
JK PN WO200066622-A1.
JL PD
JM 09-NOV-2000.
JN XX
JO XX 05-MAY-2000; 2000WO-US12371.
JP PE
JQ PR 05-MAY-1999; 99US-0132686.
JR XX
JS XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
JT PA
JU PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;
JV DR
VW WPI; 2000-656493/63.
VT
VP partial-length T20/DPI78 or T21/DPI07 formyl peptide receptor
antagonist is used to modulate inflammation -
VR
VS Claim 12; Page 24; 148pp; English.
VV
VX The present sequence is a peptide fragment of T20/DPI78. T20/DPI78 is a
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DPI78 is
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a
CC critical role in the fusion of HIV-1 and host cell membranes. T20/DPI78
CC interacts with members of the formyl peptide receptor (FPR) family and
CC thereby up-regulates an inflammatory response, and acts as a potent
CC chemotactic and activator of human peripheral blood phagocytes
CC (but not T cells). The present peptide can be used to modulate an
CC inflammatory response in a subject.
VQ Sequence 36 AA:
VY
VZ
WA Query Match 98.0%; Score 192; DB 21; Length 36;
WB Best Local Similarity 97.2%; Pred. No. 6.5e-17;
WC Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
WD
WE
WF
WG
WH
WI
WJ
WK 1 YTSLIHTLIESQNOEKNEQLLELDKWSLMNF 36
WL |||||||:|||||||:|||||||:|||||||
WM 1 YTSLIHSILIESQNOEKNEQLLELDKWSLMNF 36
WN
WO
WP
WQ
WR
```

PT Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation -  
 PS  
 PS Claim 12; Page 25; 148bp; English.  
 CC  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
 CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC chemottractant and activator of inflammatory response, and acts as a potent  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 SO  
 SO Sequence 36 AA:  
 Query Match 98.0%; Score 192; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6, 5e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0  
 QY 1 YTSLHTLEESONOEKNEDELLEDDKASLWNMF 36  
 1 YTSLHTLEESONOEKNEDELLEDDKASLWNMF 36  
 Db  
 RESULT 10  
 AAB52818  
 ID AAB52818 standard; Peptide: 36 AA.  
 XX  
 AC AAB52818;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #97.  
 XX  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.  
 OS  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200066622-A1.  
 PD  
 PD 09-NOV-2000.  
 XX  
 PF 05-MAY-2000; 2000WO-US12371.  
 XX  
 PR 05-MAY-1999; 99US-0132686.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PU Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
 XX  
 XX WPI: 2000-656493/63.  
 DR  
 DR Administration of peptide agents with a sequence corresponding to a  
 PT partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
 PT antagonist is used to modulate inflammation -  
 PS  
 PS Claim 14; Page 40; 148bp; English.  
 CC  
 CC The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
 CC helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is  
 CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
 CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
 CC interacts with members of the formyl peptide receptor (FPR) family and  
 CC thereby up-regulates an inflammatory response, and acts as a potent  
 CC chemottractant and activator of human peripheral blood phagocytes  
 CC (but not T cells). The present peptide can be used to modulate an  
 CC inflammatory response in a subject.  
 CC

RESULT	6
AAY31955	
ID	AAY31955 standard; Peptide: 36 AA.
XX	
AC	AAY31955;
DT	21-DEC-1999 (first entry)
DE	Synthetic peptide T-20 (DP-178) ..
RW	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
OS	Synthetic.
XX	Human immunodeficiency virus type 1.
FH	
FT	Key Location/Qualifiers Modified-site 1 Modified-site /note= "N-terminal acetyl" 36 Modified-site /note= "C-terminal amide"
XX	
PN	WO9948513-A1.
PD	30-SEP-1999.
XX	
PF	22-MAR-1999; 99WO-US06230.
PR	23-MAR-1998; 98US-0045920.
PR	01-MAY-1998; 98US-0071877.
PA	(TRIM-) TRIMERIS INC.
XX	
PJ	Kang M., Bray B., Lichty M., Mader C., Merutka G; WPI: 1999-591038/50.
DR	
PT	Methods of peptide synthesis, particularly used to produce T-20 or T-20 like peptides -
XX	
PS	Claim 1; Page 102; 120pp; English.
CC	
CC	The present sequence represents an N- and C-terminal modified peptide, designated T-20 (or DP-178), corresponding to amino acids 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.
CC	The invention relates to methods for the synthesis of peptides, in particular T-20 and T-20-like peptides. The method involves synthesizing specific side-chain protected peptide fragment intermediates of T-20 or a T-20-like peptide on a solid support, coupling the protected fragments in solution to form a protected T-20 or T-20-like peptide, followed by deprotection of the side chains to yield the final T-20 or T-20-like peptide. The invention also relates to individual peptide fragments (see AAY31956-73) which act as intermediates in the synthesis of peptides of interest (e.g. T-20), and to particular groups of peptide fragments which act as intermediates in the synthesis of the peptide of interest. The method allows for the large scale, economical production of high purity peptides.
CC	
SC	
Sequence	36 AA;
Query Match	98.0%; Score 192; DB 20; Length 36;
Best Local Similarity	97.2%; Pred. No. 6, 5e-17;
Matches	35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSILHTLIESONQOEKNDELLELDKASIAMNF 36      :       :      DB 1 YTSLIHSLIEESONOQEKNQELLELDKWASIAMNF 36      :       :
RAY31974	

ID	AAV31974 standard; peptide; 36 AA.
XX	
AC	AAV31974;
DT	21-DEC-1999 (first entry)
XX	
DE	HIV-1 LAI gp41 T-20 peptide.
XX	
KW	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
OS	Human immunodeficiency virus type 1.
XX	
PN	MO9948513-A1.
PD	30-SEP-1999.
XX	
PF	22-MAR-1999; 99WO-US06230.
XX	
PR	23-MAR-1998; 98US-0045920.
XX	
PR	01-MAY-1998; 98US-0071877.
XX	
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Kang M, Bray B, Lichty M, Mader C, Merutka G;
XX	
DR	WP1; 1999-591038/50.
XX	
PT	Methods of peptide synthesis, particularly used to produce T-20 or
PT	T-20 like peptides
XX	
PS	Disclosure: Page 9; 12Opp; English.
XX	
CC	The present sequence represents a peptide, designated T-20 (or
CC	DP-178), that corresponds to amino acids 638-673 of the
CC	transmembrane protein gp41 of HIV-1 LAI isolate. The invention
CC	relates to methods for the synthesis of peptides, in particular
CC	C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.
CC	The method involves synthesizing specific side-chain protected
CC	peptide fragment intermediates (see AAV31956-73) of T-20 or a
CC	T-20-like peptide on a solid support, coupling the protected
CC	fragments in solution to form a protected T-20 or T20-like peptide,
CC	followed by deprotection of the side chains to yield the final T-20
CC	or T-20-like peptide. The invention also relates to individual
CC	peptide fragments which act as intermediates in the synthesis of
CC	peptides of interest (e.g. T-20), and to particular groups of
CC	peptide fragments which act as intermediates in the synthesis of
CC	the peptide of interest. The method allows for the large scale,
CC	economical production of high purity peptides.
XX	
SO	Sequence 36 AA:
Query Match	98.0%; Score 192; DB 20; Length 36;
Best Local Similarity	97.2%; Pred. No. 6, 5e-17;
Matches 35; Conservative 1; Mismatches 0;	Indels 0; Gaps 0
QY	1 YTSLIHTLEESONOEKNDLLELDKNASLNWF 36      :     :     :     :      1 YTSLIHTLEESONOEKNDLLELDKNASLNWF 36
Dd	
RESULT 8	
AAB52655	
ID	AAB52655 standard; Peptide; 36 AA.
XX	
AC	AAB52655;
XX	
DT	23-FEB-2001 (first entry)
XX	
DE	T20/Dp178 peptide fragment #33.
XX	
KW	Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion; formyl peptide receptor family; FPR; inflammatory response up-regulation; chemoattractant.
KW	

RESULT 4  
 ID AAY22912 standard; peptide: 36 AA.  
 AC AAY22912;  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 108 from WO9820036.  
 XX  
 KM HIV, gp41 protein; constrained helical peptide; HIV infection;  
 KM vaccine; antibody; viral membrane fusion; viral infectivity;  
 KM ligand affinity purification; protein A replacement;  
 KM immunoglobulin purification; epitope mimic.  
 OS Human immunodeficiency virus.  
 XX WO9820036-A1.  
 XX 14-MAY-1998.  
 XX 05-NOV-1997; 97WO-US20069.  
 XX 16-JUN-1997; 97US-0876698.  
 XX 06-NOV-1996; 96US-0743698.  
 PA (GETH ) GENENTECH INC.  
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI, 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 PS Disclosure: Page 233-234; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 98.0%; Score 192; DB 19; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTSLIHTLIEESONQOEKNEDELLDKWASLWNF 36  
 Db 1 YTSLIHTLIEESONQOEKNEDELLDKWASLWNF 36

RESULT 5  
 ID AAY22805 standard; peptide: 36 AA.  
 AC AAY22805;  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 1 from WO9820036.  
 XX  
 KM HIV, gp41 protein; constrained helical peptide; HIV infection;  
 KM vaccine; antibody; viral membrane fusion; viral infectivity;  
 KM ligand affinity purification; protein A replacement;  
 KM immunoglobulin purification; epitope mimic.  
 OS Human immunodeficiency virus.  
 XX WO9820036-A1.  
 XX 14-MAY-1998.  
 XX 05-NOV-1997; 97WO-US20069.  
 XX 16-JUN-1997; 97US-0876698.  
 XX 06-NOV-1996; 96US-0743698.  
 PA (GETH ) GENENTECH INC.  
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI, 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 PS Disclosure: Page 143-144; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 98.0%; Score 192; DB 19; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 YTSLIHTLIEESONQOEKNEDELLDKWASLWNF 36  
 Db 1 YTSLIHTLIEESONQOEKNEDELLDKWASLWNF 36

PA (UYDU-) UNIV DUKE.  
XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
PI Pellew SR, Wild CT;  
DR WPI; 1995-036105/05.  
XX  
PT Computer search generated synthetic peptides - are inhibitors of  
PI HIV transmission  
XX  
PS Claim 11; Page 132; 182pp; English.  
XX  
CC AAR64364 is designated DP-178, and corresponds to amino acids  
CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
CC forms a putative alpha helix at the C-terminal end of the gp41  
CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
CC 558-595) which contains a leucine zipper motif. The peptides complex  
CC via non-covalent protein-protein interactions, and possess anti-viral  
CC activity. Homologues of these peptides were identified by a computer  
CC assisted peptide sequence search. The peptides inhibit transmission to  
CC uninfected cells, and can also be used as type and/or subtype specific  
CC diagnostic tools.  
XX  
SQ Sequence 36 AA;  
XX  
Query Match 98.0%; Score 192; DB 16; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36  
DB 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36  
XX  
RESULT 2  
AAR98398  
ID AAR98398 standard; peptide; 36 AA.  
XX  
AC AAR98398;  
XX  
DT 17-FEB-1997 (first entry)  
XX  
DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
XX  
XX Antifusogenic activity; antiviral capability; coiled-coil peptide;  
KM ALLMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;  
KM influenza virus; hepatitis B virus.  
XX  
XX Human immunodeficiency virus type 1.  
PN MO9619495-A1.  
XX  
PD 27-JUN-1996.  
XX  
PF 20-DEC-1995; 95WO-US16733.  
XX  
PR 06-JUN-1995; 95US-0470896.  
PR 20-DEC-1994; 94US-0360107.  
XX  
PA (TRIM-) TRIMERIS INC.  
PA (UYDU-) UNIV DUKE.  
PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
PI Matthews TJ, Pellew SR, Wild CT;  
XX  
DR WPI; 1996-309517/31.  
XX  
XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
PT isolated peptide recognised by an ALLMOTIS, 107x178x4 or PLZIP  
PT sequence search motif  
XX  
PS Disclosure; Fig 1; 471pp; English.  
XX

CC The sequences given in AAR98398-408 represent peptides which exhibit  
CC antifusogenic activity, antiviral capability and/or the ability to  
CC modulate intracellular processes involving coiled-coil peptide  
CC structures. These peptides are recognised by the ALLMOTIS,  
CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
CC hepatitis B virus, to a cell.  
XX  
SQ Sequence 36 AA;  
XX  
Query Match 98.0%; Score 192; DB 17; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36  
DB 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36  
XX  
RESULT 3  
AAW17011  
ID AAW17011 standard; peptide; 36 AA.  
XX  
AC AAW17011;  
XX  
DT 30-JUN-1997 (first entry)  
XX  
DE HIV-1 derived peptide useful for treatment of HIV infection.  
XX  
XX HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;  
KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
KM replication; transmission.  
XX  
XX Human immunodeficiency virus type 1 LAI isolate.  
OS  
XX  
XX WO9640191-A1.  
PN  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09499.  
XX  
PR 07-JUN-1995; 95US-0481957.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Johnson RM, Lambert DM;  
XX  
XX WPI; 1997-099886/09.  
DR  
XX  
XX Compens. contg. DP-178 or DP-107 in combination with other  
PT therapeutic agent - useful for treatment of HIV infection, esp. by  
PT inhibiting replication or transmission of HIV.  
XX  
XX Claim 2; Figure 1; 84pp; English.  
PS  
XX  
XX AAW17011 represents a peptide designated DP-178, a peptide derived  
CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
CC derivatives are used in combination with a therapeutic agent, e.g. a  
CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
CC by inhibiting viral replication or inhibiting transmission. They may  
CC also be used in vaccines for protecting against HIV infection.  
XX  
SQ Sequence 36 AA;  
XX  
Query Match 98.0%; Score 192; DB 18; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36  
DB 1 YTSLIHTLIESONQOEKNEDELLELDKMSLWNMF 36

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OM protein - protein search, using SW model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-540  
Perfect score: 196  
Sequence: 1 YTSLLHLEESQNOQEKNEQELLELDKWSLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A.Genesec\_101002:\*

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- 22: /SIDS2/gcgdata/genesec/genesecp-emb1/AA2001.DAT:\*
- 23: /SIDS2/gcgdata/genesec/genesecp-emb1/AA2002.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	98.0	36	16	AA64364
2	192	98.0	36	17	AA64364
3	192	98.0	36	18	AA17011
4	192	98.0	36	19	AA17011
5	192	98.0	36	20	AA17011
6	192	98.0	36	21	AA17011
7	192	98.0	36	22	AA17011
8	192	98.0	36	23	AA17011
9	192	98.0	36	24	AA17011
10	192	98.0	36	25	AA17011

11	192	98.0	36	21	AA14533	HIV-1 isolate LAI
12	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
13	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
14	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
15	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
16	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
17	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
18	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
19	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
20	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
21	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
22	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
23	192	98.0 <th>36</th> <td>21</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	21	AA14533	Core polypeptide f
24	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
25	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
26	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
27	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
28	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
29	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
30	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
31	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
32	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
33	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
34	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
35	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
36	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
37	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
38	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
39	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
40	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
41	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
42	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
43	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
44	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f
45	192	98.0 <th>36</th> <td>22</td> <td>AA14533</td> <td>Core polypeptide f</td>	36	22	AA14533	Core polypeptide f

## ALIGNMENTS

RESULT 1  
AA64364  
AA64364 standard; Peptide: 36 AA.

24-AUG-1995 (first entry)

DP-178 derived from HIV-1 isolate LAI has antiviral activity.

antiviral activity: DP-178; DP-107; diagnostic; HIV-1LAI;  
human immunodeficiency virus; transmembrane protein; gp41;  
alpha helix; leucine zipper; DP-185.

Synthetic.

Key Modified-site Location/Qualifiers  
1 /note= "optionally has an amino, acetyl, 9-fluorenylmethoxy-carbonyl, hydrophobic or macromolecular carrier gp. attached"

Modified-site 38 /note= "optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"

W09428920-A.  
22-DEC-1994.  
07-JUN-1994: 94WO-US05739.  
07-JUN-1993: 93US-0073028.

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; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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Query Match          96.9%; Score 190; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 1.5e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 YTSLIHRLIEESQNOQEKNEQELLELDKWSLWNMF 36
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Db 144 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match          96.9%; Score 190; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YTSLIHRLIEESQNOQEKNEQELLELDKWSLWNMF 36
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Db 166 YTSLIHSLIEESQNOQEKNEQELLELDKWSLWNMF 201

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Search completed: May 16, 2003, 12:10:25  
Job time : 15.759 secs

Db 2 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

; Sequence 41, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

0 ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match 96.9%; Score 190; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 2.7e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36

||||| ||||||| ||||||| ||||||| |||||||

Db 11 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

; Sequence 4, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match 96.9%; Score 190; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 3.3e-16;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36

||||| ||||||| ||||||| ||||||| |||||||

Db 16 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

; Sequence 2, Application US/10040349B

; Publication No. US20030082521A1

; GENERAL INFORMATION:

; APPLICANT: Brasseur, Robert

APPLICANT: Charlotiaux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Hadid, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match 96.9%; Score 190; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 1.1e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36

||||| ||||||| ||||||| ||||||| |||||||

Db 104 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

; Sequence 84, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPE, HEINRICH

; APPLICANT: BUDE, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; TITLE OF INVENTION: BEING IMMOBILIZED

; FILE REFERENCE: ALBRE-22

; CURRENT APPLICATION NUMBER: US/10/059,271

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: DE 101 06 295

; PRIOR FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match 96.9%; Score 190; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 1.4e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 36

||||| ||||||| ||||||| ||||||| |||||||

Db 131 YTSLSHRLIESONQOEKNEQELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

; Sequence 81, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPE, HEINRICH

; APPLICANT: BUDE, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36  
DB 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 96.9%; Score 190; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36  
DB 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 176  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 96.9%; Score 190; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 2,1e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36  
DB 1 YTSLIRLIEESONOQEKNEQELLELDKNASLWNWF 36

Query Match	96.9%;	Score 190;	DB 10;	Length 36
Best Local Similarity	97.28;	Pred. No. 2.1e-16;		

Db 1 YTSLSHSLIEESQÑQÑEKNQELLELDKWSLWNWF 36

GenCore version 5.1.4\_p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-538  
Perfect score: 196  
Sequence: 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PC7\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	190	96.9	36	9	US-09-874-475-16
2	190	96.9	36	9	US-10-116-797-1
3	190	96.9	36	9	US-09-493-346-1
4	190	96.9	36	10	US-09-796-202-10
5	190	96.9	36	10	US-09-779-451-5
6	190	96.9	36	10	US-09-834-628-1
7	190	96.9	36	10	US-09-854-816-1
8	190	96.9	36	10	US-09-854-816-108
9	190	96.9	37	9	US-09-848-616-176
10	190	96.9	46	10	US-09-779-451-41
11	190	96.9	56	10	US-09-779-451-41
12	190	96.9	177	9	US-10-040-349B-2
13	190	96.9	221	9	US-10-059-271-84
14	190	96.9	232	9	US-10-059-271-81
15	190	96.9	254	9	US-10-059-271-82
16	190	96.9	256	9	US-10-059-271-97
17	190	96.9	268	10	US-09-854-816-16
18	190	96.9	268	10	US-09-854-816-17
19	190	96.9	268	10	US-09-854-816-18

20	190	96.9	344	9	US-10-040-349B-1	Sequence 1, Appli
21	190	96.9	345	9	US-10-026-741-49	Sequence 49, Appl
22	190	96.9	345	10	US-09-779-451-8	Sequence 8, Appli
23	190	96.9	391	9	US-10-059-271-93	Sequence 93, Appli
24	190	96.9	519	10	US-09-756-551A-8	Sequence 8, Appli
25	190	96.9	853	9	US-10-003-035-33	Sequence 33, Appli
26	190	96.9	856	10	US-09-476-242-1	Sequence 1, Appli
27	190	96.9	861	9	US-10-026-741-103	Sequence 103, App
28	190	96.9	1101	9	US-10-003-035-53	Sequence 53, Appl
29	190	96.9	1186	9	US-10-003-035-55	Sequence 55, Appl
30	187	95.4	36	10	US-09-912-824-1	Sequence 1, Appli
31	187	95.4	268	10	US-09-854-816-19	Sequence 19, Appl
32	185	94.4	233	10	US-09-854-816-50	Sequence 50, Appl
33	184	93.9	268	10	US-09-854-816-9	Sequence 9, Appli
34	184	93.9	269	10	US-09-854-816-12	Sequence 12, Appl
35	184	93.9	1231	9	US-10-059-271-94	Sequence 94, Appl
36	182	92.9	268	10	US-09-854-816-13	Sequence 13, Appl
37	182	92.9	269	10	US-09-854-816-28	Sequence 28, Appl
38	181	92.3	268	10	US-09-854-816-26	Sequence 26, Appl
39	181	92.3	619	10	US-09-891-609-4	Sequence 4, Appli
40	181	92.3	646	10	US-09-891-609-2	Sequence 2, Appli
41	181	92.3	847	10	US-09-476-242-2	Sequence 2, Appli
42	180	91.8	46	10	US-09-854-816-109	Sequence 109, App
43	180	91.8	267	10	US-09-854-816-38	Sequence 38, Appl
44	180	91.8	268	10	US-09-854-816-41	Sequence 41, Appl
45	180	91.8	269	10	US-09-854-816-6	Sequence 6, Appli

## ALIGNMENTS

```

RESULT 1
US-09-874-475-16
; Sequence 16, Application US/09874475
; Publication No. US20020182592A1
; GENERAL INFORMATION:
; APPLICANT: Petropoulos, Christos J.
; APPLICANT: Parkin, Neil T.
; APPLICANT: Whitcomb, Jeanette
; APPLICANT: Huang, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
; FILE REFERENCE: 2793/65166
; CURRENT APPLICATION NUMBER: US/09/874,475
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match          96.9%; Score 190; DB 9; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.1e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36
DB 1 YTSLIHRIEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 2
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US2003004411A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; CURRENT FILING DATE: 2002-10-15

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Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497

; Sequence 497, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 497

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 96.9%; Score 190; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498

; Sequence 498, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 498

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 96.9%; Score 190; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 15

US-09-082-279B-603

; Sequence 603, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; CURRENT FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 603

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 96.9%; Score 190; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLIESONQOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:13

Job time : 10.1928 secs

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Gutnile, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 96.9%; Score 190; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOQEKNDLELDKNASLWNMF 36  
1 YTSLHSLIEESONOQEKNDLELDKNASLWNMF 36

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
8-475-668A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWMP 36  
DB 1 YTSLHSLIEESONOENKNEDELLEDKWASLWMP 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWMP 36  
DB 1 YTSLHSLIEESONOENKNEDELLEDKWASLWMP 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5,5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWMP 36  
DB 1 YTSLHSLIEESONOENKNEDELLEDKWASLWMP 36

Db 1 YTSLIHSLIESQNOQEKNEQLELDKWSLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B

Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TRANSMISSION  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLIHSLIESQNOQEKNEQLELDKWSLWNMF 36  
Db 1 YTSLIHSLIESQNOQEKNEQLELDKWSLWNMF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597

Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TRANSMISSION  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 96.9%; Score 190; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 5.5e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTSLIHSLIESQNOQEKNEQLELDKWSLWNMF 36  
Db 1 YTSLIHSLIESQNOQEKNEQLELDKWSLWNMF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A

Patent No. 6060065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TRANSMISSION  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

CURRENT APPLICATION NUMBER: US/09/071.877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 96.9%; Score 190; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 5.5e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWMPF 36

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-538

Perfect score: 196  
Sequence: 1 YTSLSHRLIEESQNOEKNEDELLELDKWSLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	36	1	US-08-073-028-1
2	190	96.9	36	3	US-08-486-099-1
3	190	96.9	36	3	US-09-071-877-1
4	190	96.9	36	3	US-08-360-107A-1
5	190	96.9	36	3	US-08-484-223B-1
6	190	96.9	36	3	US-08-919-597-1
7	190	96.9	36	3	US-08-475-668A-1
8	190	96.9	36	3	US-08-485-551A-1
9	190	96.9	36	3	US-08-471-912A-1
10	190	96.9	36	4	US-08-554-616-1
11	190	96.9	36	4	US-08-485-264A-1
12	190	96.9	36	4	US-09-082-279B-15
13	190	96.9	36	4	US-09-082-279B-497
14	190	96.9	36	4	US-09-082-279B-498
15	190	96.9	36	4	US-09-082-279B-603
16	190	96.9	36	4	US-09-082-279B-630
17	190	96.9	36	4	US-09-082-279B-631
18	190	96.9	36	4	US-09-082-279B-705
19	190	96.9	36	4	US-09-082-279B-834
20	190	96.9	36	4	US-09-082-279B-1076
21	190	96.9	36	4	US-09-082-279B-1121
22	190	96.9	36	4	US-09-082-279B-1161
23	190	96.9	36	4	US-08-965-056-1
24	190	96.9	36	4	US-08-965-056-108
25	190	96.9	36	4	US-09-045-920-1
26	190	96.9	36	4	US-08-474-349A-1
27	190	96.9	36	4	US-08-474-349A-399

28	190	96.9	36	4	US-08-474-349A-413	Sequence 413, App
29	190	96.9	36	4	US-09-315-304B-15	Sequence 15, Appl
30	190	96.9	36	4	US-09-315-304B-497	Sequence 497, App
31	190	96.9	36	4	US-09-315-304B-498	Sequence 498, App
32	190	96.9	36	4	US-09-315-304B-603	Sequence 603, App
33	190	96.9	36	4	US-09-315-304B-630	Sequence 630, App
34	190	96.9	36	4	US-09-315-304B-705	Sequence 705, App
35	190	96.9	36	4	US-09-315-304B-834	Sequence 834, App
36	190	96.9	36	4	US-09-315-304B-1076	Sequence 1076, App
37	190	96.9	36	4	US-09-315-304B-1121	Sequence 1121, App
38	190	96.9	36	4	US-09-315-304B-1161	Sequence 1161, App
39	190	96.9	36	4	US-09-315-304B-1469	Sequence 1469, App
40	190	96.9	36	4	US-09-315-304B-1470	Sequence 1470, App
41	190	96.9	36	4	US-09-315-304B-1486	Sequence 1486, App
42	190	96.9	36	4	US-09-315-304B-1511	Sequence 1511, App
43	190	96.9	36	4	US-08-255-208A-1	Sequence 1, Appl
44	190	96.9	36	4	US-09-082-279B-771	Sequence 771, App
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## ALIGNMENTS

RESULT 1  
US-08-073-028-1  
; Sequence 1, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNTE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-1  
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QY      1 YTSLIHRLIEESQNOQEKNEQELLLEDKWSLWNMF 36
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DT 01-DEC-2001 (TREMBLrel\_19, last annotation update)  
DE Envelope glycoprotein gp120.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
NCBI\_TaxID=11676;  
Virus: Retroid viruses; Retroviridae; Lentivirus

RN  
RP  
RQ  
RX  
RA  
RT  
RT  
RT  
RL  
RL  
DR  
DR  
DR  
DR  
DR  
DR  
DR  
SQ  
SQ

SEQUENCE FROM N.A.  
MEDLINE=96013815; PubMed=7474132;  
Duenning T.D., Fang H., Dordard D.W., Pincus S.H.;  
"Processing of the envelope glycoprotein gp160 in immunotoxin-  
resistant cell lines chronically infected with human immunodeficiency  
virus type 1.";  
J. Virol. 69:7122-7131(1995).  
EMBL, LA2371; AAA96326.1; -;  
InterPro: IPR000328; Env\_Gp41.  
InterPro: IPR000777; GP120.  
Pfam: PF00516; GP120; 1.  
Pfam: PF00517; GP41; 1.  
AIRS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
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Search completed: May 16, 2003, 11:19:49  
time : 27.3124 secs

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXB2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
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 SO SEQUENCE 856 AA; 97151 MW; C50BE0386FB73659 CRC64;

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 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
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 RP SEQUENCE FROM N.A.  
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 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 856;  
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 DB 638 YTSLIHSLIESQNOQEKNEQELLELDKWSLMMNF 673

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 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
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 RC STRAIN=PM213;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
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Query Match 96.9%; Score 190; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
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 RX MEDLINE=95074930; PubMed=7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 RT selected with immunotoxins from human immunodeficiency virus type 1-  
 RT infected T cells.";  
 DE J. Virol. 69:75-81(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 RT immunotoxin-resistant variant T cell line.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF070521; AAC28452.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

RT Infected with HIV type 1 (HTLV type IIB).  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12053; AAA76685.1; -;  
DR EMBL: U12036; AAA76671.1; -;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Envelope protein; glycoprotein; Polyprotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF.CRC64;  
  
Query Match 96.9%; Score 190; DB 15; Length 852;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
1 YTSLIHRIEESONOEKNEDELLELDKWSLWNNF 36  
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634 YTSLIHSLIEESONOEKNEDELLELDKWSLWNNF 669  
  
RESULT 9  
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AC 085582;  
DT 01-NOV-1996 (TRENBLREL: 01, Created)  
DT 01-NOV-1996 (TRENBLREL: 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL: 19, Last annotation update)  
DE Envelope polyprotein.  
GN ENV.  
RT Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Buckler C.E.;  
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes."  
RL J. Virol. 66:3151-3154(1992).  
DR EMBL: M19921; AAA44992.1; -;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
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Query Match 96.9%; Score 190; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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Db 636 YTSLIHSLIEESONOEKNEDELLELDKWSLWNNF 671  
  
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DT 01-NOV-1996 (TRENBLREL: 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL: 19, Last annotation update)  
DE ENV polyprotein.  
GN ENV.  
RT Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-NLA-3;  
RC MEDLINE=96036482; PubMed=7483282;  
RX Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction."  
RT Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA STRAIN-NLA-3;  
RC MEDLINE=86281827; PubMed=3016298;  
RX Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RT J. Virol. 59:284-291(1986).  
DR EMBL: 026942; AAB60578.1; -;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT CONFLICT 214 H -> L (IN REF. 2).  
FT CONFLICT 530 A -> S (IN REF. 2).  
FT CONFLICT 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220.CRC64;  
  
Query Match 96.9%; Score 190; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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|||||  
Db 636 YTSLIHSLIEESONOEKNEDELLELDKWSLWNNF 671  
  
RESULT 11  
ID 092877 PRELIMINARY; PRT; 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TRENBLREL: 08, Created)  
DT 01-NOV-1998 (TRENBLREL: 08, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL: 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Simian-Human immunodeficiency virus.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9908984; PubMed=9882298;

RN (1)  
 RC SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RC Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ NON\_TER 752 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 6  
 ID 070608 PRELIMINARY; PRT; 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirda; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
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 RC MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RC Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
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Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

DB 638 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirda; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=89352106; PubMed=2765297;  
 RA Borsetti A., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borsetti A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone.";  
 RT Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CAA7628.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-14;  
 Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 633 YTSLIHRLIESQNOEKNEQELLELDKWSLWNMF 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirda; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RC MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RX MEDLINE=95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747  
 SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64;

Query Match 96.9%; Score 190; DB 15; Length 747;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESONOEKNEDELLELDKWSLWNMF 36  
 Db 633 YTSLIHSLIEESONOEKNEDELLELDKWSLWNMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.  
 AC 070606;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RX MEDLINE=95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1;

DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748  
 SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67694B CRC64;

Query Match 96.9%; Score 190; DB 15; Length 748;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESONOEKNEDELLELDKWSLWNMF 36  
 Db 634 YTSLIHSLIEESONOEKNEDELLELDKWSLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RX MEDLINE=95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752  
 SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 190; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 1e-14;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESONOEKNEDELLELDKWSLWNMF 36  
 Db 638 YTSLIHSLIEESONOEKNEDELLELDKWSLWNMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-538  
Perfect score: 196  
Sequence: 1 YTSLIHRLIESONQOEKNEQELLEDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	645	15	0993A6 human immun
2	190	96.9	747	15	070607 human immun
3	190	96.9	748	15	070606 human immun
4	190	96.9	752	15	070604 human immun
5	190	96.9	752	15	070605 human immun
6	190	96.9	752	15	070608 human immun
7	190	96.9	851	15	078243 human immun
8	190	96.9	852	15	089797 human immun
9	190	96.9	854	15	085582 human immun
10	190	96.9	854	15	072502 human immun
11	190	96.9	856	15	092877 simian-huma
12	190	96.9	856	15	074599 human immun
13	190	96.9	854	15	074090 human immun
14	186	94.9	854	15	090178 human immun
15	186	94.9	854	15	078705 human immun
16	185	94.4	443	15	080023 human immun

17	185	94.4	856	15	0905M7 human immun
18	184	93.9	42	15	069910 human immun
19	184	93.9	616	15	0993B0 human immun
20	184	93.9	618	15	0993B2 human immun
21	184	93.9	757	15	090722 human immun
22	184	93.9	841	15	041556 human immun
23	184	93.9	848	15	069990 human immun
24	184	93.9	849	15	077368 human immun
25	184	93.9	849	15	080851 human immun
26	184	93.9	851	15	056110 human immun
27	184	93.9	851	15	080852 human immun
28	184	93.9	856	15	072993 human immun
29	184	93.9	856	15	041539 human immun
30	184	93.9	857	15	080170 human immun
31	184	93.9	859	15	080185 human immun
32	184	93.9	859	15	080180 human immun
33	184	93.9	859	15	080179 human immun
34	184	93.9	859	15	080177 human immun
35	184	93.9	859	15	080173 human immun
36	184	93.9	859	15	080850 human immun
37	184	93.9	862	15	080184 human immun
38	184	93.9	862	15	080183 human immun
39	184	93.9	862	15	080182 human immun
40	184	93.9	862	15	080178 human immun
41	184	93.9	862	15	080174 human immun
42	184	93.9	868	15	080186 human immun
43	183	93.4	858	15	071974 human immun
44	183	93.4	859	15	092937 human immun
45	182	92.9	122	15	09YX08 human immun

## ALIGNMENTS

RESULT 1  
ID 0993A6 PRELIMINARY: PRT: 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RA MEDLINE=21192672; PubMed=11287644;  
RX Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
HIV envelope glycoprotein suggests structural influences on antigen  
processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120\_1.  
DR Pfam: PF00517; GP41\_1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;

Query Match 96.9%; Score 190; DB 15; Length 645;  
Best Local Similarity 97.2%; Pred. No. 8.8e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESONQOEKNEQELLEDKWSLWMP 36  
DB 607 YTSLIHRLIESONQOEKNEQELLEDKWSLWMP 642

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FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA: 98399 MW: 5F2310146B8E8680 CRC64;

Query Match 90.3% Score 177; DB 1; Length 867;  
 Best Local Similarity 91.7%; Pred. No. 4, 8e-14;  
 Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTSLIHRIIESQNOQEKNEOELLLELDKMASLWNF 36  
 ||||:|||||||  
 DB 649 YTSLIYTLIESQNOQEKNEOELLLELDKMASLWNF 684

Search completed: May 16, 2003, 11:13:37  
 Job time : 7.07229 secs



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FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED* (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C1209B3 CRC64;
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Query Match  
Best Local Similarity 92.3%; Score 181; DB 1; Length 856;  
Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTSLSHRLIESQNOOEKNEOELLELDKWSLWNF 35
DB 638 YTSLSHRLIESQNOOEKNEOELLELDKWSLWNF 672
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RESULT 13
ENV_HV122 STANDARD; PRT; 853 AA.
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AC P12487;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
PB Submitted (NOV-1988) to the HIV data bank.
```

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DR EMBL; M22639; AAA45370.1; -
DR HIV; M22639; ENV52226.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 508 EXTENSOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
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FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 853 AA; 97043 MW; 849B0B8CBAFF7008 CRC64;
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Query Match  
Best Local Similarity 91.8%; Score 180; DB 1; Length 853;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 YTSLSHRLIESQNOOEKNEOELLELDKWSLWNF 36
DB 635 YTSLSHRLIESQNOOEKNEOELLELDKWSLWNF 670
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```
RESULT 14
ENV_HV126 STANDARD; PRT; 855 AA.
```

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AC P04580;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11708;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87248097; PubMed=3036660;
RA Sriinivasan A., Anand R., York D., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene."
RL Gene 52:71-82(1987).
```

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ENV\_HV1S1 STANDARD: PRT; 847 AA.

ID ENV\_HV1S1  
AC P19550:  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
NCBI\_TaxID=11691;  
RX MEDLINE=90347835; PubMed=2384920;  
RA "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";  
RT J. Virol. 64:4390-4398(1990).  
RL -----  
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CC -----  
CC EMBL: M65024; AAA5072.1; -  
DR HIV; M38428; ENVSEF162.  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
KM SIGNAL. 1 29  
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 203 BY SIMILARITY.  
FT DISULFID 125 194 BY SIMILARITY.  
FT DISULFID 130 155 BY SIMILARITY.  
FT DISULFID 216 245 BY SIMILARITY.  
FT DISULFID 226 237 BY SIMILARITY.  
FT DISULFID 294 328 BY SIMILARITY.  
FT DISULFID 374 435 BY SIMILARITY.  
FT DISULFID 381 408 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 847 AA; 96135 MW; 0A90317ED7FF2AB CRC64;  
Query Match 92.3%; Score 181; DB 1; Length 847;  
Best Local Similarity 91.7%; Pred. No. 1.5e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLLHRLIESQNOEKNEDELLELDKWSLWME 36  
DB 629 YTNLYLTLEESQNOEKNEDELLELDKWSLWME 664

RESULT 12

ENV\_HV1PV STANDARD: PRT; 856 AA.

ID ENV\_HV1PV  
AC P03376:  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.  
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).  
OC Viruses; Retroviridae; Lentivirus.  
NCBI\_TaxID=11700;  
RX MEDLINE=8511157; PubMed=2982104;  
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;  
RT "Nucleic acid structure and expression of the human Aids/Lymphadenopathy retrovirus."  
RL Nature 313:450-458(1985).  
CC -----  
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CC -----  
CC EMBL: K02083; AAB59873.1; -  
DR EMBL: X01762; CAN25903.1; ALT\_SEQ.  
DR PIR: A03974; VCLUVL.  
DR HIV; K02083; ENVSPV22.  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KM Aids: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.  
KM SIGNAL. 1 30  
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 54 74 BY SIMILARITY.  
FT DISULFID 119 205 BY SIMILARITY.  
FT DISULFID 126 196 BY SIMILARITY.  
FT DISULFID 131 157 BY SIMILARITY.  
FT DISULFID 218 247 BY SIMILARITY.  
FT DISULFID 228 239 BY SIMILARITY.  
FT DISULFID 286 331 BY SIMILARITY.  
FT DISULFID 328 378 BY SIMILARITY.  
FT DISULFID 378 445 BY SIMILARITY.  
FT DISULFID 385 418 BY SIMILARITY.  
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT SITE 760 760 IN-FRAME TERMINATION CODON.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 219 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 439 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600E8A7A08 CRC64;

Query Match 93.9%; Score 184; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 6, 6e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEOELLELDKWSLWMPF 36
Db 638 YTSLIYTLIESQNOQEKNEOELLELDKWSLWMPF 673

ENV_HV1S3 STANDARD; PRT; 852 AA.
ID ENV_HV1S3
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90317906; PubMed-2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT Human immunodeficiency virus type 1 cellular host range.

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RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M38427; AAA45067.1;
DR HIV; M38427; ENVSEF33.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31 BY SIMILARITY.
FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 156 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C910D CRC64;

Query Match 92.9%; Score 182; DB 1; Length 852;
Best Local Similarity 91.7%; Pred. No. 1, 2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIESQNOQEKNEOELLELDKWSLWMPF 36
Db 634 YTSLIYTLIESQNOQEKNEOELLELDKWSLWMPF 669

RESULT 11

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FT	CAROHYD	384	384	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	390	390	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	395	395	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	404	404	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	446	446	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	461	461	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	609	609	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	614	614	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	623	623	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	635	635	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	672	672	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	748	748	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
FT	CAROHYD	814	814	N-LINKED (GLCNAC . . .)	(POTENTIAL) .
SQ	SEQUENCE	853 AA:	96912 MW:	3377B93B6F22ABA	CRC64:
Query Match		95.4%;	Score 187;	DB 1;	Length 853;
Best Local Similarity		94.4%;	Pred. No. 2.8e-15;		
Matches	34; Conservative		1; Mismatches	1; Indels	0; Gaps
1	YTSLIHRLIEESQNOOEKNEOELLLELDKASLWNWF	36			
	636 YTSLIHSLLIDESQNOOEKNEOELLLELDKASLWNWF	671			

ENV_HV1WI	RESULT 8			
ID	ENV_HV1WI	STANDARD;	PRT;	856 AA.
AC	P31872;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
CN	ENV.			
OS	Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=31678;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=86218077; PubMed=2423250;			
RA	Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.			
RA	Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;			
RT	Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."			
RL	Cell 45:637-648(1986).			
CC	-I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.			
DR	PIR. A24774; VCLJ3W.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
KM	Pfam: PF00517; GP41; 1.			
KW	Aids; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL.	1	29	
FT	CHAIN	30	510	
FT	CHAIN	511	856	
FT	DISULFID	53	73	
FT	DISULFID	118	205	
FT	DISULFID	125	196	
FT	DISULFID	130	152	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	330	
FT	DISULFID	376	444	
FT	DISULFID	383	417	
FT	CARBOHYD	87	87	
FT	CARBOHYD	134	134	
FT	CARBOHYD	140	140	
FT	CARBOHYD	151	151	
FT	CARBOHYD	155	155	
FT	CARBOHYD	155	155	

FT	CARBOHYD	183	183	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	197	197	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	234	234	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	241	241	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	262	262	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	276	276	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	289	289	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	295	295	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	331	331	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	338	338	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	354	354	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	360	360	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	394	394	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	404	404	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	447	447	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	459	459	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	611	611	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	616	616	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	625	625	N-LINKED	(GLCNAC. .)	(POTENTIAL)
FT	CARBOHYD	637	637	N-LINKED	(GLCNAC. .)	(POTENTIAL)
SO	SEQUENCE	856 AA;	97526 MM;	DB681B19C40C4DE9	CR64;	

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Query March 94.4%: Score 185; DB 1; Length 856;
Best Local Similarity 94.4%; Pred. No. 5e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTSLIRLRIEESQNOEKNEQELLELDKWSIMWNMF 36
      . | | | | | | | | | | | | | | | | | | | |
DB      638 YTSLLYLNIEESQNOEKNEQELLELDKWSIMWNMF 673

RESULT 9
ENV_HV1SC STANDARD: PRT: 856 AA.
ID ENV_HV1SC
AC P05878;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgis C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Rietz M.S. Jr.;
RL "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988)
-i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
    1984 IN SOUTHERN CALIFORNIA.
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CC entities requires a license agreement (See license@isb-sib.ch).
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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

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Query Match 96.9%; Score 190; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSILHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSILHSLIEESQNOEKNEQELLELDKWSLWNMF 673

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RESULT 5
ENV_HV11M STANDARD: PRT: 856 AA.
ID ENV_HV11M
AC 070626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz G.M., Kong L.I., Weiss S.H., Walters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type 11IB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC DR GLYCOSULEDB: 070626; -
CC DR InterPro: IPR000328; Env_GP41.

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DR EMBL: U12055; AAA76690.1; -
DR GLYCOSULEDB: 070626; -
DR InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT DISULFID 88 88
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match 96.9%; Score 190; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 1.2e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSILHRLIEESQNOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSILHSLIEESQNOEKNEQELLELDKWSLWNMF 673

```

RESULT 6
ENV_HV1BR STANDARD: PRT: 861 AA.
ID ENV_HV1BR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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DR EMBL: P03377;
DR InterPro: IPR000328; Env_GP41.

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FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD <td>406</td> <td>406</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	406	406	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>448</td> <td>448</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	448	448	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>463</td> <td>463</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	463	463	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>611</td> <td>611</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	611	611	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>616</td> <td>616</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	616	616	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>624</td> <td>624</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	624	624	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>637</td> <td>637</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	637	637	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>674</td> <td>674</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	674	674	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>750</td> <td>750</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	750	750	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
FT	CARBOHYD <td>816</td> <td>816</td> <td>N-LINKED (GLCNAC. . .)<th>(POTENTIAL)</th></td>	816	816	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)
SO	SEQUENCE <td>856 AA;</td> <td>97212 MW;</td> <td>6FABI6AF85107FE0 CRC64;</td> <td></td>	856 AA;	97212 MW;	6FABI6AF85107FE0 CRC64;	
QY	1	YTSIIHRLIEESONQOEKNEDELLELDKWSIWMNF	36		
Db	638	YTSIIHSLIEESONQOEKNEDELLELDKWSIWMNF	673		
RESULT 4					
ENV_HV1H3					
ID	ENV_HV1H3	STANDARD;	PRT:	856 AA.	
AC	P04624;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OC	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentiviruses.				
OX	NCBI_Taxid=11707;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=65228248; Pubmed-2988795;				
RA	Crowl R., Gauguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;				
RA	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";				
RL	Cell 41:979-986(1985).				
CC					
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> .				
CC					
DR	EMBL: M14100; AAA44679.1; .				
DR	HIV; M14100; ENVSHXB3.				
DR	InterPro: IPR000328; Env_GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
DR	Pfam: PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.				
FT	Signal.	1	30		
FT	CHAIN	31	511	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFID	119	205	BY SIMILARITY.	
FT	DISULFID	126	196	BY SIMILARITY.	
FT	DISULFID	131	157	BY SIMILARITY.	
FT	DISULFID	218	247	BY SIMILARITY.	
FT	DISULFID	228	239	BY SIMILARITY.	
FT	DISULFID	296	331	BY SIMILARITY.	
FT	DISULFID	378	445	BY SIMILARITY.	
FT	DISULFID	385	418	BY SIMILARITY.	
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).	

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 96.9%; Score 190; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YTSLIHRLIEESONOQKNEQLELDKWSLWNNF 36
DB 633 YTSLIHSLIEESONOQKNEQLELDKWSLWNNF 668

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RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Virus: Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Lyiak K.J., Starich B.R.,
Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumister K., Ivanoff L., Peteway S.R.Jr., Pearson M.L.,
Laurenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III."
RT Nature 313:277-284 (1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382 (1990).
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```

CC EMBL; M15654; AAA44205.1;
CC PIR; A03973; VCLJH3.
CC HIV; M15654; ENVSH102.
CC InterPro; IPR000328; ENV_GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
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FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
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FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

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Query Match 96.9%; Score 190; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.2e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YTSLIHRLIEESONOQKNEQLELDKWSLWNNF 36
DB 638 YTSLIHSLIEESONOQKNEQLELDKWSLWNNF 673

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RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;

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GenCore version 5.1.4-P5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(Without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533a-538

Perfect score: 196

Sequence: 1 YTSLIHRLIESQNOQEKNEQELLELDKWSIWMWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	851	ENV_HV1B8	P04582 human immun
2	190	96.9	856	ENV_HV1B1	P03375 human immun
3	190	96.9	856	ENV_HV1H2	P04578 human immun
4	190	96.9	856	ENV_HV1H3	P04624 human immun
5	190	96.9	856	ENV_HV1LW	O70626 human immun
6	190	96.9	861	ENV_HV1BR	P03377 human immun
7	187	95.4	853	ENV_HV1MF	P19551 human immun
8	185	94.4	856	ENV_HV1W1	P13872 human immun
9	184	93.9	856	ENV_HV1SC	P05878 human immun
10	182	92.9	852	ENV_HV1S3	P15549 human immun
11	181	92.3	847	ENV_HV1S1	P19550 human immun
12	181	92.3	856	ENV_HV1PV	P13376 human immun
13	180	91.8	853	ENV_HV1Z2	P12487 human immun
14	180	91.8	855	ENV_HV1Z6	P04580 human immun
15	177	90.3	867	ENV_HV1J3	P12489 human immun
16	175	89.3	847	ENV_HV1W2	P05880 human immun
17	174	88.8	855	ENV_HV1A2	P03378 human immun
18	174	88.8	855	ENV_HV1A2	P03378 human immun
19	172	87.8	856	ENV_HV1M	P04579 human immun
20	170	86.7	853	ENV_HV1EL	P04581 human immun
21	170	86.7	855	ENV_HV1OY	P20888 human immun
22	168	85.7	843	ENV_HV1Y2	P35961 human immun
23	167	85.2	846	ENV_HV1ND	P18799 human immun
24	167	85.2	848	ENV_HV1JR	P20871 human immun
25	167	85.2	861	ENV_HV1KB	P13819 human immun
26	166	84.7	859	ENV_HV1MA	P04583 human immun
27	165	84.2	852	ENV_HV1BN	P12488 human immun
28	161	82.1	868	ENV_HV1C4	P05879 human immun
29	157	80.1	863	ENV_HV1Z8	P05881 human immun
30	149	76.0	854	ENV_SIVC2	P17281 chimpanzee
31	148	75.5	856	ENV_HV1ZH	P05881 human immun
32	91	46.4	854	ENV_SIVAT	O02837 simian immu
33	86	43.9	885	ENV_SIVS4	P12492 simian immu

34	85	43.4	860	ENV_HV2BE	P18094 human immun
35	84	42.9	881	ENV_SIVMK	P05884 simian immu
36	84	42.9	882	ENV_SIVM1	P05885 simian immu
37	82	41.8	857	ENV_HV2KR	O74126 human immun
38	82	41.8	859	ENV_HV2D2	P15831 human immun
39	81	41.3	859	ENV_HV2CA	P24105 human immun
40	81	41.3	889	ENV_SIVSP	P19503 human immun
41	80	40.8	880	ENV_SIVML	P11267 simian immu
42	79	40.3	858	ENV_HV2RO	P04577 human immun
43	78	39.8	768	ENV_SIVV1	P27757 simian immu
44	78	39.8	851	ENV_HV2D1	P17755 human immun
45	78	39.8	851	ENV_HV2G1	P16040 human immun

## ALIGNMENTS

RESULT 1	ENV_HV1B8	STANDARD:	PRT:	851 AA.
ID	ENV_HV1B8			
AC	P04582;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11684;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; Pubmed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumanster K., Ivanoff L., Pelteway S.R., Pearson M.L., Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";			
RT	Nature 313:277-284(1985).			
RL	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib.ch">license@sib.ch</a> ).			
CC	-----			
CC	EMBL: K02011; AAA4661.1; -			
DR	HIV: K02011; ENV5B8.			
DR	Glycositedb: P04582; -			
DR	InterPro: IPR000328; ENV_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	506	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	331	BY SIMILARITY.
FT	DISULFID	378	440	BY SIMILARITY.
FT	DISULFID	385	413	BY SIMILARITY.
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC. . .) (POTENTIAL).

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.8%; Score 180; DB 2; Length 357;  
Best Local Similarity 91.7%; Pred. No. 4,8e-14;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSIHRILIESQNOQEKNEQELLELDKWSLWNMF 36  
DB 139 YTGILYRLIESQNOQEKNEQELLELDKWSLWNMF 174

RESULT 12

S54384

envelope polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

Reference number: S54377

Accession: S54384

Status: preliminary

Molecule type: genomic RNA

A:Residues: 1-853 <THX>

A:Cross-references: EMBL:M2639; NID:g329377; PIDN:AAA45370.1; PID:g329385

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: polypeptide

Query Match 91.8%; Score 180; DB 2; Length 853;  
Best Local Similarity 91.7%; Pred. No. 1.3e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSIHRILIESQNOQEKNEQELLELDKWSLWNMF 36  
DB 635 YTGILYRLIESQNOQEKNEQELLELDKWSLWNMF 670

RESULT 13

VCLJZR

env polypeptide precursor - human immunodeficiency virus Zr-6

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus Zr-6

C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999

C:Accession: D26192

R:Srivatsan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from zaire: nucleoti

Reference number: A26192; MUID:87248097; PMID:3036660

Accession: D26192

Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-85/Product: env polypeptide #status predicted <MAT>

F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>

F:501-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,145,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 91.8%; Score 180; DB 1; Length 855;  
Best Local Similarity 91.7%; Pred. No. 1.3e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSIHRILIESQNOQEKNEQELLELDKWSLWNMF 36

DB 637 YTGILYRLIESQNOQEKNEQELLELDKWSLWNMF 672

RESULT 14

A41621

env polypeptide M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: A41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence divers

A:Reference number: A41621; MUID:92107924; PMID:1763038

A:Accession: A41621

Molecule type: DNA

A:Residues: 1-445 <BUR>

A:Cross-references: GB:M77228; NID:g328627; PIDN:AB03790.1; PID:g555013

A>Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TM>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding si

Query Match 90.3%; Score 177; DB 2; Length 445;  
Best Local Similarity 88.9%; Pred. No. 1.4e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSIHRILIESQNOQEKNEQELLELDKWSLWNMF 36  
DB 380 YTSIYRLIESQNOQEKNEQELLELDKWSLWNMF 415

RESULT 15

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JREF)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 90.3%; Score 177; DB 2; Length 847;  
Best Local Similarity 91.7%; Pred. No. 2.9e-13;  
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YTSIHRILIESQNOQEKNEQELLELDKWSLWNMF 36

DB 629 YTSIYRLIESQNOQEKNEQELLELDKWSLWNMF 664

Search completed: May 16, 2003, 11:25:11  
Job time: 13.1446 secs



env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doranberger, J.A.; Papas, T.S.; Chraych, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAAA42  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/DNA: signal sequence #status predicted <SIG>  
F:1-30/Product: signal sequence #status predicted <SIG>  
F:252-443/Product: exterior membrane glycoprotein #status predicted <TMN>  
F:252-443/Product: transmembrane glycoprotein #status predicted <TMN>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carboxylate (Asn) (covalent) #status predic  
Query Match 96.9%; Score 190; DB 1; Length 856;  
Best Local Similarity 97.2%; Pred. No. 8.1e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 36  
DB 638 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 673  
RESULT 4  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allizon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <MAT>  
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/DNA: signal sequence #status predicted <SIG>  
F:1-30/Product: signal sequence #status predicted <SIG>  
F:517-861/Product: exterior membrane glycoprotein #status predicted <TMN>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TMN>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carboxylate (Asn) (covalent) #status predic  
Query Match 96.9%; Score 190; DB 1; Length 861;  
Best Local Similarity 97.2%; Pred. No. 8.2e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 36  
DB 643 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 678  
RESULT 5  
env polyprotein P - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polyprotein

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Buger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi  
A:Reference number: A41621; MUID:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:424-443/Product: transmembrane glycoprotein #status predicted <TMN>  
F:9,23,36,48,76,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 94.4%; Score 185; DB 2; Length 443;  
Best Local Similarity 94.4%; Pred. No. 1.5e-14;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 36  
DB 378 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 413  
RESULT 6  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1).  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyp  
F:1-29/DNA: signal sequence #status predicted <SIG>  
F:1-29/Product: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-841/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,  
Query Match 94.4%; Score 185; DB 1; Length 856;  
Best Local Similarity 94.4%; Pred. No. 3.2e-14;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 36  
DB 638 YTSLHRLIEESONOENKNEDELLEDKWASLWNNF 673  
RESULT 7  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-538

Perfect score: 196

Sequence: 1 YTSLLHRLIESQNOEKNEDELLDLKWSLWNF 36

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	190	96.9	851	2 S33985	env polypeptide - huma
2	190	96.9	854	2 S13288	env polypeptide - huma
3	190	96.9	856	1 VCLJH3	env polypeptide pr
4	190	96.9	861	1 VCLJH3	env polypeptide pr
5	185	94.4	443	2 CA1621	env polypeptide P
6	185	94.4	856	1 VCLJ3W	env polypeptide pr
7	184	93.9	861	1 VCLJ3C	env polypeptide pr
8	181	92.3	358	2 S21998	env polypeptide pr
9	181	92.3	358	2 S21998	env polypeptide pr
10	181	92.3	856	1 VCLJVL	env polypeptide pr
11	180	91.8	357	2 S21996	env polypeptide pr
12	180	91.8	853	2 S43384	env polypeptide pr
13	180	91.8	853	1 VCLJ2R	env polypeptide pr
14	177	90.3	845	2 T09448	env polypeptide M
15	177	90.3	847	2 T09448	env polypeptide M
16	177	90.3	847	2 S13289	env polypeptide glycoprot
17	175	89.3	358	2 S22002	env polypeptide - huma
18	175	89.3	358	2 S22000	env polypeptide pr
19	175	89.3	358	2 S70417	env polypeptide pr
20	174	88.8	855	1 VCLJ2A	env polypeptide pr
21	172	87.8	852	2 T12016	env polypeptide glycoprot
22	172	87.8	859	1 VCLJMN	env polypeptide pr
23	171	87.2	357	2 S22006	env polypeptide pr
24	171	87.2	357	2 S22004	env polypeptide pr
25	168	85.7	357	2 S21992	env polypeptide pr
26	168	85.7	843	1 H44001	env polypeptide pr
27	167	85.2	729	1 VCLJXX	env polypeptide pr
28	167	85.2	846	1 VCLJND	env polypeptide pr
29	167	85.2	861	1 VCLJKB	env polypeptide pr

30	166	84.7	859	2 T01672	env polypeptide
31	165	84.2	454	2 B41621	env polypeptide D
32	165	84.2	852	1 VCLJBR	env polypeptide -
33	161	82.1	868	1 VCLJH4	env polypeptide -
34	159	81.1	136	2 J00265	env polypeptide
35	159	81.1	136	2 J00954	env polypeptide
36	149	76.0	854	1 VCLJST	env polypeptide
37	148	75.5	856	1 A44963	env polypeptide pr
38	145	74.0	357	2 S21990	env polypeptide pr
39	136	69.4	877	2 S49197	env polypeptide pr
40	119	60.7	863	2 A53034	env polypeptide P
41	86	43.9	151	2 S30448	env polypeptide - huma
42	86	43.9	151	2 S30452	env polypeptide - huma
43	86	43.9	151	2 S30451	env polypeptide - huma
44	86	43.9	366	2 B41565	env polypeptide -
45	86	43.9	885	2 S04322	env polypeptide -

#### ALIGNMENTS

##### RESULT 1

S33985

env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.  
submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:960199

C:Superfamily: type E retrovirus env polypeptide

Query Match 96.9%; Score 190; DB 2; Length 851;

Best Local Similarity 97.2%; Pred. No. 8.1e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLLHRLIESQNOEKNEDELLDLKWSLWNF 36

DB 633 YTSLLHRLIESQNOEKNEDELLDLKWSLWNF 668

##### RESULT 2

S13288

env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 96.9%; Score 190; DB 2; Length 854;

Best Local Similarity 97.2%; Pred. No. 8.1e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLLHRLIESQNOEKNEDELLDLKWSLWNF 36

DB 636 YTSLLHRLIESQNOEKNEDELLDLKWSLWNF 671

##### RESULT 3

VCLJH3



XX Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36  
1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 13

AA8729 AAY8729 standard; peptide: 36 AA.

AC AAY8729;

DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 84.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
anti-fusogenic; differentiation factor; interleukin; interferon;  
colony stimulating factor; hormone; angiogenic factor.

Undeidentified.

WO959615-A1.

25-NOV-1999.

20-MAY-1999; 99WO-US11219.

20-MAY-1998; 98US-0082279.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI: 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

Disclosure: Page 22; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY8651-190055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;

Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 14

AA89135 AAY89135 standard; peptide: 36 AA.

AC AAY89135;

DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 573.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
anti-fusogenic; differentiation factor; interleukin; interferon;  
colony stimulating factor; hormone; angiogenic factor.

Undeidentified.

WO959615-A1.

25-NOV-1999.

20-MAY-1999; 99WO-US11219.

20-MAY-1998; 98US-0082279.

(TRIM-) TRIMERIS INC.

Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

WPI: 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

Disclosure: Page 30; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
sequence linked to core polypeptides. The enhancer polypeptides are  
derived from various retroviral envelope (gp41) protein sequences,  
especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
pharmacokinetic properties such as increasing the half-life of any core  
polypeptide that they are linked to. The core polypeptides are any  
polypeptide that may be introduced into a living system and that can  
function as a pharmacologically useful peptide for the treatment or  
prevention of a disease. The core polypeptides are bioactive peptides  
selected from a growth factor, cytokine, differentiation factor,  
interleukin, interferon, colony stimulating factor, hormone or  
angiogenic factor. The peptides of the invention can be used for  
inhibiting viral infection and can be used in anti-viral and  
anti-fusogenic treatments. Sequences AAY8651-190055 represent core  
polypeptide fragments that can be used in the invention. Some sequences  
among those indicated also comprise enhancer fragments at terminal ends  
and form hybrid polypeptides.

Sequence 36 AA:

Query Match 96.9%; Score 190; DB 21; Length 36;

Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHRLIEESQNOEKNEDELLELDKWSLWNMF 36

DB 1 YTSLIHSLIEESQNOEKNEDELLELDKWSLWNMF 36

RESULT 15

AA89136 AAY89136 standard; peptide: 36 AA.

XX

XX Sequence 36 AA;  
SQ Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESQNOOEKNEQELLELDKWSIWMNF 36  
|||||  
DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSIWMNF 36

RESULT 11  
AAB14533  
ID AAB14533 standard; peptide: 36 AA.  
AC AAB14533;  
XX  
XX  
DT 24-NOV-2000 (first entry)

XX HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).  
XX  
XX  
XX HIV-1; gp41 C-helical domain;  
KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
KM core 6-helix bundle; viral entry inhibition; immunogenic;  
KM antibody; humoral response; broad spectrum vaccine; anti-HIV;  
KM envelope glycoprotein; prophylaxis; therapy.  
XX  
XX  
OS Human immunodeficiency virus type 1.  
XX  
XX WO200040616-A1.  
XX  
XX 13-JUL-2000.  
XX  
XX 10-JAN-2000; 2000WO-US00456.  
XX  
XX 08-JAN-1999; 99US-0115404.  
XX 07-JAN-2000; 2000US-0480336.  
XX  
XX (WILD/) WILD C T.  
XX (WEIS/) WEISS C D.  
XX  
XX WILD CT, Weiss CD;  
XX  
XX WPI: 2000-465959/40.  
XX  
XX Raising neutralizing antibody response to human immunodeficiency virus,  
XX comprises administering a polypeptide capable of forming a stable  
XX coiled-coil solution structure -  
XX  
XX  
XX Claim 13; Page 12; 97pp; English.

PS Sequences AAB14533-B14534 and AAB14569-B14602 represent specifically  
XX claimed peptides derived from the C-helical domain of the gp41  
XX envelope glycoprotein from a variety of HIV-1 isolates. The invention  
XX relates to raising a neutralising antibody response to a broad spectrum  
XX of HIV (human immunodeficiency virus) strains and isolates, comprising  
XX the administration of a peptide which corresponds to or mimics highly  
XX conserved portions of gp41 which are important in mediating the process  
XX of viral entry into host cells. Such peptides can correspond to or  
XX mimic the coiled coil solution structure of the N-helical domain  
XX (the heptad repeat region), or can correspond or mimic the C-helical  
XX domain (the transmembrane-proximal amphipathic alpha-helical segment),  
XX or the gp41 core 6-helix bundle, which is formed by the interaction  
XX of the N- and C-helical domains of three gp41 proteins. The peptides  
XX can be administered either singly or as a combination (particularly a  
XX combination of N-helical and C-helical peptides), and can be  
XX multimerised. For example, N- and C-helical domain peptides can  
XX be alternately linked together to form a peptide which mimics the  
XX core 6-helix bundle. Administration of the peptide(s) generates a  
XX humoral response, with the production of antibodies against gp41  
XX structures involved in viral entry. As these portions of gp41 are well  
XX conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
CC as a prophylactic or therapeutic vaccine to generate antibodies which  
CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
CC composition comprising polyclonal or monoclonal antibodies can be  
CC administered to reduce HIV infection of uninfected cells. Antibodies  
CC raised against entry-relevant gp41 structures may also be used  
CC therapeutically and as tools to further elucidate the mechanism of HIV  
CC cell entry.  
XX  
XX  
SQ Sequence 36 AA;  
OY Query Match 96.9%; Score 190; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESQNOOEKNEQELLELDKWSIWMNF 36  
|||||  
DB 1 YTSLIHSLIEESQNOOEKNEQELLELDKWSIWMNF 36

RESULT 12  
AAV8665  
ID AAV8665 standard; peptide: 36 AA.  
XX  
XX AAV8665;  
XX  
XX 23-MAY-2000 (first entry)  
XX  
XX Core polypeptide fragment T No. 20.  
XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KM anti-fusogenic; differentiation factor; interleukin; interferon;  
KM colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
XX  
XX  
XX WO9959615-A1.  
XX  
XX 25-NOV-1999.  
XX  
XX 20-MAY-1999; 99WO-US11219.  
XX  
XX 20-MAY-1998; 98US-0082279.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI: 2000-136792/12.  
XX  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
XX  
XX Disclosure; Page 21; 124pp; English.

PS The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,  
XX interleukin, interferon, colony stimulating factor, hormone or  
XX angiogenic factor. The peptides of the invention can be used for  
XX inhibiting viral infection and can be used in anti-viral and  
XX anti-fusogenic treatments. Sequences AAV8651-Y90055 represent core  
XX polypeptide fragments that can be used in the invention. Some sequences  
XX among those indicated also comprise enhancer fragments at terminal ends  
XX and form hybrid polypeptides.

XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 12; Page 24; 148pp; English.  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 96.9%; Score 190; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIRLIESONQOEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIRLIESONQOEKNEDELLEDKWASLWNMF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
AAB52688;  
DT 23-FEB-2001 (first entry)  
XX T20/Dp178 peptide fragment #66.  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemoattractant.  
XX Human immunodeficiency virus type 1.  
XX WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PN partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 12; Page 25; 148pp; English.  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 96.9%; Score 190; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
XX Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTSLIRLIESONQOEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIRLIESONQOEKNEDELLEDKWASLWNMF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
AAB52818;  
XX AC AAB52818;  
XX DT 23-FEB-2001 (first entry)  
XX T20/Dp178 peptide fragment #97.  
XX Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemoattractant.  
XX Human immunodeficiency virus type 1.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI: 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX Claim 14; Page 40; 148pp; English.  
XX The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

RESULT	6
AAY31955	
ID	AAY31955 standard; Peptide: 36 AA.
XX	
AC	AAY31955;
XX	
D7	21-DEC-1999 (first entry)
XX	
DE	Synthetic peptide T-20 (DP-178).
XX	
KW	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
OS	Synthetic.
OS	Human immunodeficiency virus type 1.
FT	
FH	
Key	Location/Qualifiers
I Modified-site	1 /note= "N-terminal acetyl"
J Modified-site	36 /note= "C-terminal amide"
PX	
PN	WO9948513-A1.
PD	
XZ	30-SEP-1999.
PF	
PR	22-MAR-1999; 99WO-US06230.
PR	23-MAR-1998; 98US-0045920.
PA	01-MAY-1998; 98US-0071877.
(TRIM-) TRIMERIS INC.	
Kang M., Bray B., Lachty M., Mader C., Merutka G.; WPI; 1999-591038/50.	
Methods of peptide synthesis, particularly used to produce T-20 or T-20 like peptides -	
Claim 1; Page 102; 120pp; English.	
The present sequence represents an N- and C-terminal modified peptide, designated T-20 (or DP-178), corresponding to amino acids 638-673 of the Transmembrane protein gp41 of HIV-1 LAI isolate. The invention relates to methods for the synthesis of peptides, in particular T-20 and T-20-like peptides. The method involves synthesizing specific side-chain protected peptide fragment intermediates of T-20 or a T-20-like peptide on a solid support, coupling the protected fragments in solution to form a protected T-20 or T-20-like peptide, followed by deprotection of the side chains to yield the final T-20 or T-20-like peptide. The invention also relates to individual peptide fragments (see AAY31956-73) which act as intermediates in the synthesis of peptides of interest (e.g. T-20), and to particular groups of peptide fragments which act as intermediates for the synthesis of the peptide of interest. The method allows for the large scale, economical production of high purity peptides.	
Sequence	36 AA:
Query Match	96.9%; Score 190; DB 20: Length 36;
Best Local Similarity	97.2%; Pred No. 1.8e-16;
Matches	35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 YTSLIHRILIESQNQQEKNDELLELDKWSLMMNF 36                                     Dd 1 YTSLIHSLIEESQNOQEKKNEGELLELDKWASLMMNF 36
RESULT	7
AAY31974	

ID	AA31974	standard; Peptide; 36 AA.
XX		
AC	AA31974;	
XX		
DT	21-DEC-1999	(first entry)
XX		
DE	HIV-1 LAI gp41 T-20 peptide.	
XX		
KW	T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.	
XX		
OS	Human immunodeficiency virus type 1.	
XX		
PN	W0948513-A1.	
XX		
PD	30-SEP-1999.	
XX		
PF	22-MAR-1999; 99WO-US06230.	
XX		
PR	23-MAR-1998; 98US-0045920.	
PR	01-MAY-1998; 98US-0071877.	
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
PI	Kang M, Bray B, Lichty M, Mader C, Merutka G;	
XX		
DR	WPI; 1999-591038/50.	
XX		
PT	Methods of peptide synthesis, particularly used to produce T-20 or	
PT	T-20 like peptides	
XX		
PS	Disclosure; Page 9; 120pp; English.	
XX		
CC	The present sequence represents a peptide, designated T-20 (or	
CC	DP-178), that corresponds to amino acids 638-673 of the	
CC	transmembrane protein gp41 of HIV-1 LAI isolate. The invention	
CC	relates to methods for the synthesis of peptides, in particular	
CC	C- and N-terminal modified T-20 (see AA31955) and T-20-like peptides.	
CC	The method involves synthesizing specific side-chain protected	
CC	peptide fragment intermediates (see AA31956-73) of T-20 or a	
CC	T-20-like peptide on a solid support, coupling the protected	
CC	fragments in solution to form a protected T-20 or T20-like peptide,	
CC	followed by deprotection of the side chains to yield the final T-20	
CC	or T-20-like peptide. The invention also relates to individual	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	peptides of interest (e.g. T-20), and to particular groups of	
CC	peptide fragments which act as intermediates in the synthesis of	
CC	the peptide of interest. The method allows for the large scale,	
CC	economical production of high purity peptides.	
XX		
SO	Sequence 36 AA.	
	Query Match	96.9%; Score 190; DB 20; Length 36;
	Best Local Similarity	97.2%; Pred. No. 1.8e-16;
	Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 YTSILHRLIEESONQOEKNECELELDKWSLIMNF 36	
	1 YTSILHSLIEESONQOEKNECELELDKWSLIMNF 36	
DB		
	1 YTSILHSLIEESONQOEKNECELELDKWSLIMNF 36	
RESULT 8		
ID	AA352655	
XX	AA352655 standard; Peptide; 36 AA.	
AC	AA352655;	
XX		
DT	23-FEB-2001 (first entry)	
XX		
DE	T20/DP178 peptide fragment #33.	
XX		
KW	Antiinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;	
KW	formyl peptide receptor family; FPR; inflammatory response up-regulation;	
FW	chemoattractant.	

ID	AA	Seq ID	Standard	Peptide	AA
XX	AY22912	19-AUG-1999	(first entry)		
XX	AY22912	SEQ ID NO. 108	from WO9820036		
XX	HIV; gp41 protein; constrained helical peptide; HIV infection;				
XX	vaccine; antibody; viral membrane fusion; viral infectivity;				
XX	ligand affinity purification; protein A replacement;				
XX	immunoglobulin purification; epitope mimic.				
XX	Human immunodeficiency virus.				
XX	WO9820036-A1.				
XX	14-MAY-1998.				
XX	05-NOV-1997;	97WO-US20069.			
XX	16-JUN-1997;	97US-0876698.			
XX	06-NOV-1996;	96US-0743698.			
XX	(GETH ) GENENTECH INC.				
XX	Bristled A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;				
XX	Wells JA;				
XX	WPI: 1998-286866/25.				
XX	Production of constrained helical peptide(s) by linking side chains				
XX	on termini of octa-peptide - derived from human immunodeficiency				
XX	virus gp41 protein, useful in vaccines for treatment and prevention				
XX	of infection				
XX	Disclosure; Page 233-234; 279pp; English.				
XX	Peptides AY22805-Y22912 are derived from Human immunodeficiency virus				
XX	(HIV). Specifically, AY22810-Y22910 are derived from gp41 proteins				
XX	of known HIV virus strains (AY22810, AY22871, AY22880, AY22888 and				
XX	AY22903 represent consensus sequences of various sections of the gp41				
XX	protein). Sequences derived from the peptides are used to produce				
XX	constrained helical peptides of the invention. The constrained helical				
XX	peptide is produced by synthesizing an octapeptide in which both terminal				
XX	amino acids have a side-chain that includes a group able to form an amide				
XX	bond, and cyclizing the octapeptide by reacting the specified side-chain				
XX	residues with a difunctional linker to produce two amide bonds.				
XX	The constrained helical peptides are used to treat or prevent HIV				
XX	infection, especially as vaccines that generate antibodies that				
XX	prevent viral membrane fusion or infectivity. Vaccines may contain,				
XX	constrained helical peptides derived from several different strains of				
XX	HIV. The antibodies are also useful for diagnosing HIV infection. Other				
XX	uses for the constrained helical peptides are in affinity purification				
XX	of ligands (particularly where complete binding protein is not readily				
XX	available), e.g. replacements for protein A in immunoglobulin				
XX	purification); as epitope mimics for antibody production; for isolation				
XX	of synthetic antibody clones from phage display libraries; or as stable				
XX	forms of "floppy" peptides or proteins.				
XX	Sequence 36 AA:				
XX	Query Match	96.9%;	Score 190;	DB 19;	Length 36;
XX	Best Local Similarity	97.2%;	Pred. No. 1.8e-16;		
XX	Matches 35; Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
XX	1 YTSLIHRIIEESONQOEKNEDELLDKRASLWNNF 36				
XX					
XX	1 YTSLIHRIIEESONQOEKNEDELLDKRASLWNNF 36				

Query Match	Best Local Similarity	Score 190;	DB 19;	Length 36;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	96.9%;	97.2%;	Pred. NO. 1.8e-16;	
1 YTSLHRLIEESQNOOEKNEDELLDLKWKASLWNNF 36				
1 YTSLHRLIEESQNOOEKNEDELLDLKWKASLWNNF 36				

PA (UYDU-) UNIV DUKE.  
 XX  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petterway SR, Wild CT;  
 XX  
 XX WPI; 1995-036105/05.  
 XX  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 XX  
 PS Claim 11; Page 132, 182pp; English.  
 XX  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-593) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibits transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLELDKWSLWNNF 36  
 |||||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLELDKWSLWNNF 36

RESULT 2  
 AAR98398

ID AAR98398 standard; peptide; 36 AA.

XX AC AAR98398;

XX DT 17-FEB-1997 (first entry)

XX DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

XX KW Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 ALMORT15; 107x178x4; PLZIP search motif; viral transmission; HIV;

XX KW Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus type 1.

PN WO9619495-A1.

XX PD 27-JUN-1996.

XX PF 20-DEC-1995; 95WO-US16733.

XX PR 06-JUN-1995; 95US-0470896.

XX PR 20-DEC-1994; 94US-0360107.

XX PA (TRIM-) TRIMERIS INC.

XX PA (UYDU-) UNIV DUKE.

XX PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 XX PI Matthews TJ, Petterway SR, Wild CT;

XX DR WPI; 1996-309517/31.

XX PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALMORT15, 107x178x4 or PLZIP  
 PT sequence search motif

XX PS Disclosure; Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALMORT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, Influenza virus, or  
 CC hepatitis B virus, to a cell.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLELDKWSLWNNF 36  
 |||||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLELDKWSLWNNF 36

RESULT 3  
 AAM17011

ID AAM17011 standard; peptide; 36 AA.

XX AC AAM17011;

XX DT 30-JUN-1997 (first entry)

XX DE HIV-1 derived peptide useful for treatment of HIV infection.

XX KW HIV; HIV; human; simian immunodeficiency virus; glycoprotein 41;  
 KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KW replication; transmission.

XX OS Human immunodeficiency virus type 1 LAI isolate.

XX PN WO9640191-A1.

XX PD 19-DEC-1996.

XX PF 06-JUN-1996; 96WO-US09499.

XX PR 07-JUN-1995; 95US-0481957.

XX PA (TRIM-) TRIMERIS INC.

XX PI Johnson RM, Lambert DM;

XX DR WPI; 1997-099886/09.

XX PT Compsns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.

XX Claim 2; Figure 1; 84pp; English.

XX AAM17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.

XX SQ Sequence 36 AA;

Query Match 96.9%; Score 190; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-16;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHRLIEESONOQEKNEOELLELDKWSLWNNF 36  
 |||||||  
 DB 1 YTSLIHSLIEESONOQEKNEOELLELDKWSLWNNF 36

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/note="optionally has an amino, acetyl,
9-fluorenylmethoxy-carbonyl, hydrophobic or
macromolecular carrier gp. attached"
38
/note="optionally has a carboxyl, amido, hydrophobic
or macromolecular carrier gp. attached"

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; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent version 3.0
; SEQ ID NO: 41
; LENGTH: 46
; TYPE: PRF
; ORGANISM: Human immunodeficiency virus type 1
; US-09-779-451-41

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Query Match          97.4%; Score 189; DB 10; Length 46;
Best Local Similarity 97.2%; Pred. No. 8.4e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY      1 YTSLSLIESONQOEKNEQELLELDKWSLWNMF 36
      11 YTSLSLIESONQOEKNEQELLELDKWSLWNMF 46
DB      11 YTSLSLIESONQOEKNEQELLELDKWSLWNMF 46

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Search completed: May 16, 2003, 12:10:25  
 Job time : 15.759 secs

J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovashnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-854-816-1

Query Match 97.4%; Score 189; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36

RESULT 13  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovashnik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108

Query Match 97.4%; Score 189; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6,5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36

Db 1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 37

RESULT 14  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Sebbel, Peter  
Dunant, Nicolas  
Applicant: Bachmann, Martin  
Applicant: Tissot, Alain  
Applicant: Lechner, Franziska

TITLE OF INVENTION: Molecule Antigen Array

FILE REFERENCE: 1700.0180002

CURRENT APPLICATION NUMBER: US/09/848,616

CURRENT FILING DATE: 2001-05-05

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 176

LENGTH: 37

TYPE: PPT

ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: DPL78c peptide  
US-09-848-616-176

Query Match 97.4%; Score 189; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 6,7e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 36  
1 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 37

Db 2 YTSLSLIEESONQOEKNEDELLEDKWASLWNMF 37

RESULT 15  
US-09-779-451-41  
Sequence 41, Application US/09779451  
Patent No. US20020094521A1

; Sequence 1, Application US/09854816  
 ; Patent No. US20020151473A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Andrew C. Braisted

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Phd., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-854-816-12  
Query Match 98.5%; Score 191; DB 10; Length 269;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 36  
DB 169 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 204  
RESULT 5  
US-09-854-816-46  
Sequence 46, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovastnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Phd., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
US-09-854-816-46  
Query Match 97.9%; Score 190; DB 10; Length 269;  
Best Local Similarity 97.2%; Pred. No. 4.1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 36  
DB 169 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 204  
RESULT 6  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
FILE REFERENCE: 2793/65166  
CURRENT APPLICATION NUMBER: US/09/874,475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
Query Match 97.4%; Score 189; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.5e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 36  
DB 1 YTSLYSLIEESQNOEKNEDELLELDKWSLWNNF 36  
RESULT 7  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US20030044411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116,797  
CURRENT FILING DATE: 2002-10-15  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

LENGTH: 268 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-854-816-13

Query Match 99.0%; Score 192; DB 10; Length 268;  
Best Local Similarity 97.2%; Pred. No. 2,4e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 2  
US-09-854-816-50  
Sequence 50, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasanik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-854-816-50

Query Match 98.5%; Score 191; DB 10; Length 233;  
Best Local Similarity 97.2%; Pred. No. 2,7e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 3

US-09-854-816-9  
Sequence 9, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasanik  
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-854-816-9

Query Match 98.5%; Score 191; DB 10; Length 268;  
Best Local Similarity 97.2%; Pred. No. 3,1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 36  
168 YTSLYISLIESQNOQEKNEDELLELDKWSLWNMF 203

RESULT 4

US-09-854-816-12

Sequence 12, Application US/09854816

Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasanik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of

Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

GenCore version 5.1.4\_p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-537

Perfect score: 194  
Sequence: 1 YTSILYSLIESSONQOEKNEDELLDKWASLWNVF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*\n2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep:\*\n3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*\n4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*\n5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*\n6: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*\n7: /cgn2\_6/ptodata/1/pubppaa/PCTUS\_PUBCOMB.pep:\*\n8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*\n9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*\n10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*\n11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*\n12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*\n13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*\n14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	99.0	268	10	US-09-854-816-13
2	191	98.5	233	10	US-09-854-816-50
3	191	98.5	268	10	US-09-854-816-9
4	191	98.5	269	10	US-09-854-816-12
5	190	97.9	269	10	US-09-854-816-46
6	189	97.4	36	9	US-09-874-475-16
7	189	97.4	36	9	US-10-116-797-1
8	189	97.4	36	9	US-09-493-346-1
9	189	97.4	36	10	US-09-796-202-10
10	189	97.4	36	10	US-09-779-451-5
11	189	97.4	36	10	US-09-834-628-1
12	189	97.4	36	10	US-09-854-816-1
13	189	97.4	36	10	US-09-854-816-108
14	189	97.4	37	9	US-09-848-616-176
15	189	97.4	46	10	US-09-779-451-41
16	189	97.4	56	10	US-09-779-451-4
17	189	97.4	177	9	US-10-040-349B-2
18	189	97.4	221	9	US-10-059-271-84
19	189	97.4	232	9	US-10-059-271-81

20	189	97.4	254	9	US-10-059-271-82	Sequence 82, Appl
21	189	97.4	256	9	US-10-059-271-97	Sequence 97, Appl
22	189	97.4	268	10	US-09-854-816-16	Sequence 16, Appl
23	189	97.4	268	10	US-09-854-816-17	Sequence 17, Appl
24	189	97.4	268	10	US-09-854-816-18	Sequence 18, Appl
25	189	97.4	269	10	US-09-854-816-28	Sequence 28, Appl
26	189	97.4	344	9	US-10-040-349B-1	Sequence 1, Appl1
27	189	97.4	345	9	US-10-026-741-49	Sequence 8, Appl1
28	189	97.4	391	10	US-09-779-451-8	Sequence 93, Appl1
29	189	97.4	391	9	US-10-059-271-93	Sequence 8, Appl1
30	189	97.4	519	10	US-09-756-551A-8	Sequence 33, Appl1
31	189	97.4	853	9	US-10-003-035-33	Sequence 1, Appl1
32	189	97.4	856	10	US-09-476-242-1	Sequence 103, App
33	189	97.4	861	9	US-10-026-741-103	Sequence 53, Appl
34	189	97.4	1101	9	US-10-003-035-53	Sequence 55, Appl
35	189	97.4	1186	9	US-10-003-035-55	Sequence 26, Appl
36	188	96.9	268	10	US-09-854-816-26	Sequence 4, Appl1
37	188	96.9	619	10	US-09-881-609-4	Sequence 2, Appl1
38	188	96.9	646	10	US-09-891-609-2	Sequence 109, App
39	188	96.9	847	10	US-09-476-242-2	Sequence 38, Appl
40	187	96.4	46	10	US-09-854-816-109	Sequence 41, Appl
41	187	96.4	267	10	US-09-854-816-38	Sequence 6, Appl1
42	187	96.4	268	10	US-09-854-816-41	Sequence 42, Appl
43	187	96.4	269	10	US-09-854-816-42	Sequence 43, Appl
44	187	96.4	269	10	US-09-854-816-43	
45	187	96.4	269	10	US-09-854-816-43	

## ALIGNMENTS

RESULT 1  
US-09-854-816-13  
Sequence 13, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovastnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-6674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

APPLICANT: J. Kevin Judice  
 APPLICANT: Robert S. McDowell  
 APPLICANT: J. Christopher Phelan  
 APPLICANT: Melissa A. Starovashnik  
 APPLICANT: James A. Wells  
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
 TITLE OF INVENTION: Making Same  
 NUMBER OF SEQUENCES: 113  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Winpatin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/965,056  
 FILING DATE: 05-Nov-6271198-1997  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Torchia, Phd., Timothy E.  
 REGISTRATION NUMBER: 36,700  
 REFERENCE/DOCKET NUMBER: PI005b2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-8674  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 269 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

Query Match 98.5%; Score 191; DB 4; Length 269;  
Best Local Similarity 97.2%; Pred. No. 2,7e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 YTSLSVSLIESQNOOEKNEOELLELDKWASIMNMF 36  
|||||:|||||:|||||:|||||:|||||:  
DB 169 YTSLSVTLIEESQNOOEKNEOELLELDKWASIMNMF 204

RESULT 15  
Sequence 14, Application US/07956483  
Patent No. 626179

GENERAL INFORMATION:  
APPLICANT: KIENY, Marie-Paule.  
TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED  
TITLE OF INVENTION: 9P160 VARIANT  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/956,483  
FILING DATE: 31-DEC-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: MO 92/19742
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 05392
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 017753-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
OS-07-956-483-14

Query Match          98.5%;   Score 191;   DB 4;   Length 855;
Best Local Similarity 97.2%;   Pred. No. 9,5e-16;
Matches      35;   Conservative      1;   Mismatches      0;   Indels      0;   Gaps      0;

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Query Match          98.5%  Score 191: DB 4
Best Local Similarity 97.2%  Pred: 9.5e-1
Matches      35;  Conservative      1;  Mismatches
Oy      1  YTSLYVSLTEESONOEKNEOEELLEDKNAASLNWVF  36
          |||||:|||||:|||||:|||||:|||||:|||||:
Db      638 YTSLYVTLTEESONOEKNEOEELLEDKNAASLNWVF  673

```

; SEQUENCE CHARACTERISTICS

APPLICANT: Andrew C. Braisted

RESULT 8  
US-08-388-809-6  
Sequence 6, Application US/08388809  
Patent No. 5576000  
GENERAL INFORMATION:  
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
APPLICANT: GENOVEFFA, MARKHAM, PHILIP D. GALLO, ROBERT  
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
APPLICANT: GARTNER, SUZANNE  
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK, 3.5"  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,809  
FILING DATE: 15-FEB-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,835  
FILING DATE: 25-FEB-1993  
APPLICATION NUMBER: US 07/599,491  
FILING DATE: 17-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: LESLIE A. SERUNIAN  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-4092US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 855 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-388-809-6  
Query Match 99.0%; Score 192; DB 1; Length 855;  
Best Local Similarity 97.2%; Pred. No. 7.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 636 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 671  
QY 1 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 36  
DB 636 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 671  
RESULT 9  
US-08-647-714-6  
Sequence 6, Application US/08647714  
Patent No. 5869313  
GENERAL INFORMATION:  
APPLICANT: REITZ, JR., MARVIN S.; FRANCHINI,  
APPLICANT: GENOVEFFA, MARKHAM, PHILIP D. GALLO, ROBERT  
APPLICANT: C.; LORI, FRANCO C.; POPOVIC, MIKULAS; AND  
APPLICANT: GARTNER, SUZANNE  
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK

STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK, 3.5"  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/647,714  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,809  
FILING DATE: 15-FEB-1995  
APPLICATION NUMBER: US 08/022,835  
FILING DATE: 25-FEB-1993  
APPLICATION NUMBER: US 07/599,491  
FILING DATE: 17-OCT-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: LESLIE A. SERUNIAN  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 2026-4092US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 751-6849  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ. ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 855 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-647-714-6  
Query Match 99.0%; Score 192; DB 2; Length 855;  
Best Local Similarity 97.2%; Pred. No. 7.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 636 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 671  
QY 1 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 36  
DB 636 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 671  
RESULT 10  
US-09-570-921-12  
Sequence 12, Application US/09570921  
Patent No. 6455265  
GENERAL INFORMATION:  
APPLICANT: SERRES, PIERRE-FRANCOIS  
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE  
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION  
FILE REFERENCE: 106213  
CURRENT APPLICATION NUMBER: US/09/570,921  
PRIORITY FILING DATE: 2000-05-15  
PRIOR APPLICATION NUMBER: PCT/FR98/02447  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: FR/97/14387  
PRIOR FILING DATE: 1997-11-17  
NUMBER OF SEQ. ID NOS: 144  
SOFTWARE: PatentIn Ver. 2.1  
SEQ. ID NO 12  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Human  
US-09-570-921-12  
Query Match 98.5%; Score 191; DB 4; Length 138;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
DB 99 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 134  
QY 1 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 36  
DB 99 YTSIIYSLIEESONQOEKNEOELLELDKMSLNNWF 134

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SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,739
FILING DATE: 27-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Haliday, Emily
REGISTRATION NUMBER: 38903
REFERENCE/DOCKET NUMBER: 14918-704
TELEPHONE: 415-393-2000
TELEFAX: 415-393-2286
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-492-739-28

Query Match          100.0%; Score 194; DB 4; Length 850;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 632 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 667

RESULT 6
US-08-965-056-13
Sequence 13, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Pheasant
APPLICANT: Melissa A. Starovasinik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

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LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-965-056-13

Query Match          99.0%; Score 192; DB 4; Length 268;
Best Local Similarity 97.2%; Pred. No. 2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 168 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 203

RESULT 7
US-08-022-835-6
Sequence 6, Application US/08022835
Patent No. 5420030
GENERAL INFORMATION:
APPLICANT: Reitz Jr., Marvin S.
APPLICANT: Franchini, Genevieve
APPLICANT: Markham, Phillip D.
APPLICANT: Gallo, Robert C.
APPLICANT: Lori, Franco C.
APPLICANT: Popovic, Mikulas
APPLICANT: Gartner, Suzanne
TITLE OF INVENTION: MOLECULAR CLONES OF HIV-1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: CUSHMAN, DARBY & CUSHMAN
STREET: Eleventh Floor, 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/022,835
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/599,491
FILING DATE: 17-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/78507/SRL
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 855 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-022-835-6

Query Match          99.0%; Score 192; DB 1; Length 855;
Best Local Similarity 97.2%; Pred. No. 7.2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 36
DB 636 YTSIYSLIEESONQOEKNEDELLELDKNASLWNMF 671

```

PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 642  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-642

Query Match 100.0%; Score 194; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1,3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSEESONOEKNEOELELDKWSLWNMF 36  
DB 1 YTSLSLSEESONOEKNEOELELDKWSLWNMF 36

LT 3  
US-448-603A-28

Sequence 28, Application US/08448603A  
Patent No. 5864027

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
APPLICANT: Nakamura, Gerald R.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP

STREET: 3 Embarcadero Center

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/448,603A

FILING DATE: 07-JUN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/072,833

FILING DATE: 07-JUN-93

ATTORNEY/AGENT INFORMATION:

NAME: Haliday, Emily

REGISTRATION NUMBER: 38903

REFERENCE/DOCKET NUMBER: 14918-704

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-393-2000

TELEFAX: 415-393-2286

TELEX:

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 850 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-448-603A-28

Query Match 100.0%; Score 194; DB 2; Length 850;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSEESONOEKNEOELELDKWSLWNMF 36  
DB 632 YTSLSLSEESONOEKNEOELELDKWSLWNMF 667

RESULT 4  
US-09-134-075-28  
Sequence 28, Application US/09134075  
Patent No. 6042836

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
APPLICANT: Nakamura, Gerald R.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP

STREET: 3 Embarcadero Center

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/134,075

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/448,603

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Haliday, Emily

REGISTRATION NUMBER: 38903

REFERENCE/DOCKET NUMBER: 14918-704

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-393-2000

TELEFAX: 415-393-2286

TELEX:

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 850 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-134-075-28

Query Match 100.0%; Score 194; DB 3; Length 850;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSEESONOEKNEOELELDKWSLWNMF 36  
DB 632 YTSLSLSEESONOEKNEOELELDKWSLWNMF 667

RESULT 5  
US-09-492-739-28  
Sequence 28, Application US/09492739  
Patent No. 6331404

GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
APPLICANT: Nakamura, Gerald R.  
TITLE OF INVENTION: HIV Envelope Polypeptides  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McCutchen, Doyle, Brown & Enersen, LLP

STREET: 3 Embarcadero Center

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-537

Perfect score: 194

Sequence: 1 YTSLSLIESQNOQERNEQELLELDKWSLWMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2.6/ptodata/1/1aa/PCUTS.COMB.pep.\*
- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	194	100.0	36	US-09-082-279B-642	Sequence 642, App
2	194	100.0	36	US-09-315-304B-642	Sequence 642, App
3	194	100.0	850	US-08-448-603A-28	Sequence 28, Appl
4	194	100.0	850	US-09-134-075-28	Sequence 28, Appl
5	194	100.0	850	US-09-492-739-28	Sequence 28, Appl
6	192	99.0	268	US-08-965-056-13	Sequence 13, Appl
7	192	99.0	855	US-08-022-835-6	Sequence 6, Appl
8	192	99.0	855	US-08-388-809-6	Sequence 6, Appl
9	192	99.0	855	US-08-647-714-6	Sequence 6, Appl
10	191	98.5	138	US-09-570-921-12	Sequence 12, Appl
11	191	98.5	138	US-09-570-921-27	Sequence 27, Appl
12	191	98.5	233	US-08-965-056-50	Sequence 50, Appl
13	191	98.5	268	US-08-965-056-9	Sequence 9, Appl
14	191	98.5	269	US-08-965-056-12	Sequence 12, Appl
15	191	98.5	855	US-07-956-483-14	Sequence 14, Appl
16	191	98.5	867	US-08-472-240A-5	Sequence 46, Appl
17	190	97.9	269	US-08-965-056-46	Sequence 46, Appl
18	189	97.4	36	US-08-073-028-1	Sequence 1, Appl
19	189	97.4	36	US-08-486-099-1	Sequence 1, Appl
20	189	97.4	36	US-09-071-877-1	Sequence 1, Appl
21	189	97.4	36	US-08-360-107A-1	Sequence 1, Appl
22	189	97.4	36	US-08-484-223B-1	Sequence 1, Appl
23	189	97.4	36	US-08-919-597-1	Sequence 1, Appl
24	189	97.4	36	US-08-475-668A-1	Sequence 1, Appl
25	189	97.4	36	US-08-485-551A-1	Sequence 1, Appl
26	189	97.4	36	US-08-471-913A-1	Sequence 1, Appl
27	189	97.4	36	US-08-554-616-1	Sequence 1, Appl

28	189	97.4	36	US-08-485-264A-1	Sequence 1, Appl
29	189	97.4	36	US-09-082-279B-15	Sequence 15, Appl
30	189	97.4	36	US-09-082-279B-497	Sequence 497, Appl
31	189	97.4	36	US-09-082-279B-498	Sequence 498, Appl
32	189	97.4	36	US-09-082-279B-603	Sequence 603, Appl
33	189	97.4	36	US-09-082-279B-630	Sequence 630, Appl
34	189	97.4	36	US-09-082-279B-631	Sequence 631, Appl
35	189	97.4	36	US-09-082-279B-705	Sequence 705, Appl
36	189	97.4	36	US-09-082-279B-834	Sequence 834, Appl
37	189	97.4	36	US-09-082-279B-1076	Sequence 1076, Appl
38	189	97.4	36	US-09-082-279B-1121	Sequence 1121, Appl
39	189	97.4	36	US-09-082-279B-1161	Sequence 1161, Appl
40	189	97.4	36	US-08-965-056-1	Sequence 1, Appl
41	189	97.4	36	US-08-965-056-108	Sequence 108, Appl
42	189	97.4	36	US-09-045-920-1	Sequence 1, Appl
43	189	97.4	36	US-08-474-349A-1	Sequence 399, Appl
44	189	97.4	36	US-08-474-349A-399	Sequence 413, Appl
45	189	97.4	36	US-08-474-349A-413	Sequence 413, Appl

## ALIGNMENTS

```
RESULT 1
US-09-082-279B-642
; Sequence 642, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Moïmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082, 279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 642
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-642

Query Match          100.0%; Score 194; DB 4; Length 36;
Best local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLIESQNOQERNEQELLELDKWSLWMNF 36
DB 1 YTSLSLIESQNOQERNEQELLELDKWSLWMNF 36

RESULT 2
US-09-315-304B-642
; Sequence 642, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315, 304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082, 279
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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds

(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-540

Perfect score: 196

Sequence: 1 YTSLIHTLIEESONQOEKNEDELLELDKWSLWNMF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	98.0	851	2	env polypeptide -
2	192	98.0	854	2	env polypeptide -
3	192	98.0	856	1	env polypeptide -
4	192	98.0	861	1	env polypeptide -
5	190	96.9	861	1	env polypeptide -
6	187	95.4	357	2	env polypeptide -
7	187	95.4	358	2	env polypeptide -
8	186	94.9	357	2	env polypeptide -
9	185	94.4	443	2	env polypeptide -
10	185	94.4	856	1	env polypeptide -
11	183	93.4	847	2	env polypeptide -
12	183	93.4	856	1	env polypeptide -
13	183	93.4	856	1	env polypeptide -
14	181	92.3	358	2	env polypeptide -
15	181	92.3	358	2	env polypeptide -
16	181	92.3	358	2	env polypeptide -
17	180	91.8	855	1	env polypeptide -
18	177	90.3	357	2	env polypeptide -
19	177	90.3	445	2	env polypeptide -
20	174	88.8	357	2	env polypeptide -
21	174	88.8	357	2	env polypeptide -
22	174	88.8	853	2	env polypeptide -
23	174	88.8	855	1	env polypeptide -
24	174	88.8	855	1	env polypeptide -
25	173	88.3	357	2	env polypeptide -
26	170	86.7	843	1	env polypeptide -
27	169	86.2	846	1	env polypeptide -
28	167	85.2	729	1	env polypeptide -
29	167	85.2	852	1	env polypeptide -

30	167	85.2	861	1	VCLJKB	env polypeptide pr
31	167	85.2	868	1	VCLJH4	env polypeptide -
32	166	84.7	859	2	T01672	env polypeptide -
33	163	83.2	454	2	B41621	env polypeptide D
34	159	81.1	136	2	J00266	env polypeptide -
35	159	81.1	136	2	J00954	env polypeptide -
36	151	77.0	357	2	S21990	env polypeptide pr
37	149	76.0	854	1	VCLJSI	env polypeptide pr
38	148	75.5	856	1	A44963	env polypeptide pr
39	135	68.9	877	2	S49197	env polypeptide p
40	118	60.2	863	2	A53034	env polypeptide -
41	85	43.4	881	1	VCLJG3	env polypeptide -
42	85	43.4	881	1	S03068	env polypeptide -
43	85	43.4	889	1	VCLJG5	env polypeptide -
44	84	42.9	151	2	S30448	env polypeptide -
45	84	42.9	151	2	S30452	env polypeptide -

## ALIGNMENTS

## RESULT 1

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F. Submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:660192; PIDN:CAN7628.1; PID:660199

C:Superfamily: type E retrovirus env polypeptide

Query Match

Best local similarity 98.0%; Score 192; DB 2; Length 851;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 633 YTSLIHTLIEESONQOEKNEDELLELDKWSLWNMF 668

RESULT 2

S13288 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyang, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match

Best local similarity 98.0%; Score 192; DB 2; Length 854;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 636 YTSLIHTLIEESONQOEKNEDELLELDKWSLWNMF 671

RESULT 3

VCLJH3

```

C:Species: human immunodeficiency virus type 1, HIV-1
C:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
C:RgnOrg: C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypotein
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane p
F.1-29/pomani: signal sequence #status predicted <SIG>
F.30-861/Product: env polypotein #status predicted <EPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,
Query Match 96.9%; Score 190; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 YTSLIHTLIESQNOOEKNEDELLELDKWKASLWNNF 36
|||||
DB 643 YTSLIYTLIESQNOOEKNEDELLELDKWKASLWNNF 678

```

S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1

## C;Access

A:Submitted to the EMBL Data Library, July 1991  
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detected by PCR  
A:Reference number: S21990  
A:Accession: S21994  
A:Molecule type: DNA  
A:Residues: 1-357 <STEB1>  
A:Cross-references: EMBL:X61355; NID:G60179; PIDN:CAAA3622.1; PID:G60180  
A:Steuiler, H., Storch-Hagenlocher, B., Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70421  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEB2>

C:Superfamily: type E retrovirus env polyprotein

Query March	95.4%	Score 187;	DB 2;	Length 357;
Best Local Similarity	94.4%	Pred. No. 4.7e-15;		
Matches 34; Conservative	2;	Mismatches 0;	Indels	0;
0Y	1	YTSLHTLIESQNOOEKNEDELLDLKVASIMNMF	36	
Db	139	YTLTLYTLIESQNOOEKNEDELLDLKVASIMNMF	174	

521998  
envelope protein.gp120/gp41 - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1

## C:\Access

submitted to the EMBL Data Library, July 1991  
A.Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as detected by

A:Reference number: S21990  
A:Accession: S21998  
A:Molecule type: DNA  
A:Residues: 1-358 <STE1>  
A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70425  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-222, 'X', 224-358 <STE2>  
A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 95.4%; Score 187; DB 2; Length 358;  
Matches 34; Conservative 94.4%; Pred. No. 4.8e-15; Mismatches 0; Indels 0; Gaps 0;

1 YTSLIHTLIESQNOEKNEDELLELDKWSIWMNF 36  
|||||  
Db 140 YTSIIYTLIEOSQNOEKNEDELLELDKWSIWMNF 175  
|||||

RESULT 8  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:G60181; PIDN:CAA43624.1; PID:g1067129  
A:Experimental source: patient 27L  
A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 94.9%; Score 186; DB 2; Length 357;  
Matches 34; Conservative 94.4%; Pred. No. 6.3e-15; Mismatches 1; Indels 0; Gaps 0;

1 YTSLIHTLIESQNOEKNEDELLELDKWSIWMNF 36  
|||||  
Db 139 YTGIIYTLIEOSQNOEKNEDELLELDKWSIWMNF 174  
|||||

RESULT 9  
C41621  
env polyprotein P - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat of coat protein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus-type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
R:Bunger, H.; Weiser, B.; Flaherty, K.; Gupta, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1765038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:G328631; PIDN:AAB03792.1; PID:g555015  
A>Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env

```

C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:

Query Match          94.4%:  Score 185;  DB 2;  Length 443;
Best Local Similarity 94.4%:  Pred. No. 1,1e-14;
Matches 34;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

QY 1 YTSLIHTLIEESQNOEKNEDELLELDKWSIIMNF 36
|||||:|||||:|||||:|||||:|||||:|||||:
DB 378 YTSLIHTLIEESQNOEKNEDELLELDKWSIIMNF 413

RESULT 10
VCLJ3M
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774
R:Streich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks,
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the
A:Reference number: A24774; MUID:86218077; PMID:243250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STRA>
A:Cross-references: GB:K03455; GB:M38432; NID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,

Query Match          94.4%:  Score 185;  DB 1;  Length 856;
Best Local Similarity 94.4%:  Pred. No. 2.2e-14;
Matches 34;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

QY 1 YTSLIHTLIEESQNOEKNEDELLELDKWSIIMNF 36
|||||:|||||:|||||:|||||:|||||:|||||
DB 638 YTSLIHTLIEESQNOEKNEDELLELDKWSIIMNF 673

RESULT 11
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Parag, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match          93.4%:  Score 183;  DB 2;  Length 847;
Best Local Similarity 94.4%:  Pred. No. 3.8e-14;
Matches 34;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

QY 1 YTSLIHTLIEESQNOEKNEDELLELDKWSIIMNF 36
|||||:|||||:|||||:|||||:|||||:|||||

```

Db 629 YTSIYTLIEESONQOEKNEQDELLDKWASLWNMF 664

## RESULT 12

env protein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
 R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A  
 Nature 348, 69-73, 1990  
 A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
 A:Reference number: S13288; MUID:91043044; PMID:2172833  
 A:Accession: S13289  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-847 <ORF>  
 C:Superfamily: type E retrovirus env polypeptide

Query Match 93.4%; Score 183; DB 2; Length 847;

Best Local Similarity 94.4%; Pred. No. 3.8e-14;  
 Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHTLIEESONQOEKNEQDELLDKWASLWNMF 36  
 |||:|||||:|||||:|||||:|||||:|||||  
 Db 629 YTSIYTLIEESONQOEKNEQDELLDKWASLWNMF 664

## RESULT 13

env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (hmn)

C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03974

R:Mesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.

Nature 313, 450-458, 1985

A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov

A:Reference number: A93355; MUID:85111157; PMID:2982104

A:Accession: A03974

A:Molecule type: DNA

A:Residues: 1-856 <MUE>

A:Cross-references: GB:K02083; NID:9555008; PIDN:AA59873.1; PID:9328559

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot

C:Domain: signal sequence #status predicted <STC>

F:512-856/Product: exterior membrane glycoprotein #status predicted <TM>

F:88,136,141,156,160,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406

F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic

Query Match 93.4%; Score 183; DB 1; Length 856;

Best Local Similarity 94.3%; Pred. No. 3.9e-14;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSIHTLIEESONQOEKNEQDELLDKWASLWNMF 35  
 |||:|||||:|||||:|||||:|||||:|||||  
 Db 638 YTSIHTLIEESONQOEKNEQDELLDKWASLWNMF 672

## RESULT 14

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 3L

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61352; NID:960186; PIDN:CAA43616.1; PID:960187

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STE2>

A:Cross-references: EMBL:X61352; NID:960186

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.3%; Score 181; DB 2; Length 358;

Best Local Similarity 91.7%; Pred. No. 2.5e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHTLIEESONQOEKNEQDELLDKWASLWNMF 36  
 |||:|||||:|||||:|||||:|||||:|||||  
 Db 140 YTSIYTLIEESONQOEKNEQDELLDKWASLWNMF 175

## RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 12-Apr-1995

C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22000

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <STE>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.3%; Score 181; DB 2; Length 358;

Best Local Similarity 91.7%; Pred. No. 2.5e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSIHTLIEESONQOEKNEQDELLDKWASLWNMF 36  
 |||:|||||:|||||:|||||:|||||:|||||  
 Db 140 YTSIYTLIEESONQOEKNEQDELLDKWASLWNMF 175

Search completed: May 16, 2003, 11:25:11

Job time: 12.146 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
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Query Match 98.0% Score 192; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 4,3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 YTSLHTLIEESQNOOEKNEDELLDKWASLWNF 36
Db 633 YTSLHTLIEESQNOOEKNEDELLDKWASLWNF 668
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```
RESULT 2
ENV_HV1B1 STANDARD: PRT; 856 AA.
AC P03375;
ID ENV_HV1B1 STANDARD: PRT; 856 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BHD isolate) (HIV-1).
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumanster K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Ghayee J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type 1 recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells.";
RL J. Biol. Chem. 265:10373-10382(1990).
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EMBL: M15654; AAA44205.1; -  
PIR: A03973; VCLJH3.  
HIV; M15654; ENVSBH102.  
DR Interpro: IPR000328; Env\_GP41.  
DR Interpro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane; Signal.

KW SIGNAL 1 30  
FT CHAIN 512 856 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT DISULFID 119 205 TRANSMEMBRANE GLYCOPROTEIN.  
FT DISULFID 126 196  
FT DISULFID 131 157  
FT DISULFID 218 247  
FT DISULFID 228 239  
FT DISULFID 296 331  
FT DISULFID 378 445  
FT DISULFID 385 418  
FT CARBOHYD 88 88  
FT CARBOHYD 136 136  
FT CARBOHYD 141 141  
FT CARBOHYD 156 156  
FT CARBOHYD 160 160  
FT CARBOHYD 186 186  
FT CARBOHYD 197 197  
FT CARBOHYD 230 230  
FT CARBOHYD 234 234  
FT CARBOHYD 241 241  
FT CARBOHYD 262 262  
FT CARBOHYD 276 276  
FT CARBOHYD 289 289  
FT CARBOHYD 295 295  
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FT CARBOHYD 463 463  
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FT CARBOHYD 616 616  
FT CARBOHYD 625 625  
FT CARBOHYD 637 637  
FT CARBOHYD 674 674  
FT CARBOHYD 750 750  
FT CARBOHYD 816 816  
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931BB27 CRC64;

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Query Match 98.0% Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4,3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 YTSLHTLIEESQNOOEKNEDELLDKWASLWNF 36
Db 638 YTSLHTLIEESQNOOEKNEDELLDKWASLWNF 673
```

```
RESULT 3
ENV_HV1H2 STANDARD: PRT; 856 AA.
ID ENV_HV1H2 STANDARD: PRT; 856 AA.
AC P04578; 009779;
```

[illegible]

FT	CARBOHYD	397	397	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	406	406	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	448	448	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	463	463	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	624	624	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	637	637	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	674	674	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	750	750	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
FT	CARBOHYD	816	816	N-LINKED (GLCNAC . . .)	(POTENTIAL).			
SQ	SEQUENCE	856 AA;	97212 MW;	65AB16APF5107FFED CXC64;				
Query Match		98.0%;	Score 192;	DB 1;	Length 856;			
Best Local Similarity		97.2%;	Pred. No. 4,3e-16;					
Matches 35;		Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;			
Oy	1 YTSLHHTLIIESQNQEKNKEDELLELDKWSIWMNF	36						
Dd	638 YTSLHSLIIESQNQEKNKEDELLDKWASIMWF	673						
RESULT 4								
ID	ENV_HV1H3	STANDARD:	PRT:	856 AA.				
AC	P04624:							
DT	13-AUG-1987 (Rel. 05, Created)							
DT	01-FEB-1996 (Rel. 33, Last sequence update)							
DT	15-JUL-1999 (Rel. 38, Last annotation update)							
DE	Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].							
GN	ENV.							
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).							
OC	Viruses; Retroid viruses; Retroviridae; Lentivirae.							
OX	[NCBI_TaxId=11707;							
RN	SEQUENCE FROM N.A.							
RP	MEOLINE=85228248; PubMed=2988795;							
RX	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P. ; "HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients."							
RT	Cell 41:979-986(1985).							
RL	-----							
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CC	-----							
DR	EMBL: M14100; AAAA4679.1; -							
DR	HIV; M14100; ENVSHXB3.							
DR	InterPro: IPR000328; Env_GP41.							
DR	InterPro: IPR000777; GP120.							
DR	Pfam: PF00516; GP120; 1.							
DR	Pfam: PF00517; GP41; 1.							
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.							
FT	SIGNAL	1	30					
FT	CHAIN	31	511	EXTERIOR MEMBRANE GLYCOPROTEIN.				
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.				
FT	DISULFID	119	205	BY SIMILARITY.				
FT	DISULFID	126	196	BY SIMILARITY.				
FT	DISULFID	131	157	BY SIMILARITY.				
FT	DISULFID	218	247	BY SIMILARITY.				
FT	DISULFID	228	239	BY SIMILARITY.				
FT	DISULFID	296	331	BY SIMILARITY.				
FT	DISULFID	378	445	BY SIMILARITY.				
FT	DISULFID	385	418	BY SIMILARITY.				
FT	CARBOHYD	88	88	N-LINKED (GLCNAC . . .) (POTENTIAL).				
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . . .) (POTENTIAL).				

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373668B84C1AFC CRC64;

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Query Match 98.0%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLHTLIEESONOQKNEOELLELDKWSLWNMF 36
DB 638 YTSLSHLSIEESONOQKNEOELLELDKWSLWNMF 673

```

```

RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
AC 070626;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
US Human immunodeficiency virus type 1 (IW12.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

```

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```

```

CC EMBL, U12055; AAA76690.1;
DR GLCOSU12055; 070626;
DR InterPro; IPR000328; Env_GP41.

```

```

DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

```

```

Query Match 98.0%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 YTSLHTLIEESONOQKNEOELLELDKWSLWNMF 36
DB 638 YTSLSHLSIEESONOQKNEOELLELDKWSLWNMF 673

```

```

RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
AC P03377;

```

```

DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

```

```

OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

```

Query Match 96.9%; Score 190; DB 1; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 YTSLHTLIESQNOQEKNEQELLELDKWSLWNF 36
Db 638 YTSLHTLIESQNOQEKNEQELLELDKWSLWNF 673

```

```

RESULT 8
ENV_HV1MF STANDARD: PRT: 853 AA.
ID ENV_HV1MF
AC P19551:

```

```

DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11704;

```

```

RA Waslak A.; Haggerty S., Lamonica C., Mann A.M., Meier C.,
RA "Cloning and characterization of human immunodeficiency virus type 1
RA variants diminished in the ability to induce syncytium-independent
RA cytolysis."
RL J. Virol. 64:3792-3803(1990).

```

```

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DR EMBL: M33943; AAA44850.1; -.
DR HIV: M33943; ENV5MFA.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
DR AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 510 853 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 119 203 BY SIMILARITY.

```

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FT DISULFID 126 194 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 329 BY SIMILARITY.
FT DISULFID 376 443 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 337B93B6F22ABA CRC64;

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Query Match 96.4%; Score 189; DB 1; Length 853;  
 Best Local Similarity 94.4%; Pred. No. 1e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 YTSLHTLIESQNOQEKNEQELLELDKWSLWNF 36
Db 636 YTSLHTLIESQNOQEKNEQELLELDKWSLWNF 671

```

```

RESULT 9
ENV_HV1S3 STANDARD: PRT: 852 AA.
ID ENV_HV1S3
AC P19549:

```

```

DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).

```

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FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 856 AA: 97339 MW: 5FCDBIDC3C1209B3 CRC64;

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Query Match  
Best Local Similarity 93.4%; Score 183; DB 1; Length 856;  
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 YTSLIHTLIESONOQKNEQLELDKKNASLWNMF 35
Db 638 YTSLIHTLIESONOQKNEQLELDKKNASLWNMF 672

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```

RESULT 13
ENV_HV1J3 STANDARD: PRT: 867 AA.
AC P12489:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RP MEDLINE=89352108; PubMed=2669897;
   Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
   "Nucleotide sequences of gag and env genes of a Japanese isolate of
   HIV-1 and their expression in bacteria.";
   AIDS Res. Hum. Retroviruses 5:411-419(1989).
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CC EMBL M21138; AAB03526.1; -
CC DR HIV; M21138; ENV5JH3.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120.1.
CC DR Pfam: PF00517; GP41.1.
CC KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
CC Signal.
CC KW SIGNAL.
CC RT CHAIN 1 30
CC FT CHAIN 31 516 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 517 867 TRANSMEMBRANE GLYCOPROTEIN.
CC FT DISULFID 53 73 BY SIMILARITY.

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FT DISULFID 118 217 BY SIMILARITY.
FT DISULFID 125 208 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 230 259 BY SIMILARITY.
FT DISULFID 240 251 BY SIMILARITY.
FT DISULFID 308 342 BY SIMILARITY.
FT DISULFID 368 457 BY SIMILARITY.
FT DISULFID 395 430 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA: 98399 MW: 5F23101468E8680 CRC64;

```

Query Match  
Best Local Similarity 93.4%; Score 183; DB 1; Length 867;  
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 YTSLIHTLIESONOQKNEQLELDKKNASLWNMF 36
Db 649 YTSLIHTLIESONOQKNEQLELDKKNASLWNMF 684

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RESULT 14
ENV_HV1A2 STANDARD: PRT: 855 AA.
AC P03378:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP MEDLINE=85090453; PubMed=2578227;
   Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
   RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
   RA Levy J.A., Dina D., Luciw P.A.;
   "Nucleotide sequence and expression of an AIDS-associated retrovirus
   (ARV-2).";
   Science 227:484-492(1985).
CC -----

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FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 847 AA; 96466 MW; CDIE33D73AA5BCAE CRC64;

Query Match 90.38; Score 177; DB 1; Length 847;  
 Best Local Similarity 88.9%; Pred. No. 3e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLIHTLIESONQKNEQELLELDKMASLWMP 36  
 |||:::||||||| |||||||||  
 Db 629 YTSIISLIESONQKNEQELLELDKMASLWMP 664

Search completed: May 16, 2003, 11:13:37  
 Job time : 6.07229 secs

3 PAGE BLANK (USPTO)

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-540  
Perfect score: 196  
Sequence: 1 YTSLIHTLIEESONQOEKNEOELLELDKASIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	98.0	645	15	Q993A6 human immun
2	192	98.0	747	15	Q70607 human immun
3	192	98.0	748	15	Q70606 human immun
4	192	98.0	752	15	Q70604 human immun
5	192	98.0	752	15	Q70605 human immun
6	192	98.0	752	15	Q70608 human immun
7	192	98.0	851	15	Q78243 human immun
8	192	98.0	852	15	Q89797 human immun
9	192	98.0	854	15	Q85582 human immun
10	192	98.0	854	15	Q72502 human immun
11	192	98.0	856	15	Q92877 simian-huma
12	192	98.0	856	15	Q74599 human immun
13	192	98.0	856	15	Q74090 human immun
14	190	96.9	442	15	Q69910 human immun
15	190	96.9	841	15	Q41556 human immun
16	190	96.9	849	15	Q77368 human immun

17	190	96.9	849	15	Q80851 human immun
18	190	96.9	851	15	Q56110 human immun
19	190	96.9	851	15	Q80852 human immun
20	190	96.9	856	15	Q72993 human immun
21	190	96.9	856	15	Q41539 human immun
22	190	96.9	857	15	Q80170 human immun
23	190	96.9	859	15	Q80185 human immun
24	190	96.9	859	15	Q80180 human immun
25	190	96.9	859	15	Q80179 human immun
26	190	96.9	859	15	Q80177 human immun
27	190	96.9	859	15	Q80173 human immun
28	190	96.9	859	15	Q80850 human immun
29	190	96.9	862	15	Q80184 human immun
30	190	96.9	862	15	Q80183 human immun
31	190	96.9	862	15	Q80182 human immun
32	190	96.9	862	15	Q80178 human immun
33	190	96.9	862	15	Q80174 human immun
34	190	96.9	868	15	Q80186 human immun
35	188	95.9	123	15	Q9YXR3 human immun
36	188	95.9	854	15	Q90178 human immun
37	188	95.9	854	15	Q78705 human immun
38	188	95.9	855	15	Q9E1R7 human immun
39	188	95.9	858	15	Q80867 human immun
40	188	95.9	858	15	Q80865 human immun
41	188	95.9	864	15	Q9E610 human immun
42	187	95.4	117	15	Q9Q0N5 human immun
43	187	95.4	122	15	Q9YXN9 human immun
44	187	95.4	122	15	Q9E6A9 human immun
45	187	95.4	358	15	Q78120 human immun

## ALIGNMENTS

## RESULT 1

Q993A6 ID Q993A6 PRELIMINARY; PRT; 645 AA.  
AC Q993A6;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER 1 1  
SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 98.0%; Score 192; DB 15; Length 645;

Best Local Similarity 97.2%; Pred. No. 2.1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESONQOEKNEOELLELDKASIMNMF 36  
DB 607 YTSLIHTLIEESONQOEKNEOELLELDKASIMNMF 642

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RESULT 2
070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12034; AAA76669.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732B836A5224514 CRC64;

Query Match 98.0%; Score 192; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 36
DB 633 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 668

RESULT 3
070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12032; AAA76668.1; -
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00517; Gp41; 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732B836A5224514 CRC64;

Query Match 98.0%; Score 192; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 36
DB 633 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 668

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DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120; 1.
DR Pfam: PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BBD186C67694B CRC64;

Query Match 98.0%; Score 192; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 36
DB 634 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 669

RESULT 4
070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA76666.1; -
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120; 1.
DR Pfam: PF00517; Gp41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 98.0%; Score 192; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 2.5e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 36
DB 638 YTSLIHTLEESONQOEKNEDELLELDKWSLWNMF 673

RESULT 5
070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM852;  
RX MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HTLV type IIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM852;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12031; AAA76667.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP41; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;  
Query Match 98.0%; Score 192; DB 15; Length 752;  
Best Local Similarity 97.2%; Pred. No. 2.5e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 36  
Db 638 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 673  
RESULT 6  
ID 070608 PRELIMINARY; PRT; 752 AA.  
AC 070608;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM87-2;  
RA MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HTLV type IIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM87-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12035; AAA7670.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP41; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0BEF8 CRC64;  
Query Match 98.0%; Score 192; DB 15; Length 752;  
Best Local Similarity 97.2%; Pred. No. 2.5e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 36  
Db 638 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 673

Db 638 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 673  
RESULT 7  
ID 078243 PRELIMINARY; PRT; 851 AA.  
AC 078243;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Env polyprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,  
RA Verani P., Rossi G.B.;  
RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
chronically infected HUT-78 cellular clone.";  
RL J. Viral Diseases 1:40-55(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=69352106; PubMed=2765297;  
RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
RA Masci B., Mangiano N., Verani P., Rossi G.;  
RT "Biological and molecular characterization of producer and non  
producer clones from HUT-78 infected with a patient HIV isolate.";  
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
RA Borsetti A., Saggio I., Verani P., Rossi G.;  
RT "Variability of HIV-1 virus: characteristics of an infected but not  
productive clone.";  
RL Int. J. Immunopharmacol. 3:17-23(1990).  
DR EMBL: Z11530; CAA77628.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP41; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;  
Query Match 98.0%; Score 192; DB 15; Length 851;  
Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 36  
Db 633 YTSLIHTLIESONQOEKNEDELLELDKWSLWNMF 668  
RESULT 8  
ID 089797 PRELIMINARY; PRT; 852 AA.  
AC 089797;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LM90-2;  
RA MEDLINE=95127297; PubMed=7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker

Matches	35: Conservative	1: Mismatches	0: Indels	0: Gaps	0: DB
QY	1 YTSLIHTLIEESQNOEKNQOELLLELDKWSLWMMF	36			
DB	636 YTSLIHTLIEESQNOEKNQOELLLELDKWSLWMMF	671			
RESULT 10					
ID	072502	PRELIMINARY;	PRT;	854 AA.	
AC	072502				
DT	01-NOV-1996 (TREMblrel. 01, Created)				
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)				
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)				
DE	ENV polypeptide.				
GN	ENV.				
OS	Human immunodeficiency virus type 1.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11676;				
CL	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN-NL4-3:				
RC	MEDLINE=96036482; PubMed=7483282;				
RA	Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,				
RA	Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;				
RT	"Recovery of virtually full-length HIV-1 provirus of diverse subtypes				
RT	from primary virus cultures using the polymerase chain reaction.";				
RL	Virology 213:80-86(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-NL4-3:				
RA	MEDLINE=866281827; PubMed=3016298;				
RA	Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,				
RA	Martin M.A.;				
RT	"Production of acquired immunodeficiency syndrome-associated				
RT	retrovirus in human and nonhuman cells transfected with an infectious				
RT	molecular clone.";				
RL	J. Virol. 59:284-291(1986).				
DR	EMBL: U26942; AAB60578.1;				
DR	InterPro: IPR000328; Env_GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
DR	Pfam: PF00517; GP41; 1.				
KM	AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.				
FT	CONFLICT 214 214 H -> L (IN REF. 2).				
FT	CONFLICT 530 530 A -> S (IN REF. 2).				
FT	CONFLICT 739 739 G -> D (IN REF. 2).				
SO	SEQUENCE 854 AA; 97005 MW; FP2264B3841D1220 CRC64;				
Query Match	98.0%;	Score 192;	DB 15;	Length 854;	
Best Local Similarity	97.2%;	Pred. No. 2.8e-15;			
Matches 35: Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 YTSLIHTLIEESQNOEKNQOELLLELDKWSLWMMF	36			
DB	636 YTSLIHTLIEESQNOEKNQOELLLELDKWSLWMMF	671			
RESULT 11					
ID	092877	PRELIMINARY;	PRT;	856 AA.	
AC	092877				
DT	01-NOV-1998 (TREMblrel. 08, Created)				
DT	01-NOV-1998 (TREMblrel. 08, Last sequence update)				
DT	01-DEC-2001 (TREMblrel. 19, Last annotation update)				
DE	Envelope glycoprotein.				
GN	ENV.				
OS	Simian-Human immunodeficiency virus.				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=57667;				
CL	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=99098984; PubMed=9882298;				

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodiroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodiroski J.G.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;  
 Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 36  
 Db 638 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 673  
 RESULT 12  
 ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RL J. Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAA12895.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;  
 Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 36  
 Db 638 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 673  
 RESULT 13  
 ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates.";  
 RL J. Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;  
 Query Match 98.0%; Score 192; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 36  
 Db 638 YTSLIHTLIESQNOQEKNEDELLELDKWSLWNMF 673  
 RESULT 14  
 ID 069910 PRELIMINARY; PRT; 42 AA.  
 AC 069910;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Gp41 (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=94211861; PubMed=7512731;  
 RX Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
 RT monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
 DR EMBL: U06740; AAA19153.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 42  
 SO SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;  
 Query Match 96.9%; Score 190; DB 15; Length 42;  
 Best Local Similarity 97.2%; Pred. No. 2.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 36  
 Db 7 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 42

## RESULT 15

ID 041556 PRELIMINARY; PRT: 841 AA.  
 AC 041556;  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT STRAIN=C17;  
 RC MEDLINE=98105804; Pubmed=9445059;  
 RA Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,  
 RA Walker B.D., Neumann A.U., Vermund S.H., Westsky J., Jackson S.,  
 RA Penmore E., Cao Y., Gao F., Kalams S., Kunstman K.J., McDonald D.,  
 RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;  
 RT "Immunodeficiency and virological analyses of persons infected by human  
 RT recombinant gp120 subunit vaccines.";  
 RL J. Virol. 72:1552-1576(1998).  
 DR EMBL: U84814; AAC58844.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR00777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 FT NON\_TER  
 SQ SEQUENCE 841 AA; 95802 MW; AAFCl04893D91667 CRC64;

## Query Match

96.9%; Score 190; DB 15; Length 841;

Best Local Similarity 97.2%; Pred. No. 4.9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 36  
 Db 623 YTSIHHTLIESQNOEKNEQELLELDKWSLWNMF 658

Search completed: May 16, 2003, 11:19:49  
 time : 26.3124 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-540

Perfect score: 196

Sequence: 1 YTSLHTLIEESQNOEKNEDELLELDKWSLWMP 36

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCNUS.COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	98.0	36	1	US-08-073-028-1
2	192	98.0	36	3	US-08-486-099-1
3	192	98.0	36	3	US-09-071-877-1
4	192	98.0	36	3	US-08-360-107A-1
5	192	98.0	36	3	US-08-484-223B-1
6	192	98.0	36	3	US-08-919-597-1
7	192	98.0	36	3	US-08-475-668A-1
8	192	98.0	36	3	US-08-485-551A-1
9	192	98.0	36	3	US-08-471-913A-1
10	192	98.0	36	4	US-08-554-616-1
11	192	98.0	36	4	US-08-485-264A-1
12	192	98.0	36	4	US-09-082-279B-15
13	192	98.0	36	4	US-09-082-279B-497
14	192	98.0	36	4	US-09-082-279B-498
15	192	98.0	36	4	US-09-082-279B-603
16	192	98.0	36	4	US-09-082-279B-630
17	192	98.0	36	4	US-09-082-279B-631
18	192	98.0	36	4	US-09-082-279B-705
19	192	98.0	36	4	US-09-082-279B-834
20	192	98.0	36	4	US-09-082-279B-1076
21	192	98.0	36	4	US-09-082-279B-1121
22	192	98.0	36	4	US-08-965-056-1
23	192	98.0	36	4	US-08-965-056-108
24	192	98.0	36	4	US-09-045-920-1
25	192	98.0	36	4	US-08-474-349A-1
26	192	98.0	36	4	US-08-474-349A-399
27	192	98.0	36	4	US-08-474-349A-399

28	192	98.0	36	4	US-08-474-349A-413	Sequence 413, App
29	192	98.0	36	4	US-09-315-304B-15	Sequence 15, Appl
30	192	98.0	36	4	US-09-315-304B-497	Sequence 497, App
31	192	98.0	36	4	US-09-315-304B-498	Sequence 498, App
32	192	98.0	36	4	US-09-315-304B-603	Sequence 603, App
33	192	98.0	36	4	US-09-315-304B-630	Sequence 630, App
34	192	98.0	36	4	US-09-315-304B-631	Sequence 631, App
35	192	98.0	36	4	US-09-315-304B-705	Sequence 705, App
36	192	98.0	36	4	US-09-315-304B-834	Sequence 834, App
37	192	98.0	36	4	US-09-315-304B-1076	Sequence 1076, App
38	192	98.0	36	4	US-09-315-304B-1121	Sequence 1121, App
39	192	98.0	36	4	US-09-315-304B-1161	Sequence 1161, App
40	192	98.0	36	4	US-09-315-304B-1469	Sequence 1469, App
41	192	98.0	36	4	US-09-315-304B-1470	Sequence 1470, App
42	192	98.0	36	4	US-09-315-304B-1486	Sequence 1486, App
43	192	98.0	36	4	US-08-255-208A-1	Sequence 1, Appl
44	192	98.0	37	4	US-09-082-279B-771	Sequence 771, App
45	192	98.0	37	4	US-09-082-279B-775	Sequence 775, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-1  
; Sequence 1, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO. 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-1  
Query Match 98.0%; Score 192; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Y YTSLHTLIEESQNOEKNEDELLELDKWSLWMP 36  
|||||

DB 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9,6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichly, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

DB 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PPT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9,6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

DB 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 98.0%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 9,6e-18;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOOEKNEQELLELDKWSLWMNF 36

```

Db      1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNWF 36
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RESULT 5  
115-08-48

US-08-484-2238-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:

		98.0%;	Score 192;	DB 3;	Length 36;
Query Match		Pred.	No. 9.6e-18;		
Best Local Similarity		97.2%;			
Matches 33; Conservative	1;	Mismatches	0;	Indels	0;
QY	1 YTSLHTLTIESNQOEKNEDELLFDKVASIWNMF	36			
b	1 YTSLHTLTIESNQOEKNEDELLFDKVASIWNMF	36			

RESULT 6  
US-08-919-597-1 -  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Biolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambeth, Dennis M.  
APPLICANT: Petewell, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:

Qy	1	YTSLHTLIESQNOQEKNEQELLELDKAWASIMNMF	36
		:	
		:	
Db	1	YTSLHTLIESQNOQEKNEQELLELDKAWASIMNMF	36
		:	
		:	

Query Match 98.0%; Score 192; DB 3; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 9,66-18;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
City: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pelteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRP  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 98.0%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,6e-18;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLIHTLIEESONOQEKNEDELLEDKWASLWNMF 36

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497  
Sequence 497, Application US/09082279B  
Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match

Best Local Similarity 97.2%; Score 192; DB 4; Length 36;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 YTSLIHSLIEESONOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:14

Job time: 11.1928 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-540

Sequence: 1 YTSLIHTLIESQNOEKNEOELLELDKWSLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB\_PEP.\*  
2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB\_PEP.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	98.0	36	US-09-874-475-16	Sequence 16, Appl
2	192	98.0	36	US-10-116-797-1	Sequence 1, Appl
3	192	98.0	36	US-09-493-346-1	Sequence 10, Appl
4	192	98.0	36	US-09-796-202-10	Sequence 5, Appl
5	192	98.0	36	US-09-779-451-5	Sequence 1, Appl
6	192	98.0	36	US-09-834-628-1	Sequence 1, Appl
7	192	98.0	36	US-09-854-816-1	Sequence 108, App
8	192	98.0	36	US-09-854-816-108	Sequence 176, App
9	192	98.0	37	US-09-848-616-176	Sequence 41, Appl
10	192	98.0	46	US-09-779-451-41	Sequence 2, Appl
11	192	98.0	56	US-10-040-349B-2	Sequence 84, Appl
12	192	98.0	177	US-10-059-271-84	Sequence 84, Appl
13	192	98.0	221	US-10-059-271-81	Sequence 82, Appl
14	192	98.0	232	US-10-059-271-81	Sequence 97, Appl
15	192	98.0	254	US-10-059-271-82	Sequence 16, Appl
16	192	98.0	256	US-10-059-271-97	Sequence 17, Appl
17	192	98.0	268	US-09-854-816-16	Sequence 18, Appl
18	192	98.0	268	US-09-854-816-17	Sequence 18, Appl
19	192	98.0	268	US-09-854-816-18	Sequence 18, Appl

20	192	98.0	344	US-10-040-349B-1	Sequence 1, Appl
21	192	98.0	345	US-10-026-741-49	Sequence 49, Appl
22	192	98.0	345	US-09-779-451-8	Sequence 8, Appl
23	192	98.0	391	US-10-059-271-93	Sequence 93, Appl
24	192	98.0	519	US-09-756-551A-8	Sequence 8, Appl
25	192	98.0	853	US-10-003-035-33	Sequence 33, Appl
26	192	98.0	856	US-09-476-242-1	Sequence 103, App
27	192	98.0	861	US-10-026-741-103	Sequence 53, Appl
28	192	98.0	1101	US-10-003-035-53	Sequence 55, Appl
29	192	98.0	1186	US-10-003-035-55	Sequence 9, Appl
30	190	96.9	268	US-09-854-816-9	Sequence 9, Appl
31	190	96.9	269	US-09-854-816-12	Sequence 12, Appl
32	189	96.4	36	US-09-912-824-1	Sequence 1, Appl
33	189	96.4	268	US-09-854-816-19	Sequence 19, Appl
34	188	95.9	268	US-09-854-816-28	Sequence 28, Appl
35	187	95.4	268	US-09-854-816-26	Sequence 26, Appl
36	187	95.4	619	US-09-891-609-4	Sequence 2, Appl
37	187	95.4	646	US-09-891-609-2	Sequence 2, Appl
38	187	95.4	847	US-09-476-242-2	Sequence 109, App
39	186	94.9	46	US-09-854-816-109	Sequence 38, Appl
40	186	94.9	268	US-09-854-816-38	Sequence 41, Appl
41	186	94.9	269	US-09-854-816-41	Sequence 6, Appl
42	186	94.9	269	US-09-854-816-42	Sequence 42, Appl
43	186	94.9	1231	US-10-059-271-94	Sequence 94, Appl
44	185	94.4	233	US-09-854-816-50	Sequence 50, Appl
45					

## ALIGNMENTS

```
RESULT 1
US-09-874-475-16
; Sequence 16, Application US/09874475
; Publication No. US20020182592A1
; GENERAL INFORMATION:
; APPLICANT: Petropoulos, Christos J.
; APPLICANT: Parkin, Neil T.
; APPLICANT: Whitcomb, Jeanette
; APPLICANT: Huang, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
; TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS
; FILE REFERENCE: 2793/65166
; CURRENT APPLICATION NUMBER: US/09/874,475
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 36
; TYPE: PRT
; ORGANSIM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match          98.0%; Score 192; DB 9; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLIHTLIESQNOEKNEOELLELDKWSLWNMF 36
Db      1 YTSLIHTLIESQNOEKNEOELLELDKWSLWNMF 36

RESULT 2
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US2003004441A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; CURRENT FILING DATE: 2002-10-15
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Db 1 YTSIHSLIEESQÑQKEKNEQELLELDKWASLWNWF 36



Db 2 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best local Similarity 98.0%; Score 192; DB 10; Length 46;

Best local Similarity 97.2%; Pred. No. 1,7e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

Db 11 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best local Similarity 98.0%; Score 192; DB 10; Length 56;

Best local Similarity 97.2%; Pred. No. 2,1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

Db 16 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotiaux, Benoit

APPLICANT: Chevallier, Michel

APPLICANT: El Habib, Raghabelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best local Similarity 98.0%; Score 192; DB 9; Length 177;

Best local Similarity 97.2%; Pred. No. 7,2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

Db 104 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDDE, ECKHARD

APPLICANT: NICOLAUS, STERAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match

Best local Similarity 98.0%; Score 192; DB 9; Length 221;

Best local Similarity 97.2%; Pred. No. 9,2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 36

Db 131 YTSLSHSLIEESQNOQEKNEQELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPKE, HEINRICH

APPLICANT: BUDDE, ECKHARD

APPLICANT: NICOLAUS, STERAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 81  
;; LENGTH: 232  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 98.0%; Score 192; DB 9; Length 232;  
Best Local Similarity 97.2%; Pred. No. 9.7e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLIHTLIEESQNOQEKNEQELLELDKWSLNNWF 36  
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Db 144 YTSLIHTLIEESQNOQEKNEQELLELDKWSLNNWF 179

RESULT 15  
US-10-059-271-82  
; Sequence 82, Application US/10059271  
; Publication No. US20030082208A1  
; GENERAL INFORMATION:  
; APPLICANT: REPKE, HEINRICH  
; APPLICANT: BUDE, ECKHARD  
; APPLICANT: NICOLAUS, STEFAN  
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
; FILE REFERENCE: ALBRE-22  
; CURRENT APPLICATION NUMBER: US/10/059,271  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: DE 101 06 295  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 82  
; LENGTH: 254  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 98.0%; Score 192; DB 9; Length 254;  
Best Local Similarity 97.2%; Pred. No. 1.1e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLIHTLIEESQNOQEKNEQELLELDKWSLNNWF 36  
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Db 166 YTSLIHTLIEESQNOQEKNEQELLELDKWSLNNWF 201

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Job time : 15.759 secs

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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-541  
Perfect score: 195  
Sequence: 1 YTSLIHSLAESQNOQEKNEQELLELDKWSLWNWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	193	99.0	36	16	AAR64364	DP-178 derived firm
2	193	99.0	36	17	AAR98398	DP178 corresponds
3	193	99.0	36	18	AAAI7011	HIV-1 derived peptide
4	193	99.0	36	19	AAW22912	SPO ID NO. 108 firm
5	193	99.0	36	19	AAV22805	SPO ID NO. 1 from
6	193	99.0	36	20	AAV31955	Synthetic peptide
7	193	99.0	36	20	AAV31974	HIV-1 LAI gp41 T-T
8	193	99.0	36	21	AAW52655	T20/DP178 peptide
9	193	99.0	36	21	AAW52688	T20/DP178 peptide
10	193	99.0	36	21	AAW52818	T20/DP178 peptide

11	193	99.0	36	21	AA81453	HIV-1 isolate LAI
12	193	99.0	36	21	AA86865	Core polypeptide f
13	193	99.0	36	21	AA86879	Core polypeptide f
14	193	99.0	36	21	AA89135	Core polypeptide f
15	193	99.0	36	21	AA89136	Core polypeptide f
16	193	99.0	36	21	AA89242	Core polypeptide f
17	193	99.0	36	21	AA89424	Core polypeptide f
18	193	99.0	36	21	AA89652	Core polypeptide f
19	193	99.0	36	21	AA89735	Core polypeptide f
20	193	99.0	36	21	AA89777	Core polypeptide f
21	193	99.0	36	21	AA89982	Core polypeptide f
22	193	99.0	36	21	AA89983	Core polypeptide f
23	193	99.0	36	21	AA89999	Core polypeptide f
24	193	99.0	36	21	AAU0719	HIV viral envelope
25	193	99.0	36	22	AA870741	HBX2 transmembrane
26	193	99.0	36	22	AA882961	Anti-HIV peptide T
27	193	99.0	36	22	AA867039	HIV-1 gp41 peptide
28	193	99.0	36	22	AB800024	HIV-1 gp41 peptide
29	193	99.0	36	22	AB800087	Biotin-labelled HI
30	193	99.0	36	22	AB800088	Viral DP178/107-II
31	193	99.0	36	22	AB800494	Viral DP178/107-II
32	193	99.0	36	22	AB800495	Viral DP178/107-II
33	193	99.0	36	22	AB800600	RSV F1 protein Dp1
34	193	99.0	36	22	AB800626	Viral DP178/107-II
35	193	99.0	36	22	AB800627	Viral DP178/107-II
36	193	99.0	36	22	AB800628	Viral DP178/107-II
37	193	99.0	36	22	AB800832	Viral DP178/107-II
38	193	99.0	36	22	AB801100	Viral DP178/107-II
39	193	99.0	36	22	AB801143	Viral DP178/107-II
40	193	99.0	36	22	AB801185	Fluorescein-labeled
41	193	99.0	36	22	AB801391	Viral DP178/107-II
42	193	99.0	36	22	AB801392	Viral DP178/107-II
43	193	99.0	36	22	AB801414	Viral DP178/107-II
44	193	99.0	36	22	AB801488	Viral core polypep
45	193	99.0	36	22	AB801970	Viral core polypep

## ALIGNMENTS

## RESULT 1

ID AAR64364 standard; Peptide; 36 AA.

AACR64364;

24-AUG-1995 (first entry)

DE DP-1/8 derived from HIV-1 isolate LA1 has antiviral activity.

human immunodeficiency virus: transmembrane protein: gp41: KW  
 antiviral activity; DP-1/8; DP-10/; diagnostic; HIV-1EAT; KW

[illegible]

XX

ET Modified-s

ET

ET Modified-s

ET

PN MO9428920-  
yy

PD 22-DEC-195

PE 01-JUN-1955  
XX

XX 0/ 00N 100

PA (UYDU-) UNIV DUKE.  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petterwey SR, Wild CT;  
 DR WPI: 1995-036105/05.  
 XX  
 PR Computer search generated synthetic peptides - are inhibitors of  
 PI HIV transmission  
 XX  
 PS Claim 11; Page 132; 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.

XX SQ Sequence 36 AA:

Query Match 99.0%; Score 193; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
 |||||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 2

ID AAR98398 standard; peptide; 36 AA.

XX AAR98398;

DT 17-FEB-1997 (first entry)

DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;

KW ALLMOT15; 107x178x4; PLZIP search motif; viral transmission; HIV;

KW Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus type 1.

PN WO9619495-A1.

PD 27-JUN-1996.

PS 20-DEC-1995; 95WO-US16733.

XX 06-JUN-1995; 95OS-0470896.

PR 20-DEC-1994; 94US-0360107.

XX (TRIM-) TRIMERIS INC.

PA (UYDU-) UNIV DUKE.

PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;

PI Matthews TJ, Petterwey SR, Wild CT;

DR WPI: 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure; Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, Influenza virus, or  
 CC hepatitis B virus, to a cell.

XX SQ Sequence 36 AA:

Query Match 99.0%; Score 193; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
 |||||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 3

ID AAM17011 standard; peptide; 36 AA.

XX AAM17011;

DT 30-JUN-1997 (first entry)

DE HIV-1 derived peptide useful for treatment of HIV infection.

XX HIV; STV: human; simian immunodeficiency virus; glycoprotein 41;

KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;

KW replication; transmission.

XX Human immunodeficiency virus type 1 LAI isolate.

PN WO9640191-A1.

PD 19-DEC-1996.

PS 06-JUN-1996; 96WO-US09499.

XX 07-JUN-1995; 95US-0481957.

XX (TRIM-) TRIMERIS INC.

PI Johnson RM, Lambert DM;

DR WPI: 1997-099886/09.

XX Compens. contg. DP-178 or DP-107 in combination with other

PT therapeutic agent - useful for treatment of HIV infection, esp. by

PT inhibiting replication or transmission of HIV.

XX Claim 2; Figure 1; 84pp; English.

CC AAM17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.

XX SQ Sequence 36 AA:

Query Match 99.0%; Score 193; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
 |||||||:|||||:|||||:|||||:|||||:|||||  
 DB 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 4  
AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
XX AAV22912:  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F MO9820036-A1.  
F 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminl of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure: Page 233-234; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA:  
Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5  
AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
XX AAV22805:  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
F MO9820036-A1.  
F 14-MAY-1998.  
XX  
PF 05-NOV-1997; 97WO-US20069.  
XX  
PR 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
PA (GETH ) GENENTECH INC.  
PI Braisted A, Judice JK, McDowell RS, Phehan JC, Starovasnik MA;  
PI Wells JA;  
DR WPI: 1998-286866/25.  
XX  
PT Production of constrained helical peptide(s) by linking side chains  
PT on terminl of octa:peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
PS Disclosure: Page 143-144; 279pp; English.  
XX  
CC Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
SQ Sequence 36 AA:  
Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 AAY31955  
 ID AAY31955 standard; Peptide: 36 AA.  
 AC AAY31955;  
 DT 21-DEC-1999 (first entry)  
 DE Synthetic peptide T-20 (DP-178).  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT Modified-site /note= "N-terminal acetyl"  
 PM Modified-site 36  
 PM Modified-site /note= "C-terminal amide"  
 XX W09948513-A1.  
 PN 30-SEP-1999.  
 PD 22-MAR-1999; 99WO-US06230.  
 PF 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX (TRIM-) TRIMERIS INC.  
 PI Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 DR WPI: 1999-591038/50.  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 XX Claim 1; Page 102; 120pp; English.  
 PS The present sequence represents an N- and C-terminal modified  
 CC peptide, designated T-20 (or DP-178), corresponding to amino acids  
 CC 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.  
 CC The invention relates to methods for the synthesis of peptides,  
 CC in particular T-20 and T-20-like peptides. The method involves  
 CC synthesizing specific side-chain protected peptide fragment  
 CC intermediates of T-20 or a T-20-like peptide on a solid support,  
 CC coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side  
 CC chains to yield the final T-20 or T-20-like peptide. The invention  
 CC also relates to individual peptide fragments (see AAY31956-73) which  
 CC act as intermediates in the synthesis of peptides of interest (e.g.  
 CC T-20), and to particular groups of peptide fragments which act as  
 CC intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high  
 CC purity peptides.  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID AAY31974 standard; Peptide: 36 AA.  
 XX AAY31974;  
 XX 21-DEC-1999 (first entry)  
 DT HIV-1 LAI gp41 T-20 peptide.  
 DE HIV-1 LAI gp41 T-20 peptide.  
 KW T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 OS Human immunodeficiency virus type 1.  
 PN W09948513-A1.  
 PD 30-SEP-1999.  
 PF 22-MAR-1999; 99WO-US06230.  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX (TRIM-) TRIMERIS INC.  
 PA Kang M, Bray B, Lichty M, Mader C, Merutka G;  
 PI WPI: 1999-591038/50.  
 DR Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides  
 PS Disclosure; Page 9; 120pp; English.  
 XX The present sequence represents a peptide, designated T-20 (or  
 CC DP-178), that corresponds to amino acids 638-673 of the  
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention  
 CC relates to methods for the synthesis of peptides, in particular  
 CC C- and N-terminal modified T-20 (see AAY31955) and T-20-like peptides.  
 CC The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates (see AAY31956-73) of T-20 or a  
 CC T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20  
 CC or T-20-like peptide. The invention also relates to individual  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC peptides of interest (e.g. T-20), and to particular groups of  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides.  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 AAB52655  
 ID AAB52655 standard; Peptide: 36 AA.  
 AC AAB52655;  
 DT 23-FEB-2001 (first entry)  
 DE T20/DP178 peptide fragment #33.  
 KW Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KW chemottractant.

XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 24; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX SQ Sequence 36 AA;  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKMASLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEQELLELDKMASLWNMF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
XX  
XX AAB52688;  
XX  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #66.  
XX KW Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX KM  
XX KW  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PN partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 25; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
XX SQ Sequence 36 AA;  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKMASLWNMF 36  
DB 1 YTSLSHLSLEESQNOQEKNEQELLELDKMASLWNMF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
XX  
XX AAB52818;  
XX  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #97.  
XX KW Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; Inflammatory response up-regulation;  
XX chemoattractant.  
XX KM  
XX KW  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR WPI; 2000-656493/63.  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagonist is used to modulate inflammation -  
XX  
XX Claim 14; Page 40; 148pp; English.  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

Sequence	36 AA.	99.0%	Score 193;	DB 21;	Length 36;
Query Match		97.2%;	Pred. No. 7.6e-17;		
Best Local Similarity		Matches 35;	Conservative 1;	Mismatches 0;	Indels 0;
					Gaps 0;
Db	1 YTSLSHLSIESONOENKEOELLLEDDKWSLWMPF 36				
	1 YTSLSHLSIESONOENKEOELLLEDDKWSLWMPF 36				
RESULT 11					
AAB14533					
ID	AAB14533 standard; peptide: 36 AA.				
AC	AAB14533;				
XX					
XX					
XX					
DT	24-NOV-2000 (first entry)				
	HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).				
KM	HIV-1; gp41 C-helical domain;				
KM	gp41 transmembrane-proximal amphipathic alpha-helical segment;				
KM	core 6-helix bundle; viral entry inhibition; immunogenic;				
KM	antibody; humoral response; broad spectrum vaccine; anti-HIV;				
KM	envelope glycoprotein; prophylaxis; therapy.				
XX					
OS	Human immunodeficiency virus type 1.				
XX					
PN	WO20040616-A1.				
XX					
PD	13-JUL-2000.				
XX					
PF	10-JAN-2000; 2000WO-US00456.				
PR	08-JAN-1999; 98US-0115404.				
PR	07-JAN-2000; 2000US-0480336.				
XX					
PA	(WILD/) WILD C.T.				
PA	(WEIS/) WEISS C.D.				
PI	Wild CT, Weiss CD;				
DR	WPI: 2000-465959/40.				
XX					
PT	Raising neutralizing antibody response to human immunodeficiency virus,				
PT	comprises administering a polypeptide capable of forming a stable				
PT	coiled-coil solution structure -				
PS	Claim 13; Page 12; 97pp; English.				
XX					
CC	Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically				
CC	claimed peptides derived from the C-helical domain of the gp41				
CC	envelope glycoprotein from a variety of HIV-1 isolates. The invention				
CC	relates to raising a neutralising antibody response to a broad spectrum				
CC	of HIV (human immunodeficiency virus) strains and isolates, comprising				
CC	the administration of a peptide which corresponds to or mimics highly				
CC	conserved portions of gp41 which are important in mediating the process				
CC	of viral entry into host cells. Such peptides can correspond to or				
CC	mimic the coiled coil solution structure of the N-helical domain				
CC	(the heptid repeat region), or can correspond or mimic the C-helical				
CC	domain (the transmembrane-proximal amphipathic alpha-helical segment),				
CC	or the gp41 core 6-helix bundle, which is formed by the interaction				
CC	of the N- and C-helical domains of three gp41 proteins. The peptides				
CC	can be administered either singly or as a combination (particularly a				
CC	combination of N-helical and C-helical peptides), and can be				
CC	multimerised. For example, N- and C-helical domain peptides can				
CC	be alternately linked together to form a peptide which mimics the				
CC	core 6-helix bundle. Administration of the peptide(s) generates a				
CC	humoral response, with the production of antibodies against gp41				
CC	structures involved in viral entry. As these portions of gp41 are well				
CC	conserved, such antibodies may be effective against a broad range of				

	HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry.
SQ	Sequence    36 AA:
Query Match	99.0%; Score 193; DB 21; Length 36;
Best Local Similarity	97.2%; Pred. No. 7.6e-17;
Matches	35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy	1 YTSLIHSLEESONOEKNEOELLELDKASIMNWF 36        :       :
Dd	1 YTSLIHSLEESONOEKNEOELLELDKASIMNWF 36
<b>RESULT 12</b>	
ID	AAV88665
AC	AAV88665 standard; peptide; 36 AA.
XX	AAV88665;
DT	23-MAY-2000 (first entry)
DE	Core polypeptide fragment T NO. 20.
KM	Retrovirus: hybrid polypeptide: enhancer: gp41; envelope protein: HIV-1; HIV-2; SIV; pharmacokinetic: half-life; growth factor: cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.
OS	Unidentified.
PJ	WO9959615-A1.
PD	25-NOV-1999.
PF	20-MAY-1999; 99WO-US11219.
PR	20-MAY-1998; 98US-0082279.
PA	(TRIM-) TRIMERIS INC.
PI	Barney S., Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PT	A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence -
PS	Disclosure; page 21; 124pp; English.
XX	The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAV88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.

XX Sequence 36 AA;  
 SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36  
 DB 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36

RESULT 13  
 ID AAY88729 standard; peptide; 36 AA.  
 AC AAY88729;  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 84.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

Unidentified.

OS WO9595615-A1.  
 PN 25-NOV-1999.  
 PD 20-MAY-1999; 99WO-US11219.  
 PF 20-MAY-1998; 98US-0082279.  
 PR (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI: 2000-136792/12.  
 DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure; Page 22; 12app; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
 sequence linked to core polypeptides. The enhancer polypeptides are  
 derived from various retroviral envelope (gp41) protein sequences,  
 especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 polypeptide that they are linked to. The core polypeptides are any  
 polypeptide that may be introduced into a living system and that can  
 function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 selected from a growth factor, cytokine, differentiation factor,  
 interleukin, interferon, colony stimulating factor, hormone or  
 angiogenic factor. The peptides of the invention can be used for  
 inhibiting viral infection and can be used in anti-viral and  
 anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 polypeptide fragments that can be used in the invention. Some sequences  
 among those indicated also comprise enhancer fragments at terminal ends  
 and form hybrid polypeptides.

XX Sequence 36 AA;  
 SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36

DB 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36

RESULT 14  
 ID AAY89135 standard; peptide; 36 AA.  
 AC AAY89135;  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 573.

Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 anti-fusogenic; differentiation factor; interleukin; interferon;  
 colony stimulating factor; hormone; angiogenic factor.

Unidentified.

OS WO9595615-A1.  
 PN 25-NOV-1999.  
 PD 20-MAY-1999; 99WO-US11219.  
 PF 20-MAY-1998; 98US-0082279.  
 PR (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI: 2000-136792/12.  
 DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure; Page 30; 12app; English.

The invention relates to hybrid polypeptides comprising enhancer peptide  
 sequence linked to core polypeptides. The enhancer polypeptides are  
 derived from various retroviral envelope (gp41) protein sequences,  
 especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 polypeptide that they are linked to. The core polypeptides are any  
 polypeptide that may be introduced into a living system and that can  
 function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 selected from a growth factor, cytokine, differentiation factor,  
 interleukin, interferon, colony stimulating factor, hormone or  
 angiogenic factor. The peptides of the invention can be used for  
 inhibiting viral infection and can be used in anti-viral and  
 anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core  
 polypeptide fragments that can be used in the invention. Some sequences  
 among those indicated also comprise enhancer fragments at terminal ends  
 and form hybrid polypeptides.

XX Sequence 36 AA;  
 SQ Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 7.6e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36  
 DB 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36

RESULT 15  
 ID AAY89136 standard; peptide; 36 AA.  
 DT AAY89136

AC AAY89136;

XX 23-MAY-2000 (first entry)

XX Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS Unidentified.

PN WO959615-A1.

PD 25-NOV-1999.

XX 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM.

DR WPI: 2000-136792/12.

XX A new hybrid polypeptide with enhanced pharmacokinetic properties

XX comprises enhancer sequence -

XX Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA;

Query Match 99.0%; Score 193; DB 21; Length 36;

Best local Similarity 97.2%; Pred. No. 7.6e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLEESONQOEKNEQELLELDKWSLNNWF 36

DB 1 YTSLSHLEESONQOEKNEQELLELDKWSLNNWF 36

Search completed: May 16, 2003, 11:12:06

Job time : 32.4578 secs

GenCore version 5.1.4-p5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-541  
Perfect score: 195  
Sequence: 1 YTSLSHLSLEESQNOEKNEQELLEDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
A number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	851	2 S33985	env polyprotein -
2	193	99.0	854	2 S13288	env protein - huma
3	193	99.0	856	1 VCLJH3	env polyprotein pr
4	193	99.0	861	1 VCLJIV	env polyprotein pr
5	184	94.4	443	2 C41621	env polyprotein p
6	184	94.4	856	1 VCLJVL	env polyprotein pr
7	184	94.4	856	1 VCLJ3W	env polyprotein pr
8	184	94.4	861	1 VCLJSC	env polyprotein pr
9	181	92.8	357	2 S21994	env polyprotein g
10	181	92.8	358	2 S21998	env polyprotein g
11	180	92.3	357	2 S21996	env polyprotein g
12	179	91.8	859	1 VCLJMN	env polyprotein pr
13	178	91.3	855	1 VCLJAZ	env polyprotein pr
14	177	90.8	847	2 T09448	env polyprotein pr
15	177	90.8	847	2 S13289	env polyprotein pr
16	176	90.3	445	2 A41621	env polyprotein M
17	175	89.7	358	2 S22002	env polyprotein g
18	175	89.7	358	2 S22000	env polyprotein g
19	175	89.7	358	2 S70417	env polyprotein g
20	175	89.7	852	2 T12016	env polyprotein g
21	174	89.2	357	2 S22004	env polyprotein g
22	172	88.2	357	2 S21992	env polyprotein g
23	172	88.2	853	2 S54384	env polyprotein g
24	172	88.2	855	1 VCLJZR	env polyprotein pr
25	171	87.7	843	1 S22006	env polyprotein pr
26	171	87.7	843	1 H44001	env polyprotein pr
27	170	87.2	846	1 VCLJND	env polyprotein pr
28	168	86.2	852	1 VCLJBR	env polyprotein pr
29	166	85.1	729	1 VCLJRX	env polyprotein pr

30	166	85.1	861	1 VCLJKB	env polyprotein pr
31	165	84.6	859	2 T01672	env polyprotein pr
32	162	83.1	454	2 B41621	env polyprotein D
33	161	82.6	868	1 VCLJH4	env polyprotein -
34	158	81.0	136	2 JU0266	env polyprotein -
35	158	81.0	136	2 JU0266	env polyprotein -
36	153	78.5	854	1 VCLJ51	env polyprotein pr
37	147	75.4	856	1 A44963	env polyprotein pr
38	145	74.4	357	2 S21990	env polyprotein g
39	134	68.7	877	2 S49197	env polyprotein g
40	117	60.0	863	2 A53034	env polyprotein p
41	88	45.1	881	1 VCLJG3	env polyprotein -
42	88	45.1	881	2 S03068	env polyprotein -
43	88	45.1	889	1 VCLJG5	env polyprotein -
44	87	44.6	151	2 S30448	env polyprotein -
45	87	44.6	151	2 S30452	env polyprotein -

## ALIGNMENTS

RESULT 1  
S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAAT7628.1; PID:960199  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 99.0%; Score 193; DB 2; Length 851;  
Matches 35; Conservative 1; Mismatches 0; Indels 0;

Qy 1 YTSLSHLSLEESQNOEKNEQELLEDKWSLWNF 36  
Db 633 YTSLSHLSLEESQNOEKNEQELLEDKWSLWNF 668

RESULT 2  
S13288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, N.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polyprotein

Query Match  
Best Local Similarity 99.0%; Score 193; DB 2; Length 854;  
Matches 35; Conservative 1; Mismatches 0; Indels 0;

Qy 1 YTSLSHLSLEESQNOEKNEQELLEDKWSLWNF 36  
Db 636 YTSLSHLSLEESQNOEKNEQELLEDKWSLWNF 671

RESULT 3  
VCLJH3

```

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Accession: A03973
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R:Ratner, L.; Haseltine, W.; Patarca, R.; Layak, K.J.; Starcich, B.; Josephs, S.F.; Doran,
Berger, J.A.; Papas, T.S.; Chirghey, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMN>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,730,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 4,1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 36
Db 638 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 673

RESULT 4
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 99.0%; Score 193; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 4,1e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 36
Db 643 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 678

RESULT 5
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein

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```

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 94.4%; Score 184; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 2,3e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 36
Db 378 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 413

RESULT 6
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
R:Messing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MEB>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,730,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 94.4%; Score 184; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 4,9e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 35
Db 638 YTSLIHSLSSESONQOEKNEOELLELDKASLWMWF 672

RESULT 7
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

```



C:Superfamily: type E retrovirus env polypotein

Query Match 92.3%; Score 180; DB 2; Length 357;  
Best Local Similarity 88.9%; Pred. No. 5.5e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 139 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 174

# RESULT 12

VCLJMN

env polypotein precursor - human immunodeficiency virus type 1 (isolate MN)

N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: A28922  
P:Quigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
P:Quigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: A28922  
A:Molecule type: DNA  
A:Residues: 1-859 <GUR>  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane prote  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-859/Product: env polypotein #status predicted <EPP>  
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401

Query Match 91.8%; Score 179; DB 1; Length 859;  
Best Local Similarity 91.7%; Pred. No. 1.9e-13;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 642 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 677

# RESULT 13

VCLJMA

env polypotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-S  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: GB:K02007; NID:9328658; PIDN:AAB59882.1; PID:9328666  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  
F:87,129,140,146,161,165,191,200,244,265,292,334,341,358,364,388,394,400,445,458  
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.3%; Score 178; DB 1; Length 855;  
Best Local Similarity 88.9%; Pred. No. 2.5e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 637 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 672

# RESULT 14

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
C:Accession: T09448  
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz  
submitted to the EMBL Data Library, July 1996  
A:Reference number: T09448  
A:Accession: T09448  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781  
C:Genetics:

A:Gene: env  
C:Superfamily: type E retrovirus env polypotein  
Query Match 90.8%; Score 177; DB 2; Length 847;  
Best Local Similarity 88.9%; Pred. No. 3.3e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 629 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 664

# RESULT 15

S13289

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namaz, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13289; MUID:91043044; PMID:2172833  
A:Accession: S13289  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
C:Superfamily: type E retrovirus env polypotein

Query Match 90.8%; Score 177; DB 2; Length 847;  
Best Local Similarity 88.9%; Pred. No. 3.3e-13;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 629 YTSLSHLSLEESONQOEKNEDELLELDKWSLWNMF 664

Search completed: May 16, 2003, 11:25:12  
Job time: 13.146 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(Without alignments)  
245,895 Million cell updates/sec

Title: US-09-623-533A-541

Perfect score: 195  
Sequence: 1 YTSLSHLEESQNOEKNEQELLEDKWASLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	851	1	ENV_HV1B8
2	193	99.0	856	1	ENV_HV1B1
3	193	99.0	856	1	ENV_HV1B2
4	193	99.0	856	1	ENV_HV1B3
5	193	99.0	856	1	ENV_HV1B4
6	193	99.0	856	1	ENV_HV1B5
7	190	97.4	853	1	ENV_HV1B6
8	186	95.4	852	1	ENV_HV1B7
9	184	94.4	856	1	ENV_HV1B8
10	184	94.4	856	1	ENV_HV1B9
11	181	92.8	847	1	ENV_HV1C1
12	179	91.8	856	1	ENV_HV1C2
13	178	91.3	847	1	ENV_HV1C3
14	178	91.3	847	1	ENV_HV1C4
15	178	91.3	847	1	ENV_HV1C5
16	177	90.8	867	1	ENV_HV1C6
17	177	90.8	867	1	ENV_HV1C7
18	173	88.7	853	1	ENV_HV1C8
19	172	88.2	853	1	ENV_HV1C9
20	172	88.2	853	1	ENV_HV1D1
21	171	87.7	843	1	ENV_HV1D2
22	170	87.2	846	1	ENV_HV1D3
23	170	87.2	846	1	ENV_HV1D4
24	168	86.2	852	1	ENV_HV1D5
25	167	85.6	848	1	ENV_HV1D6
26	166	85.1	861	1	ENV_HV1D7
27	165	84.6	859	1	ENV_HV1D8
28	161	82.6	868	1	ENV_HV1D9
29	160	82.1	863	1	ENV_HV1D10
30	153	78.5	854	1	ENV_HV1D11
31	147	75.4	856	1	ENV_HV1D12
32	92	47.2	854	1	ENV_HV1D13
33	88	45.1	881	1	ENV_HV1D14

## ALIGNMENTS

RESULT 1	ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615;				
RA	Rather L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Pettey S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Chrayev J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";				
RA	Nature 313:277-284(1985).				
RT					
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CC	EMBL: K02011; AAA44661.1; -				
CC	HIV: K02011; ENVSRB8.				
DR	Glycosylated: P04582; -				
DR	InterPro: IPR000328; ENV_GPA1.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120.1.				
DR	Pfam: PF00516; GP120.1.				
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL.	1	30		
FT	CHAIN	31	506		
FT	CHAIN	507	851		
FT	DISULFID	54	74		
FT	DISULFID	119	205		
FT	DISULFID	126	196		
FT	DISULFID	131	157		
FT	DISULFID	218	247		
FT	DISULFID	228	239		
FT	DISULFID	296	331		
FT	DISULFID	378	440		
FT	DISULFID	385	413		
FT	CARBOHYD	88	88		
FT	CARBOHYD	136	136		
FT	CARBOHYD	141	141		

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

```

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 99.0%; Score 193; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLSHLSLEESONOQKNEOELLELDKNASLNMWF 36
DB 633 YTSLSHLSLEESONOQKNEOELLELDKNASLNMWF 668

```

```

RESULT 2
ENV_HV1B1 STANDARD; PRT: 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_TaxID=11678;

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RA MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Dorn E.R., Ratslki S.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Peteway J.S. Jr., Pearson M.L.,
RA Laubenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RN Nature 313:277-284(1985).

```

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RA DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RA MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
RT potential glycosylation sites of the type I recombinant human
RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
RT Chinese hamster ovary cells.";
RL J. Biol. Chem. 265:10373-10382(1990).

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```

CC EMBL: M15654; AAA4205.1;
CC PIR: A03973; VCLJH3.
CC HIV: M15654; ENVSBH102.
CC Interpro: IPR000328; Env_GP41.
CC Interpro: IPR00777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Aids; Coat protein; Glycoprotein; Transmembrane;
CC Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT DISULFID 88 88
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931BB27 CRC64;

```

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Query Match 99.0%; Score 193; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 YTSLSHLSLEESONOQKNEOELLELDKNASLNMWF 36
DB 638 YTSLSHLSLEESONOQKNEOELLELDKNASLNMWF 673

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RESULT 3
ENV_HV1H2 STANDARD; PRT: 856 AA.
AC P04578; O09779;

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

```

```

Query Match          99.0% Score 193; DB 1; Length 856;
Best Local Similarity 97.2% Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLSHLSLEESONOEKNEOELLELDKASLWNMF 36
    |||||:|||||:|||||:|||||:|||||:|||||
DB 638 YTSLSHLSLEESONOEKNEOELLELDKASLWNMF 673

```

```

RESULT 5
ENV_HVILM STANDARD; PRT; 856 AA.
ID ENV_HVILM
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
CC DR GlycosultedB: 070626; -
CC DR NCBI_TaxID=11686;
CC DR InterPro: IPR000328; Env_GP41.

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```

DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 512 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CE7E6687 CRC64;

```

```

Query Match          99.0% Score 193; DB 1; Length 856;
Best Local Similarity 97.2% Pred. No. 7.3e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTSLSHLSLEESONOEKNEOELLELDKASLWNMF 36
    |||||:|||||:|||||:|||||:|||||:|||||
DB 638 YTSLSHLSLEESONOEKNEOELLELDKASLWNMF 673

```

```

RESULT 6
ENV_HVILR STANDARD; PRT; 861 AA.
ID ENV_HVILR
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
OX [1]

```



```

FT CARBOHD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 97.4%; Score 190; DB 1; Length 853;
Best Local Similarity 94.4%; Pred. No. 1.7e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHSLLEESONOEKNEQELLELDKWSLWNMF 36
|||||:|||||:|||||:|||||:|||||:
636 YTSLSHSLDESONOENKNEQELLELDKWSLWNMF 671

RESULT 8
ENV_HV1S3 STANDARD; PRT; 852 AA.
ID ENV_HV1S3 STANDARD; PRT; 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OX Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11690;
[1]
RP MEDLINE-90317906; PubMed-2370688;
RX York-Higgins D., Cheng-Wayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
RT replication, and cytopathicity are linked to the envelope region of
RT the viral genome."
RL J. Virol. 64:4016-4020(1990).
-----
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-----
CC EMBL: M38427; AAA45067.1; -
CC DR HIV; M38427; ENVSEF33.
CC DR InterPro: IPR000328; Env.GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC signal.
CC FT SIGNAL 1 31 BY SIMILARITY.
CC FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
CC FT DISULFID 53 73 BY SIMILARITY.
CC FT DISULFID 118 206 BY SIMILARITY.
CC FT DISULFID 125 197 BY SIMILARITY.
CC FT DISULFID 130 156 BY SIMILARITY.
CC FT DISULFID 219 248 BY SIMILARITY.
CC FT DISULFID 229 240 BY SIMILARITY.
CC FT DISULFID 297 331 BY SIMILARITY.
CC FT DISULFID 377 439 BY SIMILARITY.

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FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96603 MW; EEF7BF8D2C9910D CRC64;

Query Match 95.4%; Score 186; DB 1; Length 852;
Best Local Similarity 94.4%; Pred. No. 5.2e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHSLLEESONOEKNEQELLELDKWSLWNMF 36
|||||:|||||:|||||:|||||:|||||:
634 YTSLSHSLLEESONOEKNEQELLELDKWSLWNMF 669

RESULT 9
ENV_HV1PV STANDARD; PRT; 856 AA.
ID ENV_HV1PV STANDARD; PRT; 856 AA.
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OX Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11700;
[1]
RP MEDLINE-8511157; PubMed-2982104;
RX Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus."
RL Nature 313:450-458(1985).
-----
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-----
CC EMBL: K02083; AAB59873.1; -
CC DR EMBL: X01762; CAA25903.1; ALT_SEQ.

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FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA: 97055 MW: DAF4DA60DEBA7A08 CRC64;  
 Query Match 94.4%; Score 184; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 9, 1e-15;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36  
 DB 638 YTSLSYLTLEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 11  
 ID ENV\_HV1W1 STANDARD; PRT; 856 AA.  
 AC P31872;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS ENV.  
 OC Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=31678;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86218077; PubMed=2423250;  
 RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;  
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."  
 RL Cell 45:637-648(1986).  
 RT -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.  
 CC PIR: A24774; VCLJ3W.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 205 BY SIMILARITY.  
 FT DISULFID 125 196 BY SIMILARITY.  
 FT DISULFID 130 152 BY SIMILARITY.  
 FT DISULFID 218 247 BY SIMILARITY.  
 FT DISULFID 228 239 BY SIMILARITY.  
 FT DISULFID 296 330 BY SIMILARITY.  
 FT DISULFID 376 444 BY SIMILARITY.  
 FT DISULFID 383 417 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 856 AA: 97526 MW: DB68D1E49C40ADE9 CRC64;  
 Query Match 94.4%; Score 184; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 9, 1e-15;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36  
 DB 638 YTSLSYLTLEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 12  
 ID ENV\_HV1S1 STANDARD; PRT; 847 AA.  
 AC P19550;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 OS ENV.  
 OC Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
 OX NCBI\_TaxID=11691;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90347835; PubMed=2284920;  
 RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;  
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation."  
 RL J. Virol. 64:4390-4398(1990).  
 CC -----  
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 CC -----  
 DR EMBL: M65024; AAA45072.1; -  
 DR HIV: M38428; ENVSEF162.  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29  
 FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.  
 FT CHAIN 847 847 TRANSMEMBRANE GLYCOPROTEIN.  
 FT DISULFID 53 73 BY SIMILARITY.  
 FT DISULFID 118 203 BY SIMILARITY.  
 FT DISULFID 125 194 BY SIMILARITY.  
 FT DISULFID 130 155 BY SIMILARITY.  
 FT DISULFID 216 245 BY SIMILARITY.  
 FT DISULFID 226 237 BY SIMILARITY.  
 FT DISULFID 294 328 BY SIMILARITY.  
 FT DISULFID 374 435 BY SIMILARITY.  
 FT DISULFID 381 408 BY SIMILARITY.  
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).





FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 855 AA: 97438 MW: A3BC20573AAC41A2 CRC64;

Query Match 91.3%; Score 178; DB 1; Length 855;  
Best Local Similarity 88.9%; Pred. No. 4.8e-14;  
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNLIHSLEESONOEKNEOELELDKWSLWMP 36  
DB 637 YNLIHSLEESONOEKNEOELELDKWSLWMP 672

Job completed: May 16, 2003, 11:13:38  
Job time : 7.07229 secs

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GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-541

Perfect score: 195

Sequence: 1 YTSLHSLIESONQOEKNEQLLELDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rotent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	645	15	0993A6 human immun
2	193	99.0	747	15	070607 human immun
3	193	99.0	748	15	070606 human immun
4	193	99.0	752	15	070604 human immun
5	193	99.0	752	15	070605 human immun
6	193	99.0	752	15	070608 human immun
7	193	99.0	851	15	078243 human immun
8	193	99.0	852	15	089797 human immun
9	193	99.0	854	15	085582 human immun
10	193	99.0	854	15	072502 human immun
11	193	99.0	856	15	092877 simian-huma
12	193	99.0	856	15	074599 human immun
13	193	99.0	856	15	074090 human immun
14	189	96.9	854	15	090178 human immun
15	189	96.9	854	15	078705 human immun
16	188	96.4	856	15	0905M7 human immun

17	187	95.9	616	15	0993B0 human immun
18	187	95.9	618	15	0993B2 human immun
19	187	95.9	757	15	090722 human immun
20	187	95.9	848	15	069980 human immun
21	186	95.4	855	15	09E1R7 human immun
22	186	95.4	858	15	080867 human immun
23	186	95.4	858	15	080865 human immun
24	186	95.4	864	15	09E610 human immun
25	185	94.9	122	15	09YXR6 simian-huma
26	185	94.9	838	15	003806 human immun
27	185	94.9	854	15	078225 human immun
28	185	94.9	855	15	003805 human immun
29	184	94.4	42	15	069910 human immun
30	184	94.4	443	15	080023 human immun
31	184	94.4	841	15	041556 human immun
32	184	94.4	849	15	077368 human immun
33	184	94.4	849	15	080851 human immun
34	184	94.4	851	15	056110 human immun
35	184	94.4	851	15	080852 human immun
36	184	94.4	856	15	072993 human immun
37	184	94.4	856	15	041539 human immun
38	184	94.4	857	15	080170 human immun
39	184	94.4	858	15	080190 human immun
40	184	94.4	858	15	080188 human immun
41	184	94.4	859	15	080185 human immun
42	184	94.4	859	15	080180 human immun
43	184	94.4	859	15	080179 human immun
44	184	94.4	859	15	080177 human immun
45	184	94.4	859	15	080173 human immun

## ALIGNMENTS

## RESULT 1

ID 0993A6 PRELIMINARY; PRT; 645 AA.  
AC 0993A6;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update).  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
DE ENV.  
GN Human immunodeficiency virus type 1.  
OS Viruses; Retroviruses; Retroviridae; Lentivirus.  
OC NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AKK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;  
KW Transmembrane.  
FT NON\_TER 1 1  
SO SEQUENCE 645 AA; 72485 MW; B076514BE9336ZEC CRC64;

## Query Match

Best Local Similarity 99.0%; Score 193; DB 15; Length 645;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLHSLIESONQOEKNEQLLELDKWSLWNF 36  
DB 607 YTSLHSLIESONQOEKNEQLLELDKWSLWNF 642

## RESULT 2

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070607 ID 070607 PRELIMINARY: PRT: 747 AA.
AC 070607:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RM [2]
RN SEQUENCE FROM N.A.
RC STRAIN=LM87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR InterPro: IPR000328; ENV_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match
Best Local Similarity 99.0%; Score 193; DB 15; Length 747;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36
DB 633 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 668

RESULT 3
070606 ID 070606 PRELIMINARY: PRT: 748 AA.
AC 070606:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RM [2]
RN SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR InterPro: IPR000328; ENV_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match
Best Local Similarity 99.0%; Score 193; DB 15; Length 752;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36
DB 633 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 5
070605 ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

```
DR InterPro: IPR000328; ENV_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67694B CRC64;
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Query Match
Best Local Similarity 99.0%; Score 193; DB 15; Length 748;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36
DB 634 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 669
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## RESULT 4

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070604 ID 070604 PRELIMINARY: PRT: 752 AA.
AC 070604:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RM [2]
RN SEQUENCE FROM N.A.
RC STRAIN=LM851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12030; AAA7666.1; -
DR InterPro: IPR000328; ENV_Gp41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match
Best Local Similarity 99.0%; Score 193; DB 15; Length 752;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 36
DB 638 YTSLSHLSLEESONQOEKNEDELLEDKWASLWNMF 673

RESULT 5
070605 ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 6  
 O70608 PRELIMINARY; PRT; 752 AA.  
 AC O70608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752 752  
 SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 2.8e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 673

DB 638 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 673

RESULT 7  
 O78243 PRELIMINARY; PRT; 851 AA.  
 AC O78243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai Q.,  
 Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 RT chronically infected HUT-78 cellular clone.";  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Macchi B., Mangano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 RT producer clones from HUT-78 infected with a patient HIV isolate.";  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 RT productive clone.";  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CAA77628.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 KW SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 633 YTSLSLSLEESONOEKNEDELLELDKWSLWMP 668

RESULT 8  
 O89797 PRELIMINARY; PRT; 852 AA.  
 AC O89797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LM90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Viral variability and serum antibody response in a laboratory worker

RT Infected with HIV type 1 (HTLV type IIIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U12053; AAA76685.1; -  
DR EMBL; U12036; AAA76671.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229DAEB33CF CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 852;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
1 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 36  
634 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 669  
  
RESULT 9  
085582 PRELIMINARY; PRT; 854 AA.  
AC 085582;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Envelope polyprotein.  
RN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-86281827; PubMed-3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone.";  
RT J. Virol. 59:284-291(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E.;  
RN Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-92219406; PubMed-1373204;  
RA Dai L.C., Litcau R., Takahashi K., Ennis F.A.;  
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes.";  
RT J. Virol. 66:3151-3154(1992).  
DR EMBL; M19921; AAA4992.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
1 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 36  
636 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 671  
  
RESULT 10  
072502 PRELIMINARY; PRT; 854 AA.  
AC 072502;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Env polyprotein.  
RN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96036482; PubMed-7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction.";  
RT Virology 213:80-86(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ML4-3;  
RX MEDLINE-86281827; PubMed-3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone.";  
RT J. Virol. 59:284-291(1986).  
DR EMBL; U26942; AAB60578.1; -  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
FT CONFLICT 214 H -> L (IN REF. 2).  
FT CONFLICT 530 A -> S (IN REF. 2).  
FT CONFLICT 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
  
Query Match 99.0%; Score 193; DB 15; Length 854;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
1 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 36  
636 YTSLSHLSLEESONOQEKNEQELLELDKWSLWNMF 671  
  
RESULT 11  
092877 PRELIMINARY; PRT; 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
RT Envelope glycoprotein.  
RN ENV.  
OS Simian-Human immunodeficiency virus.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_Taxid=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-99098984; PubMed-9882298;

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
RA Steenbeke T., Halloran M., Fanton J.W., Axelhelm M.K., Letvin N.L.,  
RA Sodroski J.G.;  
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
RT responsible for the pathogenicity of a multiply passaged simian-human  
RT immunodeficiency virus (SHIV-HXBc2).";  
RL J. Virol. 73:976-984(1999).  
RN (2)  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axelhelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00517; GP120.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 12  
ID 074599 PRELIMINARY; PRT; 856 AA.  
AC Q74599;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=90101366; PubMed=1688473;  
RA Cloyd M.W., Moore B.E.;  
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
RT (HIV-1) Isolates.";  
RL Virology 174:103-116(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RA Iwatani Y.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: D86068; BAA12995.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00516; GP120.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 13  
O74090

ID 074090 PRELIMINARY; PRT; 856 AA.  
AC Q74090;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
RA Halloran M., Axelhelm M.W., Letvin N.L., Sodroski J.G.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF041850; AAD12142.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00517; GP120.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 99.0%; Score 193; DB 15; Length 856;  
Best Local Similarity 97.2%; Pred. No. 3.2e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
DB 638 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 673

RESULT 14  
ID 090178 PRELIMINARY; PRT; 854 AA.  
AC 090178;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MCK1;  
RX MEDLINE=95074930; PubMed=7983770;  
RA Fang H., Pincus S.H.;  
RT "Unique insertion sequence and pattern of CD4 expression in variants  
RT infected with immunotoxins from human immunodeficiency virus type 1-  
RT infected T cells.";  
RL J. Virol. 69:75-81(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Fang H., Pincus S.H.;  
RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
RT immunotoxin-resistant variant T cell line";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF070521; AAC28452.1; -  
DR InterPro: IPR000328; Env-GP41.  
DR Pfam: PF00517; GP120.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 96.9%; Score 189; DB 15; Length 854;  
 Best Local Similarity 94.4%; Pred. No. 9.8e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONOEKNEQELLELDKWSLWNF 36  
 |||||||:|||||:|||||:|||||:|||||  
 DB 636 YTSLSHSLIESONOEKNEQELLELDKWSLWNF 671

## RESULT 15

Q78705 PRELIMINARY; PRT; 854 AA.  
 AC Q78705;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96013815; PubMed=7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.,  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1.";  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AAA96326.1;-;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 96.9%; Score 189; DB 15; Length 854;  
 Best Local Similarity 94.4%; Pred. No. 9.8e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONOEKNEQELLELDKWSLWNF 36  
 |||||||:|||||:|||||:|||||:|||||  
 DB 636 YTSLSHSLIESONOEKNEQELLELDKWSLWNF 671

Search completed: May 16, 2003, 11:19:50  
 Time : 27.3124 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-541

Perfect score: 195  
Sequence: 1 YTSLSHLSLEESONQOEKNEDELLEIDRWASLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	193	99.0	36	1 US-08-073-028-1	Sequence 1, Appl
2	193	99.0	36	1 US-08-486-099-1	Sequence 1, Appl
3	193	99.0	36	3 US-09-071-877-1	Sequence 1, Appl
4	193	99.0	36	3 US-08-360-107A-1	Sequence 1, Appl
5	193	99.0	36	3 US-08-484-223B-1	Sequence 1, Appl
6	193	99.0	36	3 US-08-919-597-1	Sequence 1, Appl
7	193	99.0	36	3 US-08-475-668A-1	Sequence 1, Appl
8	193	99.0	36	3 US-08-485-551A-1	Sequence 1, Appl
9	193	99.0	36	3 US-08-471-913A-1	Sequence 1, Appl
10	193	99.0	36	4 US-08-554-616-1	Sequence 1, Appl
11	193	99.0	36	4 US-08-485-264A-1	Sequence 1, Appl
12	193	99.0	36	4 US-09-082-279B-15	Sequence 15, Appl
13	193	99.0	36	4 US-09-082-279B-497	Sequence 497, App
14	193	99.0	36	4 US-09-082-279B-498	Sequence 498, App
15	193	99.0	36	4 US-09-082-279B-603	Sequence 603, App
16	193	99.0	36	4 US-09-082-279B-630	Sequence 630, App
17	193	99.0	36	4 US-09-082-279B-631	Sequence 631, App
18	193	99.0	36	4 US-09-082-279B-705	Sequence 705, App
19	193	99.0	36	4 US-09-082-279B-834	Sequence 834, App
20	193	99.0	36	4 US-09-082-279B-1076	Sequence 1076, App
21	193	99.0	36	4 US-09-082-279B-1121	Sequence 1121, App
22	193	99.0	36	4 US-09-082-279B-1161	Sequence 1161, App
23	193	99.0	36	4 US-08-965-056-1	Sequence 1, Appl
24	193	99.0	36	4 US-08-965-056-108	Sequence 108, App
25	193	99.0	36	4 US-09-045-920-1	Sequence 1, Appl
26	193	99.0	36	4 US-08-474-349A-1	Sequence 1, Appl
27	193	99.0	36	4 US-08-474-349A-399	Sequence 399, App

28	193	99.0	36	4 US-08-474-349A-413	Sequence 413, App
29	193	99.0	36	4 US-09-315-304B-15	Sequence 15, Appl
30	193	99.0	36	4 US-09-315-304B-497	Sequence 497, App
31	193	99.0	36	4 US-09-315-304B-498	Sequence 498, App
32	193	99.0	36	4 US-09-315-304B-603	Sequence 603, App
33	193	99.0	36	4 US-09-315-304B-630	Sequence 631, App
34	193	99.0	36	4 US-09-315-304B-705	Sequence 705, App
35	193	99.0	36	4 US-09-315-304B-834	Sequence 834, App
36	193	99.0	36	4 US-09-315-304B-1076	Sequence 1076, App
37	193	99.0	36	4 US-09-315-304B-1121	Sequence 1121, App
38	193	99.0	36	4 US-09-315-304B-1161	Sequence 1161, App
39	193	99.0	36	4 US-09-315-304B-1469	Sequence 1469, App
40	193	99.0	36	4 US-09-315-304B-1470	Sequence 1470, App
41	193	99.0	36	4 US-09-315-304B-1486	Sequence 1486, App
42	193	99.0	36	4 US-08-255-208A-1	Sequence 1, Appl
43	193	99.0	37	4 US-09-082-279B-771	Sequence 771, App
44	193	99.0	37	4 US-09-082-279B-775	Sequence 775, App
45	193	99.0	37	4 US-09-082-279B-775	Sequence 775, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-1  
Sequence 1, Application US/08073028  
Patent No. 5464933  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Mathews, Thomas J.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-073-028-1  
Query Match 99.0%; Score 193; DB 1; Length 36;  
Best local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
1 YTSLSHLSLEESONQOEKNEDELLEIDRWASLWMP 36  
|||||

Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1

; Sequence 1, Application US/08486099

; Patent No. 6013263

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; TITLE OF INVENTION: B VIRUS TRANSMISSION

; NUMBER OF SEQUENCES: 209

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/486,099

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1

; Sequence 1, Application US/09071877

; Patent No. 6015881

; GENERAL INFORMATION:

; APPLICANT: Kang, Myung-Chol

; APPLICANT: Bray, Brian

; APPLICANT: Lichy, Maynard

; APPLICANT: Mader, Catherine

; APPLICANT: Merutka, Gene

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

; FILE REFERENCE: 7872-050

; CURRENT APPLICATION NUMBER: US/09/071,877

; CURRENT FILING DATE: 1998-05-01

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1

; Sequence 1, Application US/08360107A

; Patent No. 6017536

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; TITLE OF INVENTION: TRANSMISSION

; NUMBER OF SEQUENCES: 149

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/360,107A

; FILING DATE: 20-DEC-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-013

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 99.0%; Score 193; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESONOEKNEQELLELDKWSLWMPF 36

## RESULT 5

US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995

## CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONOEKNEQELLELDKWSLWMPF 36  
DB 1 YTSLSHLSIESONOEKNEQELLELDKWSLWMPF 36

## RESULT 6

US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown

MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESONOEKNEQELLELDKWSLWMPF 36  
DB 1 YTSLSHLSIESONOEKNEQELLELDKWSLWMPF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
DB-475-668A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6033794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 99.0%; Score 193; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2,3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 10  
US-08-554-616-1  
; Sequence 1, Application US/08554616  
; Patent No. 6133418  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/554,616  
; FILING DATE: 06-NOV-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/073,028  
; FILING DATE: 07-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQLLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESONQOEKNEQLLELDKWSLWNMF 36

RESULT 11  
US-08-485-264A-1  
; Sequence 1, Application US/08485264A  
; Patent No. 6228983  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,264A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-485-264A-1  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQLLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESONQOEKNEQLLELDKWSLWNMF 36

RESULT 12  
US-09-082-279B-15  
; Sequence 15, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15  
Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQLLELDKWSLWNMF 36  
|||||:|||||:|||||:|||||:|||||

Db 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 13

US-09-082-279B-497

Sequence 497, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

## RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 99.0%; Score 193; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.3e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

DB 1 YTSLSHLSLEESONQOEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:22:14  
Job time: 10.1928 secs

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-541  
Perfect score: 195  
Sequence: 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLNNMF 36

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCF\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCUTS\_PUBCOMB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	193	99.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	193	99.0	36	9 US-09-493-346-1	Sequence 1, Appl
4	193	99.0	36	10 US-09-779-202-10	Sequence 10, Appl
5	193	99.0	36	10 US-09-779-451-5	Sequence 5, Appl
6	193	99.0	36	10 US-09-834-628-1	Sequence 1, Appl
7	193	99.0	36	10 US-09-854-816-1	Sequence 1, Appl
8	193	99.0	36	10 US-09-854-816-108	Sequence 108, App
9	193	99.0	37	9 US-09-848-616-176	Sequence 176, App
10	193	99.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	193	99.0	56	10 US-09-779-451-4	Sequence 4, Appl
12	193	99.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	193	99.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	193	99.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	193	99.0	254	9 US-10-059-271-82	Sequence 82, Appl
16	193	99.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	193	99.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	193	99.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	193	99.0	268	10 US-09-854-816-18	Sequence 18, Appl

20	193	99.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	193	99.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	193	99.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	193	99.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	193	99.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	193	99.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	193	99.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	193	99.0	861	9 US-10-026-741-103	Sequence 103, Appl
28	193	99.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	193	99.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	190	97.4	36	10 US-09-912-624-1	Sequence 1, Appl
31	190	97.4	268	10 US-09-854-816-19	Sequence 19, Appl
32	187	95.9	1231	9 US-10-059-271-94	Sequence 94, Appl
33	186	95.4	269	10 US-09-854-816-28	Sequence 28, Appl
34	185	94.9	268	10 US-09-854-816-13	Sequence 13, Appl
35	184	94.4	233	10 US-09-854-816-50	Sequence 50, Appl
36	184	94.4	268	10 US-09-854-816-9	Sequence 9, Appl
37	184	94.4	269	10 US-09-854-816-12	Sequence 12, Appl
38	183	93.8	269	10 US-09-854-816-46	Sequence 46, Appl
39	181	92.8	268	10 US-09-854-816-26	Sequence 26, Appl
40	181	92.8	619	10 US-09-891-609-4	Sequence 4, Appl
41	181	92.8	646	10 US-09-891-609-2	Sequence 2, Appl
42	181	92.8	847	10 US-09-476-242-2	Sequence 2, Appl
43	180	92.3	46	10 US-09-854-816-109	Sequence 109, App
44	180	92.3	267	10 US-09-854-816-38	Sequence 38, Appl
45	180	92.3	268	10 US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLNNMF 36  
Db 1 YTSLSHLSLEESQNOEKNEQELLELDKWSLNNMF 36

RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US2003004411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Maddon, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Application No. US20030082185A1  
GENERAL INFORMATION:  
APPLICANT: Madison, William C  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 99.0%; Score 193; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE: NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:  
APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: Dp178  
US-09-834-628-1

Query Match 99.0%; Score 193; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSHLSLEESQNOQEKNEQELLELDKWSLWNMF 36

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005r2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 108:

US-09-854-816-108

Query Match          99.0%: Score 193; DB 10; Length 36;
Best Local Similarity 97.2%: Pred. No. 1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 YTSLSHLSLESQNOEKNEQELLELDKVASLWNMF 36
Dbb 1 YTSLSHLSLESQNOEKNEQELLELDKVASLWNMF 36

RESULT 9
US-09-848-616-176
Sequence 176, Application US/09848616
Publication No. US20030054010A1
GENERAL INFORMATION:
APPLICANT: Sebbel, Peter
APPLICANT: Dunant, Nicolas
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
CURRENT APPLICATION NUMBER: US/09/848,616
CURRENT FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 176
LENGTH: 37
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DP178c peptide
US-09-848-616-176

Query Match          99.0%: Score 193; DB 9; Length 37;
Best Local Similarity 97.2%: Pred. No. 1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 YTSLSHLSLESQNOEKNEQELLELDKVASLWNMF 36
Dbb 1 YTSLSHLSLESQNOEKNEQELLELDKVASLWNMF 36

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Db 2 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 1,3e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 36

Db 11 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900.0300003

CURRENT APPLICATION NUMBER: US/09/779,451

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 99.0%; Score 193; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 1,6e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 36

Db 16 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotteaux, Benoit

APPLICANT: Chevallier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 5,3e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 36

Db 104 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match

Best Local Similarity 99.0%; Score 193; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 6,7e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 36

Db 131 YTSLSHSLIESONQOEKNEQELLELDKWSLWNMF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPE, HEINRICH

APPLICANT: BUDE, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

```

; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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Query Match          99.0%; Score 193; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 7,1e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 36
|||||:|||||:|||||:|||||:|||||:
Db 144 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKER, HEINRICH
; APPLICANT: BUDDER, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

```

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Query Match          99.0%; Score 193; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 7,8e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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0Y 1 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 36
|||||:|||||:|||||:|||||:|||||:
Db 166 YTSLIHSLIESQNOEKNEQELLELDKWSLWNMF 201

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Search completed: May 16, 2003, 12:10:26  
Job time : 16.759 secs

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GenCore version 5.1.4.P5.4578  
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## OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533A-1  
Perfect score: 195  
Sequence: 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/PC105\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query Match	Length	ID	Description
1	195	100.0	36	US-09-874-475-16	Sequence 16, Appl
2	195	100.0	36	US-10-116-797-1	Sequence 1, Appl
3	195	100.0	36	US-09-493-346-1	Sequence 1, Appl
4	195	100.0	36	US-09-796-202-10	Sequence 10, Appl
5	195	100.0	36	US-09-779-451-5	Sequence 5, Appl
6	195	100.0	36	US-09-834-628-1	Sequence 1, Appl
7	195	100.0	36	US-09-854-816-1	Sequence 1, Appl
8	195	100.0	36	US-09-854-816-108	Sequence 108, App
9	195	100.0	37	US-09-848-616-176	Sequence 176, App
10	195	100.0	46	US-09-779-451-41	Sequence 41, Appl
11	195	100.0	56	US-09-779-451-41	Sequence 4, Appl
12	195	100.0	177	US-10-040-349B-2	Sequence 2, Appl
13	195	100.0	221	US-10-059-271-84	Sequence 84, Appl
14	195	100.0	232	US-10-059-271-81	Sequence 81, Appl
15	195	100.0	254	US-10-059-271-82	Sequence 82, Appl
16	195	100.0	256	US-10-059-271-97	Sequence 97, Appl
17	195	100.0	268	US-09-854-816-16	Sequence 16, Appl
18	195	100.0	268	US-09-854-816-17	Sequence 17, Appl
19	195	100.0	268	US-09-854-816-18	Sequence 18, Appl

20	195	100.0	344	9	US-10-040-349B-1	Sequence 1, Appl
21	195	100.0	345	9	US-10-026-741-49	Sequence 49, Appl
22	195	100.0	345	10	US-09-779-451-8	Sequence 8, Appl
23	195	100.0	391	9	US-10-059-271-93	Sequence 93, Appl
24	195	100.0	519	10	US-09-756-551A-8	Sequence 8, Appl
25	195	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
26	195	100.0	856	10	US-09-476-242-1	Sequence 1, Appl
27	195	100.0	861	9	US-10-026-741-103	Sequence 103, App
28	195	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
29	195	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
30	192	98.5	36	10	US-09-912-824-1	Sequence 1, Appl
31	192	98.5	268	10	US-09-854-816-19	Sequence 19, Appl
32	189	96.9	1231	9	US-10-059-271-94	Sequence 94, Appl
33	187	95.9	268	10	US-09-854-816-13	Sequence 13, Appl
34	186	95.4	233	10	US-09-854-816-50	Sequence 50, Appl
35	186	95.4	268	10	US-09-854-816-9	Sequence 9, Appl
36	186	95.4	269	10	US-09-854-816-12	Sequence 12, Appl
37	185	94.9	269	10	US-09-854-816-46	Sequence 46, Appl
38	184	94.4	269	10	US-09-854-816-28	Sequence 28, Appl
39	183	93.8	268	10	US-09-854-816-26	Sequence 26, Appl
40	183	93.8	619	10	US-09-891-609-4	Sequence 4, Appl
41	183	93.8	646	10	US-09-891-609-2	Sequence 2, Appl
42	183	93.8	847	10	US-09-476-242-2	Sequence 2, Appl
43	182	93.3	46	10	US-09-854-816-109	Sequence 109, App
44	182	93.3	267	10	US-09-854-816-38	Sequence 38, Appl
45	182	93.3	268	10	US-09-854-816-41	Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
FILE REFERENCE: 2793/5516  
CURRENT APPLICATION NUMBER: US/09/874.475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36  
DB 1 YTSLSHSLIESQNOEKNEQELLDKWSLWNF 36

RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US2003004411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Madon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116.797  
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 3

US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 100.0%; Score 195; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JEP/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human Immunodeficiency virus type 1  
US-09-779-451-5

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 6

US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: Dp178  
US-09-834-628-1

Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-854-816-1  
Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
MOLECULE TYPE: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 100.0%; Score 195; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 7.7e-17;  
Matches 36; Conservative 0; Mismatches 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
Db 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Sebbel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 176  
LENGTH: 37  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 100.0%; Score 195; DB 9; Length 37;  
Best Local Similarity 100.0%; Pred. No. 8e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36  
1 YTSLSHLSIESONQOEKNEDELLELDKWSLWNMF 36

Db 2 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 37

RESULT 10

US-09-779-451-41

Sequence 41, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900 0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 100.0%; Score 195; DB 10; Length 46;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 11 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 46

RESULT 11

US-09-779-451-4

Sequence 4, Application US/09779451

Patent No. US20020094521A1

GENERAL INFORMATION:

APPLICANT: Wild, Carl T.

APPLICANT: Allaway, Graham P.

TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

FILE REFERENCE: 1900 0300003

CURRENT APPLICATION NUMBER: US/09/779,451

CURRENT FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: US 60/235,901

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/181,543

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 77

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 100.0%; Score 195; DB 10; Length 56;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 16 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 51

RESULT 12

US-10-040-349B-2

Sequence 2, Application US/10040349B

Publication No. US20030082521A1

GENERAL INFORMATION:

APPLICANT: Brasseur, Robert

APPLICANT: Charlotteaux, Benoit

APPLICANT: Chevalier, Michel

APPLICANT: El Habib, Raphaelle

APPLICANT: Krell, Tino

TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

FILE REFERENCE: 01-078-A

CURRENT APPLICATION NUMBER: US/10/040,349B

CURRENT FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)...(177)

OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 100.0%; Score 195; DB 9; Length 177;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 104 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 139

RESULT 13

US-10-059-271-84

Sequence 84, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPRE, HEINRICH

APPLICANT: BUDDÉ, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

FILE REFERENCE: ALBRE-22

CURRENT APPLICATION NUMBER: US/10/059,271

CURRENT FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: DE 101 06 295

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide

US-10-059-271-84

Query Match

Best Local Similarity 100.0%; Score 195; DB 9; Length 221;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 36

Db 131 YTSLSHSLIESQNOEKNEQELLELDKWSLWMNF 166

RESULT 14

US-10-059-271-81

Sequence 81, Application US/10059271

Publication No. US20030082208A1

GENERAL INFORMATION:

APPLICANT: REPRE, HEINRICH

APPLICANT: BUDDÉ, ECKHARD

APPLICANT: NICOLAUS, STEFAN

TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 81  
;; LENGTH: 232  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-81

Query Match 100.0%; Score 195; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 5.5e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
|||||  
Db 144 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 179

RESULT 15  
US-10-059-271-82  
;; Sequence 82, Application US/10059271  
;; Publication No. US20030082208A1  
;; GENERAL INFORMATION:  
;; APPLICANT: REPKKE, HEINRICH  
;; APPLICANT: BUDDDE, ECKHARD  
;; APPLICANT: NICOLAUS, STEFAN  
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND  
;; TITLE OF INVENTION: BEING IMMOBILIZED  
;; FILE REFERENCE: ALBRE-22  
;; CURRENT APPLICATION NUMBER: US/10/059,271  
;; CURRENT FILING DATE: 2002-01-31  
;; PRIOR APPLICATION NUMBER: DE 101 06 295  
;; PRIOR FILING DATE: 2001-02-02  
;; NUMBER OF SEQ ID NOS: 97  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO: 82  
;; LENGTH: 254  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
;; OTHER INFORMATION: peptide  
US-10-059-271-82

Query Match 100.0%; Score 195; DB 9; Length 254;  
Best Local Similarity 100.0%; Pred. No. 6.1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 36  
|||||  
Db 166 YTSLSHSLIEESQNOEKNEQELLELDKVASLWNMF 201

Search completed: May 16, 2003, 12:10:21  
Job time : 16.759 secs

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GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-3  
Perfect score: 198  
Sequence: 1 YTNVITLLESONQOEKNEQELLEDKXASLMWVF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	198	100.0	36	21	AAV89837	Core polypeptide f
2	198	100.0	36	22	AAU70180	HIV viral envelope
3	198	100.0	36	22	ABB01244	Viral Dp178/107-11
4	198	100.0	36	22	ABB01245	Viral Dp178/107-11
5	198	100.0	36	22	ABB02830	Viral core polypep
6	198	100.0	36	22	AAU13790	Dp178-1like/Dp107-1
7	198	100.0	36	22	AAU13791	Dp178-1like/Dp107-1
8	198	100.0	36	22	AAV82245	Virus related pept
9	198	100.0	36	22	AAV82337	Core polypeptide T
10	198	100.0	36	22	AAV82338	Core polypeptide T

11	198	100.0	36	22	AAV54786	HIV antiviral acti
12	198	100.0	269	19	AAV22834	SEQ ID NO. 30 from
13	198	100.0	269	19	AAV22835	SEQ ID NO. 31 from
14	198	100.0	269	23	ABG68305	Envelope protein g
15	198	100.0	269	23	ABG68306	Envelope protein g
16	198	100.0	275	19	AAW33615	SOD/env-5b protein
17	198	100.0	725	21	AAV77309	HIV-1 env5b/human
18	198	100.0	700	11	AAV05795	HIV-1 env mutcin 1
19	198	100.0	855	19	AAV53112	ENV protein contai
20	198	100.0	855	21	AAV77298	HIV-1 (ATCC CRL 85
21	198	100.0	855	21	AAV77302	HIV-1 (ATCC CRL 85
22	198	100.0	860	18	AAW31284	HIV-SF2 virus gp12
23	198	100.0	863	13	AAV61509	Sequence of ARV-2
24	198	100.0	863	13	AAV29706	env gene decoded f
25	193	97.5	36	16	AAV67698	Dp-178 homologue d
26	193	97.5	36	17	AAV89839	Dp185 corresponds
27	193	97.5	36	18	AAV17012	Dp-178-like peptid
28	193	97.5	36	21	AAV89836	Core polypeptide f
29	193	97.5	36	22	AAV67040	HIV-1 gp41 peptide
30	193	97.5	36	22	AAU14012	Dp178 homologue, P
31	193	97.5	854	19	AAV43070	HIV-1 gp120 protei
32	190	96.0	268	19	AAV22830	SEQ ID NO. 26 from
33	190	96.0	268	23	ABG68301	Envelope protein g
34	190	96.0	619	23	AAV75156	N-terminal mutant
35	190	96.0	646	23	AAV75155	Modified full-leng
36	190	96.0	847	21	AAV97073	Variant HIV-1 SF16
37	187	94.4	36	21	AAV89665	Core polypeptide f
38	187	94.4	36	22	ABB01073	Viral Dp178/107-11
39	187	94.4	36	22	ABB02524	Viral core polypep
40	187	94.4	36	22	AAU13619	Dp178-1like/Dp107-1
41	187	94.4	36	22	AAV78066	Core polypeptide T
42	187	94.4	268	19	AAV22811	SEQ ID NO. 7 from
43	187	94.4	268	23	ABG68282	Envelope protein g
44	187	94.4	269	19	AAV22832	SEQ ID NO. 28 from
45	187	94.4	269	23	ABG68303	Envelope protein g

## ALIGNMENTS

RESULT 1  
AAV89837  
ID AAV89837 standard; peptide: 36 AA.  
XX  
AC AAV89837;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 1406.  
XX  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN W09959615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US11219.  
XX  
PR 20-MAY-1998; 98US-0082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KL, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
comprises enhancer sequence -

XX Disclosure: Page 45; 124pp; English.  
 PS  
 XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fibrogenic treatments. Sequences AA98651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

CC Sequence 36 AA:

Query Match 100.0%; Score 198; DB 21; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTITITLLEESQNOEKNEDELLEDKWASLWNMF 36  
 ||||||||||||||||||||||||||||||||||  
 DB 1 YNTITITLLEESQNOEKNEDELLEDKWASLWNMF 36

RESULT 2  
 AAU70180

ID AAU70180 standard; Peptide: 36 AA.

AC AAU70180;

DT 14-FEB-2002 (first entry)

DE HIV viral envelope protein stabilising peptide #2.

XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 KW alpha-helical region; ectodomain.

XX Homo sapiens.

OS WO200170262-A2.

PD 27-SEP-2001.

PF 15-MAR-2001; 2001WO-US08108.

PR 17-MAR-2000; 2000US-189981P.

XX (PANA-) PANACOS PHARM INC.

PA Wild CT, Allaway GP;

PI WPI; 2001-626098/72.

XX Immunogenic composition for inhibiting HIV infection, comprises viral  
 PT envelope protein or its fragment exterior to viral membrane, a  
 PT stabilising peptide, and optionally, viral cell surface receptor or  
 PT its fragment

XX Claim 6; Page 45; 84pp; English.

XX The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of  
 CC HIV-1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and

CC AAU70677-AAU70743 represent stabilising peptides modelling the  
 CC alpha-helical regions of the ectodomain of the HIV-1 transmembrane  
 CC protein to stabilise fusion-active intermediate structures, which can be  
 CC used as vaccine immunogens. Immunogenic compositions comprise a viral  
 CC envelope protein or its fragment exterior to the viral membrane, a  
 CC stabilising peptide to disrupt formation of structural intermediates  
 CC necessary for viral fusion and entry, and optionally, a viral cell  
 CC surface receptor or its fragment. The stabilising peptide is capable of  
 CC associating with the envelope protein or its fragment to form a  
 CC stabilised, fusion active structure. Antibody binding assays are used to  
 CC determine the ability of immunogen vaccines to generate an immune  
 CC response to various forms of envelope. Virus neutralisation assays can be  
 CC used to characterise the antibody response raised against HIV-1 gp41  
 CC domains. The sequences and methods are useful for inhibiting HIV  
 CC infection, for inducing an immune response in an animal and for raising  
 CC antibodies.

SQ Sequence 36 AA:

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTITITLLEESQNOEKNEDELLEDKWASLWNMF 36  
 ||||||||||||||||||||||||||||||||||  
 DB 1 YNTITITLLEESQNOEKNEDELLEDKWASLWNMF 36

RESULT 3  
 ABB01244

ID ABB01244 standard; Peptide: 36 AA.

AC ABB01244;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T1405.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX Viridiae.

OS Key Location/Qualifiers

FT Modified-site 1 /note="N-terminal is substituted by Ac"

FT Modified-site 36 /note="C-terminal amide"

FT WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

XX (TRIM-) TRIMERIS INC.

PA Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

PI WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection

XX Disclosure; Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region

CC HRI1 respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36

LT 4  
 1245

ID ABB01245 standard; Peptide: 36 AA.

AC ABB01245;

DT 03-JAN-2002 (first entry)

DE Viral DP178/107-like region peptide T1406.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 KW infection.

XX Viridiac.

OS WO200164013-A2.

PN 07-SEP-2001.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 PI WPI; 2001-514829/56.

PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

PS Disclosure: Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36

RESULT 5

ID ABB02830 standard; Peptide: 36 AA.

AC ABB02830;

DT 03-JAN-2002 (first entry)

DE Viral core polypeptide, SEQ ID NO: 1357.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;  
 KW infection.

OS Viridiac.

PN WO200164013-A2.

PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US03988.

PR 29-FEB-2000; 2000US-0515965.

PA (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 PI WPI; 2001-514829/56.

PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

PS Disclosure: Page 524; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HRI  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 22; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36  
 DB 1 YNTNTYTLLESQNOEKNEQELLELDKWSIWMNF 36

RESULT 6

ID AAU13790 standard; Peptide: 36 AA.

AC AAU13790;

DT 21-NOV-2001 (first entry)

DE		DP178-1like/DP107-1like peptide T-1405.
XX		
KM		Anti-retroviral; DP178-1like; DP107-1like; transmembrane protein gp41;
KW		antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX		
OS		Human immunodeficiency virus 1 isolate LAI.
XX		Synthetic.
FT	Key	Location/Qualifiers
FT	Modified-site	1
FT	/note= "N-terminal is substituted by Ac"	
FT	Modified-site	36
FT	/note= "C-terminal amide"	
XX		
PN	MO200151673-A2.	
PD	19-JUL-2001.	
XX		
PF	05-JUL-2000; 2000WO-US35727.	
XX		
PA	09-JUL-1999; 99US-0350841.	
XX		
PI	(TRIM-) TRIMERIS INC.	
XX		
PT	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;	
XX		
DR	WPI: 2001-442157/47.	
XX		
PT	Identifying a compound that inhibits the formation of or disrupts a	
PT	DP107/DP178 complex, especially compounds with antifusogenic, antiviral	
PT	or intracellular modulatory activity, by detecting the formation of a	
PT	DP107/DP178 complex -	
PS	Disclosure; Page 77; 259pp; English.	
XX		
CC	The present invention relates to peptides which exhibit anti-retroviral	
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise	
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds	
CC	to amino acids 639-673 of the transmembrane protein gp41 from human	
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide	
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention	
CC	also relates to a method of identifying compounds that inhibit the	
CC	formation of or disrupts a DP107/DP178 complex. The method comprises	
CC	detecting the formation of a DP107/DP178 complex, both in the presence	
CC	or absence of a test compound, in a reaction mixture containing DP107	
CC	and DP178 peptides. The method is useful for identifying compounds,	
CC	including small molecule compounds, which may themselves exhibit	
CC	antifusogenic, antiviral or intracellular modulatory activity. The	
CC	DP178-like/DP107-like peptides are useful to inhibit human and non-human	
CC	retroviral, particularly HIV, transmission to uninfected cells. The	
CC	present sequence represents one of the DP178-like/DP107-like peptides	
CC	of the invention.	
XX		
SQ	Sequence	36 AA:
XX		
Query Match	100.0%; Score 198; DB 22; Length 36;	
Best Local Similarity	100.0%; Pred. No. 1,4e-17;	
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	1 YTNITYTLLLESQNQQEKNEQELLELDKWSLMNMF 36	
Dd	1 YTNITYTLLLESQNQQEKNEQELLELDKWSLMNMF 36	
RESULT 7		
ID	AAU13791 standard; Peptide; 36 AA.	
AC	AAU13791	
XX		
DT	AAU13791;	
XX		
DT	21-NOV-2001 (first entry)	
XX		
DE	DP178-1like/DP107-1like peptide T-1406.	

XX	Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;
KW	antifusogenic; antiviral; HIV transmission; mutant; mutein.
XX	
OS	Human immunodeficiency virus 1 isolate LAI.
XX	Synthetic.
PN	WO200151673-A2.
PD	19-JUL-2001.
XX	
PF	05-JUL-2000; 2000WO-US35727.
XX	
PR	09-JUL-1999; 99US-0350841.
XX	
PA	(TRIM-) TRIMERIS INC.
PL	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
DR	WPI: 2001-442157/47.
XX	
PT	Identifying a compound that inhibits the formation of or disrupts a
PT	DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT	or intracellular modulatory activity, by detecting the formation of a
XX	DP107/DP178 complex -
PS	
XX	Disclosure; Page 77; 259pp; English.
CC	
CC	The present invention relates to peptides which exhibit anti-retroviral
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds
CC	to amino acids 639-673 of the transmembrane protein gp41 from human
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC	also relates to a method of identifying compounds that inhibit the
CC	formation of or disrupts a DP107/DP178 complex. The method comprises
CC	detecting the formation of a DP107/DP178 complex, both in the presence
CC	or absence of a test compound, in a reaction mixture containing DP107
CC	and DP178 peptides. The method is useful for identifying compounds,
CC	including small molecule compounds, which may themselves exhibit
CC	antifusogenic, antiviral or intracellular modulatory activity. The
CC	DP178-like/DP107-like peptides are useful to inhibit human and non-human
CC	retroviral, particularly HIV, transmission to uninfected cells. The
CC	present sequence represents one of the DP178-like/DP107-like peptides
CC	of the invention.
CC	
SO	Sequence    36 AA:
XX	
XX	
Query Match	100.0%; Score 198; DB 22; Length 36;
Best Local Similarity	100.0%; Pred. No. 1,4e-17;
Matches    36; Conservative    0; Mismatches    0; Indels         0; Gaps         0;	
OY	1 YTNITYTLLLESQNOEKNEDELELLDKWASIMNPF 36       
Dd	1 YTNITYTLLLESQNOEKNEDELELLDKWASIMNPF 36
RESULT 8	
ID	AAB92245
AC	AAB92245 standard; Peptide: 36 AA.
XX	
XX	AAB92245;
XX	
DT	22-JUN-2001 (first entry)
DE	Virus related peptide SEQ ID NO:1421.
XX	
KW	Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW	blood component; modification; succinimidyl; maleimido group; amino;
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX	
XX	Homo sapiens
OS	Synthetic.
DS	

XX WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US13576.  
 XX 17-MAY-1999; 99US-0134406.  
 XX 10-SEP-1999; 99US-0153406.  
 XX 15-OCT-1999; 99US-0159783.  
 XX (CONJ-) CONJUCHEM INC.  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX MPI; 2001-112059/12.  
 XX Modifying and attaching therapeutic peptides to albumin prevents  
 XX peptidase degradation, useful for increasing length of in vivo activity  
 XX  
 XX Disclosure; Page 662; 733pp; English.  
 XX The present invention describes a modified therapeutic peptide (I)  
 XX comprising a therapeutically active amino acid region (II) and a  
 XX reactive group (III) (e.g. succinimidyl and maleimido groups) attached to  
 XX a less therapeutically active amino acid region (IV), which covalently  
 XX bonds with amino/hydroxyl/thiol groups on blood components to form a  
 XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 XX factors and neurotransmitters, to protect them from peptidase activity  
 XX in vivo for the treatment of various disorders. Endogenous therapeutic  
 XX peptides are not suitable as drug candidates as they require frequent  
 XX administration due to rapid degradation by peptidases in the body.  
 XX Modifying and attaching therapeutic peptides to albumin prevents or  
 XX reduces the action of peptidases to increase length of activity (half  
 XX life) and specificity as bonding to large molecules decreases  
 XX intracellular uptake and interference with physiological processes.  
 XX AAB90829 to AAB92441 represent peptides which can be used in the  
 XX exemplification of the present invention.  
 XX  
 XX Sequence 36 AA:  
 XX  
 XX Query Match 100.0%; Score 198; DB 22; Length 36;  
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 YTNITITLLEESONQOEKNEDELLELDKWSLNNMF 36  
 XX ||||||||||||||||||||||||||||||||||||  
 XX 1 YTNITITLLEESONQOEKNEDELLELDKWSLNNMF 36  
 XX  
 XX RESULT 9  
 XX AAB78237  
 XX ID AAB78237 standard; Peptide; 36 AA.  
 XX  
 XX AC AAB78237;  
 XX  
 XX DT 19-APR-2001 (first entry)  
 XX DE Core polypeptide T1405.  
 XX DE Core polypeptide T1405.  
 XX DE Core polypeptide; enhancer; antiviral; anti-HIV;  
 XX KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 XX KW coiled-coil peptide interaction; fusion-related disorder;  
 XX KW bacterial infection; viral infection.  
 XX  
 XX OS Unidentified.  
 XX  
 XX PN WO200103723-A1.  
 XX  
 XX PD 18-JAN-2001.  
 XX  
 XX

PF 10-JUL-2000; 2000WO-US18772.  
 XX  
 XX 09-JUL-1999; 99US-0350641.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 XX  
 XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX MPI; 2001-147136/15.  
 XX  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 XX e.g. viral infections, comprises an enhancer peptide linked to a core  
 XX polypeptide -  
 XX  
 XX Disclosure; Page 58; 151pp; English.  
 XX  
 XX The present sequence is a core polypeptide which may be linked to  
 XX an enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 XX polypeptide exhibits enhanced pharmacokinetic properties relative to  
 XX those exhibited by the core polypeptide when introduced into a living  
 XX system. It is used to increase the in vitro or ex vivo half-life of  
 XX the core polypeptide. The hybrid and core polypeptides can be used for  
 XX modulating fusogenic events and intracellular processes involving  
 XX coiled-coil peptide interactions. Other uses include preventing,  
 XX treating and/or diagnosing disorders involving fusion events (e.g.  
 XX modulation of neurotransmitter exchange and sperm-egg fusion),  
 XX intracellular processes involving coiled-coil peptides (e.g. bacterial  
 XX infections) and viral infections that involve cell-cell and/or  
 XX virus-cell fusion (e.g. viral infections caused by human  
 XX CC immunodeficiency virus, respiratory syncytial virus, Epstein-Barr  
 XX CC virus, hepatitis B virus, Mason-Pfizer virus and polio virus).  
 XX The enhancer peptide sequence increases the half-life and reduces the  
 XX clearance rate of therapeutic peptides, which increases their efficacy  
 XX and minimises the incidence and severity of adverse side effects.  
 XX In addition, this increases the sensitivity of the diagnostic procedure  
 XX in which they are used.  
 XX  
 XX Sequence 36 AA:  
 XX  
 XX Query Match 100.0%; Score 198; DB 22; Length 36;  
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 YTNITITLLEESONQOEKNEDELLELDKWSLNNMF 36  
 XX ||||||||||||||||||||||||||||||||||||  
 XX 1 YTNITITLLEESONQOEKNEDELLELDKWSLNNMF 36  
 XX  
 XX RESULT 10  
 XX AAB78238  
 XX ID AAB78238 standard; Peptide; 36 AA.  
 XX  
 XX AC AAB78238;  
 XX  
 XX DT 19-APR-2001 (first entry)  
 XX DE Core polypeptide T1406.  
 XX DE Core polypeptide T1406.  
 XX DE Core polypeptide; enhancer; antiviral; anti-HIV;  
 XX KW virucide; hepatotropic; antiinflammatory; hybrid polypeptide;  
 XX KW coiled-coil peptide interaction; fusion-related disorder;  
 XX KW bacterial infection; viral infection.  
 XX  
 XX OS Unidentified.  
 XX  
 XX PN WO200103723-A1.  
 XX  
 XX PD 18-JAN-2001.  
 XX  
 XX PF 10-JUL-2000; 2000WO-US18772.  
 XX  
 XX PR 09-JUL-1999; 99US-0350641.  
 XX  
 XX



DR WPI: 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 PS  
 PS Claim 11: Page 171-172; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 XX Sequence 269 AA;  
 SQ  
 Query Match 100.0%; Score 198; DB 19; Length 269;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 36  
 Db 169 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 204  
 RESULT 13  
 AAY22835  
 ID AAY22835 standard; Protein: 269 AA.  
 XX  
 AC AAY22835;  
 XX  
 XX 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 31 from W09820036.  
 XX  
 XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 XX Human immunodeficiency virus.  
 OS  
 XX W09820036-A1.  
 PN  
 XX 14-MAY-1998.  
 PD  
 XX 05-NOV-1997; 97WO-US20069.  
 PF  
 XX 16-JUN-1997; 97US-0876698.  
 PR  
 PR 06-NOV-1996; 96US-0743696.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX

DR WPI: 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termini of octa-peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 PS  
 PS Claim 11: Page 172-173; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 XX Sequence 269 AA;  
 SQ  
 Query Match 100.0%; Score 198; DB 19; Length 269;  
 Best Local Similarity 100.0%; Pred. NO. 1.3e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 36  
 Db 169 YTNNTYTLLESQNOEKNEQELLEDKWSLMMNF 204  
 RESULT 14  
 ABG68305  
 ID ABG68305 standard; Protein: 269 AA.  
 XX  
 AC ABG68305;  
 XX  
 XX 07-OCT-2002 (first entry)  
 DE Envelope protein gp41 from HIV clade B strain #24.  
 XX  
 XX HIV; glycoprotein; gp41; antigen; helical conformation;  
 KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;  
 KW viral envelope protein; vaccine; virucide; anti-HIV.  
 XX  
 XX Human immunodeficiency virus type 1 clade B.  
 OS  
 XX US6271198-B1.  
 PN  
 XX 07-AUG-2001.  
 PD  
 XX 05-NOV-1997; 97US-0965056.  
 PF  
 XX 16-JUN-1997; 97US-049787P.  
 PR  
 PR 06-NOV-1996; 96US-0743696.  
 XX  
 XX 16-JUN-1997; 97US-0876698.  
 XX  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 XX

```

PT alpha-helical conformation -
xx
xx Disclosure: Column 177-178: 175pp: English.
xx
xx The invention relates to cyclic peptides (A) with a constrained helical
cc conformation, derived from gp41 (glycoprotein 41, a viral envelope
cc protein) protein of human immunodeficiency virus (HIV). The cyclic
cc peptides have formulas given in the specification part of which are
cc derived from a consensus sequence of gp41 derived from HIV clades A, B,
cc C, D, E or O. The peptides are used to cause induction of a specific
cc immune response, resulting in antibodies that prevent virus-induced
cc membrane fusion. The peptides are used to treat subjects with, or at risk
cc of, HIV infection, either as antilusion/anti-infection agents or,
cc preferably where associated with a carrier, as an immunogen (including as
cc vaccine) to raise antibodies. The antibodies may be used for diagnosis or
cc prevention/treatment of HIV infection (i.e. acquired immunodeficiency
cc syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
cc cases of health care accidents. The peptides can be based on specific HIV
cc strains, e.g. breakthrough isolates of HIV that have developed during
cc vaccine trials, so a combination of them should cover a wide range of
cc protection. The present sequence is gp41 protein from a particular
cc HIV clade used to derive a consensus sequence of gp41.
xx
xx
xx Sequence 269 AA:
xx
xx
xx Query Match 100.0%; Score 198; DB 22; Length 269;
xx Best Local Similarity 100.0%; Pred. No. 1.3e-16;
xx Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
xx
xx
xx 1 YNTNTYVTLLEESQNOEKNEQELLELDKWSLMMNF 36
xx ||||||||||||||||||||||||||||||||
xx Db 169 YNTNTYVTLLEESQNOEKNEQELLELDKWSLMMNF 204

```

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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-1  
Perfect score: 195  
Sequence: 1 YTSLSHSLIESONQOEKNEQELLELDKWSLMMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	645	15	Q993A6 human immun
2	195	100.0	747	15	Q70607 human immun
3	195	100.0	748	15	Q70606 human immun
4	195	100.0	752	15	Q70604 human immun
5	195	100.0	752	15	Q70605 human immun
6	195	100.0	752	15	Q70608 human immun
7	195	100.0	851	15	Q78243 human immun
8	195	100.0	852	15	Q89797 human immun
9	195	100.0	854	15	Q85582 human immun
10	195	100.0	854	15	Q72502 human immun
11	195	100.0	856	15	Q92877 simian-huma
12	195	100.0	856	15	Q74599 human immun
13	195	100.0	856	15	Q74090 human immun
14	191	97.9	854	15	Q90178 human immun
15	191	97.9	854	15	Q78705 human immun
16	190	97.4	856	15	Q90SM7 human immun

17	189	96.9	616	15	Q993B0 human immun
18	189	96.9	618	15	Q993B2 human immun
19	189	96.9	757	15	Q9Q722 human immun
20	189	96.9	848	15	Q69990 human immun
21	187	95.9	838	15	Q03806 human immun
22	187	95.9	854	15	Q78225 human immun
23	187	95.9	855	15	Q03805 human immun
24	186	95.4	443	15	Q69910 human immun
25	186	95.4	443	15	Q80023 human immun
26	186	95.4	841	15	Q41556 human immun
27	186	95.4	849	15	Q77368 human immun
28	186	95.4	849	15	Q8Q851 human immun
29	186	95.4	851	15	Q56110 human immun
30	186	95.4	851	15	Q8Q852 human immun
31	186	95.4	856	15	Q72993 human immun
32	186	95.4	856	15	Q41539 human immun
33	186	95.4	857	15	Q8U170 human immun
34	186	95.4	858	15	Q8U190 human immun
35	186	95.4	858	15	Q8U188 human immun
36	186	95.4	859	15	Q8U180 human immun
37	186	95.4	859	15	Q8U179 human immun
38	186	95.4	859	15	Q8U177 human immun
39	186	95.4	859	15	Q8U173 human immun
40	186	95.4	859	15	Q8Q850 human immun
41	186	95.4	859	15	Q8U184 human immun
42	186	95.4	862	15	Q8U183 human immun
43	186	95.4	862	15	Q8U182 human immun
44	186	95.4	862	15	Q8U178 human immun
45	186	95.4	862	15	Q8U178 human immun

## ALIGNMENTS

RESULT 1  
Q993A6 PRELIMINARY: PRT: 645 AA.  
AC Q993A6:  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
White S.W., Doherty P.C., Hurwitz J.L.;  
RT "Localization of CD4 T cell epitope hotspots to exposed strands of  
HIV envelope glycoprotein suggests structural influences on antigen  
processing.";  
RT Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
RL EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env.GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120.1.  
DR Pfam: PF00517; GP41.1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
FT NON\_TER  
SQ SEQUENCE 645 AA: 72485 MW: B076514BE93362EC CRC64;

Query Match 100.0%; Score 195; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 1,7e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESONQOEKNEQELLELDKWSLMMWF 36  
DB 607 YTSLSHSLIESONQOEKNEQELLELDKWSLMMWF 642

## RESULT 2

070607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B., Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RA "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747 747  
 SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245P14 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 747;  
 Best Local Similarity 100.0%; Pred. No. 2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 36  
 |||||  
 Db 633 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 668

## RESULT 3

070606 PRELIMINARY: PRT: 748 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B., Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RA "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1;

DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748 748  
 SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67694B CRC64;

Query Match 100.0%; Score 195; DB 15; Length 748;  
 Best Local Similarity 100.0%; Pred. No. 2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 36  
 |||||  
 Db 634 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 669

## RESULT 4

070604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B., Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RA "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752 752  
 SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 36  
 |||||  
 Db 638 YTSLSHSLIEESONQOEKNEDELLELDKNASLWNMF 673

## RESULT 5

070605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses: Retroviridae: Lentivirus.  
 OX NCBI\_Taxid=11676;

LN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM852;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM852;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12031; AAA76667.1; -;  
DR InterPro: IPR000328; Env GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
NON\_TER 752 752  
SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 36  
Db 638 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 673

RESULT 6  
ID 070608 PRELIMINARY; PRT; 752 AA.  
AC 070608;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM87-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM87-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12035; AAA76670.1; -;  
DR InterPro: IPR000328; Env GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
NON\_TER 752 752  
SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8E8 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 2e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 36  
Db 638 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 673

Db 638 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 673

RESULT 7  
ID 078243 PRELIMINARY; PRT; 851 AA.  
AC 078243;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Env polypotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,  
Verani P., Rossi G.B.;  
RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
chronically infected HUT-78 cellular clone.";  
RL J. Viral Diseases 1:40-55(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-89352106; PubMed-2765297;  
RA Federico M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Maccini B., Mangano N., Verani P., Rossi G.;  
RT "Biological and molecular characterization of producer and non  
producer clones from HUT-78 infected with a patient HIV isolate.";  
RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Tilti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Borsetti A., Saggio I., Verani P., Rossi G.;  
RT "Variability of HIV-1 virus: characteristics of an infected but not  
productive clone.";  
RL Int. J. Immunopharmacol. 3:17-23(1990).  
DR EMBL: Z11530; CAAT7628.1; -;  
DR InterPro: IPR000328; Env GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane.  
NON\_TER 851 AA; 96630 MW; 1A3767B987E98027 CRC64;  
SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 851;  
Best Local Similarity 100.0%; Pred. No. 2.2e-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 36  
Db 633 YTSLSHSLIESQNOEKNEQELLELDKWSIWMNF 668

RESULT 8  
ID 089797 PRELIMINARY; PRT; 852 AA.  
AC 089797;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LM90-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker

RT Infected with HIV type 1 (HTLV type IIIB).  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 [12]  
 RC SEQUENCE FROM N.A.  
 RA STRAIN-LW90-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U12053; AAA76685.1;  
 DR EMBL; U12036; AAA76671.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 Transmembrane.  
 SO SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;

Query Match 100.0%; Score 195; DB 15; Length 852;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 634 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 669

RESULT 9  
 ID 085582 PRELIMINARY: PRT: 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RT J. Virol. 59:284-291(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92219406; PubMed=1373204;  
 RT Dai L.C., Litaeva R., Takahashi K., Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes."  
 RL J. Virol. 66:3151-3154(1992).  
 DR EMBL; M19921; AAA44992.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 100.0%; Score 195; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 636 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 671

RESULT 10  
 ID 072502 PRELIMINARY: PRT: 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE ENV polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-NL4-3;  
 RX MEDLINE=96036482; PubMed=7483282;  
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
 Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
 RT from primary virus cultures using the polymerase chain reaction."  
 RT Virology 213:80-86(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NL4-3;  
 RX MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 Martin M.A.;  
 RT "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone."  
 RL J. Virol. 59:284-291(1986).  
 DR EMBL; U26942; AAB60578.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT CONFLICT 214 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 739 G -> D (IN REF. 2).  
 SO SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 100.0%; Score 195; DB 15; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||  
 DB 636 YTSLSHSLIESQNOEKNEQELLELDKWSLWNMF 671

RESULT 11  
 ID 092877 PRELIMINARY: PRT: 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TRENBLREL. 08, Created)  
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Simian-Human immunodeficiency virus.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99098984; PubMed=9882298;

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fenton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenesis of a multiply passaged simian-human  
 RT immunodeficiency virus (SHIV-HXBc2).";  
 RL J. Virol. 73:976-984(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AADL2142.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36  
 Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673  
 RESULT 12  
 Q74599 PRELIMINARY; PRT; 856 AA.  
 AC Q74599;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates";  
 RL Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RA Iwataani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAI12995.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97287 MW; 238042A234C6685 CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36  
 Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673  
 RESULT 13  
 Q74090

ID Q74090 PRELIMINARY; PRT; 856 AA.  
 AC Q74090;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates";  
 RL Virology 174:103-116(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RA Iwataani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAI3003.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;  
 Query Match 100.0%; Score 195; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 2,3e-15;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 36  
 Db 638 YTSLSHLSIESQNOQEKNEQELLELDKWSLWME 673  
 RESULT 14  
 Q090178 PRELIMINARY; PRT; 854 AA.  
 AC Q090178;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=95074930; PubMed=7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 RT selected with immunotoxins from human immunodeficiency virus type 1-  
 RT infected T cells";  
 RL J. Virol. 69:75-81(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 RT immunotoxin-resistant variant T cell line";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF070521; AAC28452.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.9%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESQNOEKNQELLEDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 636 YTSLSHSLIEESQNOEKNQELLEDKWSLWNMF 671

## RESULT 15

078705 PRELIMINARY; PRT; 854 AA.  
 ID 078705  
 AC 078705;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 VR Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RX MEDLINE=96013815; PubMed=7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1."  
 RL J. Virol. 69:7122-7131(1995).  
 DR EMBL; LA2371; AA696326.1;  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SO SEQUENCE 854 AA; 97199 MW; 58951216533E256 CRC64;

Query Match 97.9%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 6.9e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIEESQNOEKNQELLEDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 636 YTSLSHSLIEESQNOEKNQELLEDKWSLWNMF 671

Search completed: May 16, 2003, 11:19:42  
 Time : 28.3124 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-1  
Sequence: 1 YTSLSHLSIESQNOEKNEQELLELDKWSLNMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	195	100.0	36 1 US-08-073-028-1	Sequence 1, Appli
2	195	100.0	36 3 US-08-486-099-1	Sequence 1, Appli
3	195	100.0	36 3 US-09-071-877-1	Sequence 1, Appli
4	195	100.0	36 3 US-08-360-107A-1	Sequence 1, Appli
5	195	100.0	36 3 US-08-484-223B-1	Sequence 1, Appli
6	195	100.0	36 3 US-08-919-597-1	Sequence 1, Appli
7	195	100.0	36 3 US-08-475-668A-1	Sequence 1, Appli
8	195	100.0	36 3 US-08-485-551A-1	Sequence 1, Appli
9	195	100.0	36 3 US-08-471-913A-1	Sequence 1, Appli
10	195	100.0	36 4 US-08-554-616-1	Sequence 1, Appli
11	195	100.0	36 4 US-08-485-264A-1	Sequence 1, Appli
12	195	100.0	36 4 US-09-082-279B-15	Sequence 15, Appli
13	195	100.0	36 4 US-09-082-279B-497	Sequence 497, App
14	195	100.0	36 4 US-09-082-279B-498	Sequence 498, App
15	195	100.0	36 4 US-09-082-279B-603	Sequence 603, App
16	195	100.0	36 4 US-09-082-279B-630	Sequence 630, App
17	195	100.0	36 4 US-09-082-279B-631	Sequence 631, App
18	195	100.0	36 4 US-09-082-279B-705	Sequence 705, App
19	195	100.0	36 4 US-09-082-279B-834	Sequence 834, App
20	195	100.0	36 4 US-09-082-279B-1076	Sequence 1076, App
21	195	100.0	36 4 US-09-082-279B-1121	Sequence 1121, App
22	195	100.0	36 4 US-09-082-279B-1161	Sequence 1161, App
23	195	100.0	36 4 US-08-965-056-1	Sequence 1, Appli
24	195	100.0	36 4 US-08-965-056-108	Sequence 108, App
25	195	100.0	36 4 US-09-045-920-1	Sequence 1, Appli
26	195	100.0	36 4 US-08-474-349A-1	Sequence 1, Appli
27	195	100.0	36 4 US-08-474-349A-399	Sequence 399, App

28	195	100.0	36 4 US-08-474-349A-413	Sequence 413, App
29	195	100.0	36 4 US-09-315-304B-15	Sequence 15, Appli
30	195	100.0	36 4 US-09-315-304B-497	Sequence 497, App
31	195	100.0	36 4 US-09-315-304B-498	Sequence 498, App
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35	195	100.0	36 4 US-09-315-304B-705	Sequence 705, App
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37	195	100.0	36 4 US-09-315-304B-1076	Sequence 1076, App
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40	195	100.0	36 4 US-09-315-304B-1469	Sequence 1469, App
41	195	100.0	36 4 US-09-315-304B-1470	Sequence 1470, App
42	195	100.0	36 4 US-09-315-304B-1486	Sequence 1486, App
43	195	100.0	36 4 US-08-255-208A-1	Sequence 1, Appli
44	195	100.0	37 4 US-09-082-279B-771	Sequence 771, App
45	195	100.0	37 4 US-09-082-279B-775	Sequence 775, App

ALIGNMENTS

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RESULT 1
US-08-073-028-1
; Sequence 1, Application US/08073028
; Patent No. 5464933
;
GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
;
US-08-073-028-1
Query Match 100.0%; Score 195; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Gaps 0;
1 YTSLSHLSIESQNOEKNEQELLELDKWSLNMWF 36
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Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelletway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Marutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-09-071-877-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelletway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 100.0%; Score 195; DB 3; Length 36;

Best Local Similarity 100.0%; Pred. No. 5.5e-18;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLIEESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESONQOEKNEQELLEDKWSASLWNMF 36  
Db 1 YTSLSHSLIEESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSHSLIEESONQOEKNEQELLEDKWSASLWNMF 36  
Db 1 YTSLSHSLIEESONQOEKNEQELLEDKWSASLWNMF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
08-475-668A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36  
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DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/0848551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 100.0%; Score 195; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36  
|||||  
DB 1 YTSLSHLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8664/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1

Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Danl P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 100.0%; Score 195; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.5e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36  
DB 1 YTSLSLSLIEESQNOEKNEQELLELDKWSLWNNF 36

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Db      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 13
US-09-082-279B-497
; Sequence 497, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 497
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-497
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
Db      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 14
US-09-082-279B-498
; Sequence 498, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 498
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-498
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
Db      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
RESULT 15
US-09-082-279B-603
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; Sequence 603, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 603
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-603
Query Match      100.0%; Score 195; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.5e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
Db      1 YTSLSHSLIEESONQOEKNEQELLELDKWSASLWNMF 36
Search completed: May 16, 2003, 11:22:09
Job time : 11.1928 secs
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GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-1

Perfect score: 195  
Sequence: 1 YTSLSHSLIESQNOEKNEQLELDKWSLIMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_101002:\*\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	195	100.0	36	16	DP-178 derived fro
2	195	100.0	36	17	DP178 corresponds
3	195	100.0	36	18	HIV-1 derived pept
4	195	100.0	36	19	SEQ ID NO. 108 fro
5	195	100.0	36	19	SEQ ID NO. 1 from
6	195	100.0	36	20	Synthetic peptide
7	195	100.0	36	20	HIV-1 LAI gp41 T-2
8	195	100.0	36	21	T20/DP178 peptide
9	195	100.0	36	21	T20/DP178 peptide
10	195	100.0	36	21	T20/DP178 peptide

11	195	100.0	36	21	AA14533	HIV-1 isolate LAI
12	195	100.0	36	21	AAV88665	Core polypeptide f
13	195	100.0	36	21	AAV88729	Core polypeptide f
14	195	100.0	36	21	AAV89135	Core polypeptide f
15	195	100.0	36	21	AAV89136	Core polypeptide f
16	195	100.0	36	21	AAV89242	Core polypeptide f
17	195	100.0	36	21	AAV89424	Core polypeptide f
18	195	100.0	36	21	AAV89692	Core polypeptide f
19	195	100.0	36	21	AAV89735	Core polypeptide f
20	195	100.0	36	21	AAV89777	Core polypeptide f
21	195	100.0	36	21	AAV89982	Core polypeptide f
22	195	100.0	36	21	AAV89983	Core polypeptide f
23	195	100.0	36	21	AAV89999	Core polypeptide f
24	195	100.0	36	22	AAU70179	HIV viral envelope
25	195	100.0	36	22	AAU70741	HB2 transmembrane
26	195	100.0	36	22	AAU70741	Anti-HIV peptide T
27	195	100.0	36	22	AAV67039	HIV-1 gp41 peptide
28	195	100.0	36	22	AB800024	HIV-1 gp41 peptide
29	195	100.0	36	22	AB800087	Biotin-labelled HI
30	195	100.0	36	22	AB800088	Viral DP178/107-11
31	195	100.0	36	22	AB800494	Viral DP178/107-11
32	195	100.0	36	22	AB800495	Viral DP178/107-11
33	195	100.0	36	22	AB800600	Viral DP178/107-11
34	195	100.0	36	22	AB800626	Fluorescein-label
35	195	100.0	36	22	AB800627	Viral DP178/107-11
36	195	100.0	36	22	AB800628	Viral DP178/107-11
37	195	100.0	36	22	AB800832	Viral DP178/107-11
38	195	100.0	36	22	AB801100	Viral DP178/107-11
39	195	100.0	36	22	AB801143	Viral DP178/107-11
40	195	100.0	36	22	AB801185	Fluorescein-label
41	195	100.0	36	22	AB801391	Viral DP178/107-11
42	195	100.0	36	22	AB801392	Viral DP178/107-11
43	195	100.0	36	22	AB801414	Viral DP178/107-11
44	195	100.0	36	22	AB801488	Viral core polypep
45	195	100.0	36	22	AB801970	Viral core polypep

## ALIGNMENTS

RESULT 1

ID	Score	Query Match	Length	ID	Description
16	195	100.0	36	21	AA14533
17	195	100.0	36	21	AAV88665
18	195	100.0	36	21	AAV88729
19	195	100.0	36	21	AAV89135
20	195	100.0	36	21	AAV89136
21	195	100.0	36	21	AAV89242
22	195	100.0	36	21	AAV89424
23	195	100.0	36	21	AAV89692
24	195	100.0	36	21	AAV89735
25	195	100.0	36	21	AAV89777
26	195	100.0	36	21	AAV89982
27	195	100.0	36	21	AAV89983
28	195	100.0	36	21	AAV89999
29	195	100.0	36	22	AAU70179
30	195	100.0	36	22	AAU70741
31	195	100.0	36	22	AAU70741
32	195	100.0	36	22	AAV67039
33	195	100.0	36	22	AB800024
34	195	100.0	36	22	AB800087
35	195	100.0	36	22	AB800088
36	195	100.0	36	22	AB800494
37	195	100.0	36	22	AB800495
38	195	100.0	36	22	AB800600
39	195	100.0	36	22	AB800626
40	195	100.0	36	22	AB800627
41	195	100.0	36	22	AB800628
42	195	100.0	36	22	AB800832
43	195	100.0	36	22	AB801100
44	195	100.0	36	22	AB801143
45	195	100.0	36	22	AB801185

AA14533 standard; Peptide; 36 AA.

24-AUG-1995 (first entry)

DP-178 derived from HIV-1 isolate LAI has antiviral activity.

antiviral activity: DP-178; DP-107; diagnostic; HIV-1LAI;

human immunodeficiency virus; transmembrane protein; gp41;

alpha helix; leucine zipper; DP-185.

Synthetic.

Key

Modified-site

Location/Qualifiers

1

/note="Optionally has an amino, acetyl, 9-fluorenylmethoxy-carboxyl, hydrophobic or macromolecular carrier gp. attached"

Modified-site

38

/note="Optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"

MO9428920-A.

22-DEC-1994.

07-JUN-1994;

94AU-US05739.

07-JUN-1993;

93US-0073028.



RESULT 4  
ID AAY22912 standard; Peptide: 36 AA.  
AC AAY22912;  
DT 19-AUG-1999 (first entry)  
DE SEQ ID NO. 108 from WO9820036.  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
OS Human immunodeficiency virus.  
XX WO9820036-A1.  
XX 14-MAY-1998.  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-JUN-1997; 97US-0876698.  
XX 06-NOV-1996; 96US-0743698.  
XX (GENTH ) GENENTECH INC.  
XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovassnik MA;  
XX Wells JA;  
XX WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
XX on termal of octa:peptide - derived from human immunodeficiency  
XX virus gp41 protein, useful in vaccines for treatment and prevention  
XX of infection  
XX  
XX Disclosure: Page 233-234; 279pp; English.  
XX  
XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
XX (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
XX of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
XX AAY22903 represent consensus sequences of various sections of the gp41  
XX protein). Sequences derived from the peptides are used to produce  
XX constrained helical peptides of the invention. The constrained helical  
XX peptide is produced by synthesizing an octapeptide in which both terminal  
XX amino acids have a side-chain that includes a group able to form an amide  
XX bond, and cyclizing the octapeptide by reacting the specified side-chain  
XX residues with a difunctional linker to produce two amide bonds.  
XX The constrained helical peptides are used to treat or prevent HIV  
XX infection, especially as vaccines that generate antibodies that  
XX prevent viral membrane fusion or infectivity. Vaccines may contain  
XX constrained helical peptides derived from several different strains of  
XX HIV. The antibodies are also useful for diagnosing HIV infection. Other  
XX uses for the constrained helical peptides are in affinity purification  
XX of ligands (particularly where complete binding protein is not readily  
XX available, e.g. replacements for protein A in immunoglobulin  
XX purification); as epitope mimics for antibody production; for isolation  
XX of synthetic antibody clones from phage display libraries, or as stable  
XX forms of "floppy" peptides or proteins.  
XX  
XX Sequence 36 AA:  
SQ

Query Match 100.0%; Score 195; DB 19; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOQEKNEDELLFDKWSIWNMF 36  
DB 1 YTSLSHSLIESQNOQEKNEDELLFDKWSIWNMF 36

RESULT 5  
ID AAY22805 standard; Peptide: 36 AA.  
AC AAY22805;  
DT 19-AUG-1999 (first entry)  
DE SEQ ID NO. 1 from WO9820036.  
KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
KW vaccine; antibody; viral membrane fusion; viral infectivity;  
KW ligand affinity purification; protein A replacement;  
KW immunoglobulin purification; epitope mimic.  
OS Human immunodeficiency virus.  
XX WO9820036-A1.  
XX 14-MAY-1998.  
XX 05-NOV-1997; 97WO-US20069.  
XX 16-JUN-1997; 97US-0876698.  
XX 06-NOV-1996; 96US-0743698.  
XX (GENTH ) GENENTECH INC.  
XX Braisted A, Judice JK, McDowell RS, Phelan JC, Starovassnik MA;  
XX Wells JA;  
XX WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
XX on termal of octa:peptide - derived from human immunodeficiency  
XX virus gp41 protein, useful in vaccines for treatment and prevention  
XX of infection  
XX  
XX Disclosure: Page 143-144; 279pp; English.  
XX  
XX Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
XX (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
XX of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
XX AAY22903 represent consensus sequences of various sections of the gp41  
XX protein). Sequences derived from the peptides are used to produce  
XX constrained helical peptides of the invention. The constrained helical  
XX peptide is produced by synthesizing an octapeptide in which both terminal  
XX amino acids have a side-chain that includes a group able to form an amide  
XX bond, and cyclizing the octapeptide by reacting the specified side-chain  
XX residues with a difunctional linker to produce two amide bonds.  
XX The constrained helical peptides are used to treat or prevent HIV  
XX infection, especially as vaccines that generate antibodies that  
XX prevent viral membrane fusion or infectivity. Vaccines may contain  
XX constrained helical peptides derived from several different strains of  
XX HIV. The antibodies are also useful for diagnosing HIV infection. Other  
XX uses for the constrained helical peptides are in affinity purification  
XX of ligands (particularly where complete binding protein is not readily  
XX available, e.g. replacements for protein A in immunoglobulin  
XX purification); as epitope mimics for antibody production; for isolation  
XX of synthetic antibody clones from phage display libraries, or as stable  
XX forms of "floppy" peptides or proteins.  
XX  
XX Sequence 36 AA:  
SQ

Query Match 100.0%; Score 195; DB 19; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOQEKNEDELLFDKWSIWNMF 36  
DB 1 YTSLSHSLIESQNOQEKNEDELLFDKWSIWNMF 36

```

RESULT 6
AAV31955
ID AAV31955 standard; Peptide; 36 AA.
AC AAV31955;
XX
XX 21-DEC-1999 (first entry)
XX
XX Synthetic peptide T-20 (DP-178).
XX
XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
XX
XX Synthetic.
XX
XX Human immunodeficiency virus type 1.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminal acetyl"
XX FT 36
XX Modified-site 36 /note= "C-terminal amide"
XX
XX MO9948513-A1.
XX
XX 30-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06230.
XX
XX 23-MAR-1998; 98US-0045920.
XX
XX 01-MAY-1998; 98US-0071877.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Kang M, Bray B, Lichy M, Mader C, Merutka G;
XX
XX WPI; 1999-591038/50.
XX
XX Methods of peptide synthesis, particularly used to produce T-20 or
XX T-20 like peptides
XX
XX Claim 1; Page 102; 120pp; English.
XX
XX The present sequence represents an N- and C-terminal modified
XX peptide, designated T-20 (or DP-178), corresponding to amino acids
XX 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.
XX The invention relates to methods for the synthesis of peptides,
XX in particular T-20 and T-20-like peptides. The method involves
XX synthesizing specific side-chain protected peptide fragment
XX intermediates of T-20 or a T-20-like peptide on a solid support,
XX coupling the protected fragments in solution to form a protected
XX T-20 or T-20-like peptide, followed by deprotection of the side
XX chains to yield the final T-20 or T-20-like peptide. The invention
XX also relates to individual peptide fragments (see AAV31955-73) which
XX act as intermediates in the synthesis of peptides of interest (e.g.
XX T-20), and to particular groups of peptide fragments which act as
XX intermediates in the synthesis of the peptide of interest. The
XX method allows for the large scale, economical production of high
XX purity peptides.
XX
XX Sequence 36 AA:
SQ
Query Match 100.0%; Score 195; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4, 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36
DB 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36
RESULT 7
AAV31974

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```

ID AAV31974 standard; Peptide; 36 AA.
XX
XX AAV31974;
AC
XX 21-DEC-1999 (first entry)
XX
XX HIV-1 LAI gp41 T-20 peptide.
XX
XX T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.
XX
XX Human immunodeficiency virus type 1.
XX
XX MO9948513-A1.
XX
XX 30-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06230.
XX
XX 23-MAR-1998; 98US-0045920.
XX
XX 01-MAY-1998; 98US-0071877.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Kang M, Bray B, Lichy M, Mader C, Merutka G;
XX
XX WPI; 1999-591038/50.
XX
XX Methods of peptide synthesis, particularly used to produce T-20 or
XX T-20 like peptides
XX
XX Disclosure; Page 9; 120pp; English.
XX
XX The present sequence represents a peptide, designated T-20 (or
XX DP-178), that corresponds to amino acids 638-673 of the
XX transmembrane protein gp41 of HIV-1 LAI isolate. The invention
XX relates to methods for the synthesis of peptides, in particular
XX C- and N-terminal modified T-20 (see AAV31955) and T-20-like peptides.
XX The method involves synthesizing specific side-chain protected
XX peptide fragment intermediates (see AAV31955-73) of T-20 or a
XX T-20-like peptide on a solid support, coupling the protected
XX fragments in solution to form a protected T-20 or T-20-like peptide,
XX followed by deprotection of the side chains to yield the final T-20
XX or T-20-like peptide. The invention also relates to individual
XX peptide fragments which act as intermediates in the synthesis of
XX peptides of interest (e.g. T-20), and to particular groups of
XX peptide fragments which act as intermediates in the synthesis of
XX the peptide of interest. The method allows for the large scale,
XX economical production of high purity peptides.
XX
XX Sequence 36 AA:
SQ
Query Match 100.0%; Score 195; DB 20; Length 36;
Best Local Similarity 100.0%; Pred. No. 4, 1e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36
DB 1 YTSLSHSLIEESONQOEKNEDELLELDKMASLWNMF 36
RESULT 8
AAV52655
ID AAV52655 standard; Peptide; 36 AA.
AC AAV52655;
XX
XX 23-FEB-2001 (first entry)
XX
XX T20/DP178 peptide fragment #33.
XX
XX Antiinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;
XX chemottractant.
XX

```

XX Human immunodeficiency virus type 1.  
OS  
XX  
PN WO20006622-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
DR WPI: 2000-656493/63.  
XX  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
antagonist is used to modulate inflammation -  
XX  
● Claim 12; Page 24; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
SQ Sequence 36 AA:  
XX  
Query Match 100.0%; Score 195; DB 21; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
|||  
1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
DB  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide: 36 AA.  
XX  
● AAB52688;  
XX  
DI 23-FEB-2001 (first entry)  
XX  
DE T20/Dp178 peptide fragment #66.  
XX  
KM Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KM chemoattractant.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO20006622-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
DR WPI: 2000-656493/63.

XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
PS Claim 12; Page 25; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
SQ Sequence 36 AA:  
XX  
Query Match 100.0%; Score 195; DB 21; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4,1e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
|||  
1 YTSLSLSLIESQNOQEKNEQELLELDKWSLWNMF 36  
DB  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide: 36 AA.  
XX  
AC AAB52818;  
XX  
DI 23-FEB-2001 (first entry)  
XX  
DE T20/Dp178 peptide fragment #97.  
XX  
KM Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KM chemoattractant.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO20006622-A1.  
XX  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
DR WPI: 2000-656493/63.  
XX  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
PS Claim 14; Page 40; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
 SQ Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36  
 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36

Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36

RESULT 11  
 AAB14533  
 ID AAB14533 standard; peptide: 36 AA.  
 XX AAB14533;  
 XX 24-NOV-2000 (first entry)

HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).

KM HIV-1; gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KM envelope glycoprotein; prophylaxis; therapy.

XX Human immunodeficiency virus type 1.  
 XX WO200040616-A1.  
 XX 13-JUL-2000.  
 XX 10-JAN-2000; 2000WO-US00456.  
 XX 08-JAN-1999; 99US-0115404.  
 XX 07-JAN-2000; 2000US-0480336.

PA (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 PI Wild CT, Weiss CD;  
 DR WPI: 2000-465959/40.

PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -

PS Claim 13; Page 12; 97pp; English.

XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralising antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
 SQ Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36  
 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36

Db 1 YTSLIHSLEESQNOEKNEQELLELDKWSLIMNF 36

RESULT 12  
 AAY88665  
 ID AAY88665 standard; peptide: 36 AA.  
 XX AAY88665;  
 XX 23-MAY-2000 (first entry)

DE Core polypeptide fragment T No. 20.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; HIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.  
 XX WO9959615-A1.  
 XX 25-NOV-1999.  
 XX 20-MAY-1999; 99WO-US11219.  
 XX 20-MAY-1998; 98US-0082279.

PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI: 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

PS Disclosure; Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and STV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA: 100.0%; Score 195; DB 21; Length 36;  
 SO Query Match Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36  
 DB 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36

RESULT 13  
 ID AAY88729 standard; peptide; 36 AA.  
 AC AAY88729;  
 XX 23-MAY-2000 (first entry)  
 DT Core polypeptide fragment T No. 84.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.  
 XX Unidentified.  
 OS  
 XX W0959615-A1.  
 PN 25-NOV-1999.  
 PD 20-MAY-1999; 99WO-US11219.  
 XX 20-MAY-1998; 98US-0082279.  
 PR (TRIM-) TRIMERIS INC.  
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI: 2000-136792/12.  
 DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX Disclosure; Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 sequence linked to core polypeptides. The enhancer polypeptides are  
 derived from various retroviral envelope (gp41) protein sequences,  
 especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 polypeptide that they are linked to. The core polypeptides are any  
 polypeptide that may be introduced into a living system and that can  
 function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 selected from a growth factor, cytokine, differentiation factor,  
 interleukin, interferon, colony stimulating factor, hormone or  
 angiogenic factor. The peptides of the invention can be used for  
 inhibiting viral infection and can be used in anti-viral and  
 anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 polypeptide fragments that can be used in the invention. Some sequences  
 among those indicated also comprise enhancer fragments at terminal ends  
 and form hybrid polypeptides.

XX Sequence 36 AA:  
 SO Query Match Best Local Similarity 100.0%; Score 195; DB 21; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36

DB 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36  
 ID AAY89135 standard; peptide; 36 AA.  
 AC AAY89135;  
 XX 23-MAY-2000 (first entry)  
 DT Core polypeptide fragment T No. 573.

XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.  
 XX Unidentified.  
 OS  
 XX W0959615-A1.  
 PN 25-NOV-1999.  
 PD 20-MAY-1999; 99WO-US11219.  
 XX 20-MAY-1998; 98US-0082279.  
 PR (TRIM-) TRIMERIS INC.  
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI: 2000-136792/12.  
 DR A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX Disclosure; Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 sequence linked to core polypeptides. The enhancer polypeptides are  
 derived from various retroviral envelope (gp41) protein sequences,  
 especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 pharmacokinetic properties such as increasing the half-life of any core  
 polypeptide that they are linked to. The core polypeptides are any  
 polypeptide that may be introduced into a living system and that can  
 function as a pharmacologically useful peptide for the treatment or  
 prevention of a disease. The core polypeptides are bioactive peptides  
 selected from a growth factor, cytokine, differentiation factor,  
 interleukin, interferon, colony stimulating factor, hormone or  
 angiogenic factor. The peptides of the invention can be used for  
 inhibiting viral infection and can be used in anti-viral and  
 anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 polypeptide fragments that can be used in the invention. Some sequences  
 among those indicated also comprise enhancer fragments at terminal ends  
 and form hybrid polypeptides.

XX Sequence 36 AA:  
 SO Query Match Best Local Similarity 100.0%; Score 195; DB 21; Length 36;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36  
 DB 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLMMWF 36

RESULT 15  
 ID AAY89136 standard; peptide; 36 AA.

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX

DE Core polypeptide fragment T No. 574.

XX Retrovirus; hybrid polypeptide; enhancer; gp41, envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

OS W09959615-A1.

XX 25-NOV-1999.

PD 20-MAY-1999; 99WO-US11219.

XX 20-MAY-1998; 98US-0082279.

XX (TRIM-) TRIMERIS INC.

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

DR WPI; 2000-136792/12.

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 comprises enhancer sequence -

PS Disclosure: Page 30; 124pp; English.

XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

SQ Sequence 36 AA;

Query Match 100.0%; Score 195; DB 21; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.1e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36  
 ||||||||||||||||||||||||||||||||||||  
 Db 1 YTSLSHSLIESQNOQEKNEQELLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:12:00  
 Job time : 33.4578 secs

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-1

Perfect score: 195  
Sequence: 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	195	100.0	851	2 S13288	env polypeptide -
2	195	100.0	854	2 S13288	env polypeptide - huma
3	195	100.0	856	1 VCLJH3	env polypeptide pr
4	195	100.0	861	1 VCLJLV	env polypeptide pr
5	186	95.4	443	2 C41621	env polypeptide p
6	186	95.4	856	1 VCLJ3W	env polypeptide pr
7	186	95.4	861	1 VCLJ3C	env polypeptide pr
8	183	93.8	357	2 S21994	env polypeptide pr
9	183	93.8	358	2 S21998	env polypeptide pr
10	182	93.3	357	2 S21996	env polypeptide pr
11	179	91.8	847	2 T09448	env polypeptide pr
12	179	91.8	847	2 S13289	env polypeptide pr
13	178	91.8	445	2 A41621	env polypeptide M
14	178	91.8	445	2 S22002	env polypeptide M
15	177	90.8	358	2 S22000	env polypeptide g
16	177	90.8	358	2 S70417	env polypeptide g
17	177	90.8	852	2 T12016	env polypeptide g
18	177	90.8	852	2 VCLJMN	env polypeptide pr
19	176	90.3	357	2 S22004	env polypeptide pr
20	176	90.3	855	1 VCLJAJ	env polypeptide pr
21	174	89.2	853	2 S54384	env polypeptide pr
22	174	89.2	855	1 VCLJZR	env polypeptide pr
23	173	88.7	357	2 S22006	env polypeptide pr
24	173	88.7	843	1 H44001	env polypeptide pr
25	172	88.2	846	1 VCLJND	env polypeptide pr
26	170	87.2	357	2 S21992	env polypeptide g
27	170	87.2	852	1 VCLJBR	env polypeptide g
28	168	86.2	729	1 VCLJHX	env polypeptide pr
29	168	86.2	729	1 VCLJHX	env polypeptide pr

30	168	86.2	861	1 VCLJKB	env polypeptide pr
31	167	85.6	859	2 T01672	env polypeptide pr
32	164	84.1	454	2 B41621	env polypeptide D
33	163	83.6	868	1 VCLJH4	env polypeptide -
34	160	82.1	136	2 J00266	env polypeptide -
35	160	82.1	136	2 J00266	env polypeptide -
36	151	77.4	854	1 VCLJST	env polypeptide pr
37	149	76.4	856	1 A44963	env polypeptide pr
38	147	75.4	357	2 S21990	env polypeptide pr
39	136	69.7	877	2 S49197	env polypeptide p
40	119	61.0	863	2 A53034	env polypeptide p
41	86	44.1	881	1 VCLJG3	env polypeptide -
42	86	44.1	881	1 S03068	env polypeptide -
43	86	44.1	889	1 VCLJG5	env polypeptide -
44	85	43.6	151	2 S30448	env polypeptide -
45	85	43.6	151	2 S30452	env polypeptide -

## ALIGNMENTS

## RESULT 1

S33985 env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F. submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199

C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 195; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

DB 633 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 668

RESULT 2

env polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 195; DB 2; Length 854;

Best Local Similarity 100.0%; Pred. No. 2e-15;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 36

DB 636 YTSLSHSLIEESQNOEKNEQLELDKRWASLWMP 671

RESULT 3

VCLJH3

```

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, J.A.; Papas, T.S.; Grzybicki, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <MAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:12-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 4

```

env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, J.A.; Papas, T.S.; Grzybicki, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 195; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 5

```

env polypeptide precursor - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, J.A.; Papas, T.S.; Grzybicki, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <MAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:12-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 195; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 2e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 6

```

env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, J.A.; Papas, T.S.; Grzybicki, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 95.4%; Score 186; DB 2; Length 443;
Best Local Similarity 94.4%; Pred. No. 1.1e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7

```

env polypeptide precursor - human immunodeficiency virus type 1 (isolate WMCI)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran, J.A.; Papas, T.S.; Grzybicki, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.; Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <MAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <Sig>
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:12-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 95.4%; Score 186; DB 2; Length 443;
Best Local Similarity 94.4%; Pred. No. 1.1e-14;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

C:Accession: A24774  
 R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774, MIMD:86218077, PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 95.4%; Score 186; DB 1; Length 856;  
 Best Local Similarity 94.4%; Pred. No. 2.4e-14;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 638 YTSLLITLIEESONQOEKNEDELLELDKWSLWMP 673

RESULT 8  
 WCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MIMD:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <GP>  
 F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 95.4%; Score 186; DB 1; Length 861;  
 Best Local Similarity 94.4%; Pred. No. 2.4e-14;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 643 YTSLLITLIEESONQOEKNEDELLELDKWSLWMP 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi  
 A:Reference number: S21994  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEL>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.8%; Score 183; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 2e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 139 YTSLLITLIEESONQOEKNEDELLELDKWSLWMP 174

RESULT 10  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222, 'X', 224-358 <STEL>  
 A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 93.8%; Score 183; DB 2; Length 358;  
 Best Local Similarity 91.7%; Pred. No. 2e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

DB 140 YTSLLITLIEESONQOEKNEDELLELDKWSLWMP 175

RESULT 11  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 C:Accession: S70422; S21996  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MIMD:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>  
 A:Cross-references: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.3%; Score 182; DB 2; Length 357;

Best Local Similarity 91.7%; Pred. No. 2, 7e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 139 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 174

#### RESULT 12

envelope glycoprotein - human immunodeficiency virus type 1 (strain JFRL)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Pan, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

Accession number: Z16673

Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-References: EMBL:063632; NID:91465777; PID:91465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

#### Query Match

Best Local Similarity 91.8%; Score 179; DB 2; Length 847;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 629 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 664

#### RESULT 13

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13289; MUID:91043044; PMID:2172833

Accession: S13289

Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polypeptide

#### Query Match

Best Local Similarity 91.8%; Score 179; DB 2; Length 847;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 629 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 664

#### RESULT 14

AA1621

env polypeptide M - human immunodeficiency virus type 1 (fragment)

N:Alternate names: coat polypeptide

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999

C:Accession: AA1621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity

A:Reference number: AA1621; MUID:92107924; PMID:1763038

A:Accession: AA1621

A:Molecule type: DNA

A:Residues: 1-445 <BUR>

A:Cross-References: GB:M77228; NID:9328627; PID:AA03790.1; PID:9555013

A>Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TMN>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding st

#### Query Match

Best Local Similarity 91.3%; Score 178; DB 2; Length 445;

Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 380 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 415

#### RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 3L

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <STEL>

A:Cross-References: EMBL:X61352; NID:960186; PID:CAA43616.1; PID:960187

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <STEL2>

A:Cross-References: EMBL:X61352; NID:960186

C:Superfamily: type E retrovirus env polypeptide

#### Query Match

Best Local Similarity 90.8%; Score 177; DB 2; Length 358;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 36

DB 140 YTSLSHLSIESONQOEKNEDELLEDKNASLWNMF 175

Search completed: May 16, 2003, 11:25:05

Job time: 13.1446 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644. MW; D16A3C90857785F1 CR64;

```

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Query Match 100.0%; Score 195; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YTSLSHSLIEESONOQEKNEQELLELDKWSLWNMF 36
DB 633 YTSLSHSLIEESONOQEKNEQELLELDKWSLWNMF 668

```

```

RESULT 2
ENV_HV1B1 STANDARD: PRT; 856 AA.
AC P03375;
ID ENV_HV1B1
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide GPI60 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
Viruses; Retrovird viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284(1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
RA Gregory T.J.;
RT "Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells.";
RL J. Biol. Chem. 265:10373-10382(1990).
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```

CC EMBL: M15654; AAA44205.1; -
DR PIR: A03973; VCLJH3
DR HIV: M15654; ENVSBI102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
KW SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFEB1A18931BB27 CR64;

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Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YTSLSHSLIEESONOQEKNEQELLELDKWSLWNMF 36
DB 638 YTSLSHSLIEESONOQEKNEQELLELDKWSLWNMF 673

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RESULT 3
ENV_HV1H2 STANDARD: PRT; 856 AA.
AC F04578; 009779;

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FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	448	448	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	463	463	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	611	611	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	624	624	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	637	637	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	674	674	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	750	750	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL).		
SO	SEQUENCE	856 AA;	97212 MW;	66AB16AF85107FFED CRC64;			
Query Match		100.0%;	Score 195;	DB 1;	Length 856;		
Best Local Similarity		100.0%;	Pred. No. 3,2e-16;				
Matches 36;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Oy	1	YTSLHSLIESQNOEKNEDELLFLDKWASLMMWF	36				
Db	638	YTSLHSLIESQNOEKNEDELLFLDKWASLMMWF	673				
RESULT 4							
ENV_HV1H3	STANDARD:	PRT:	856 AA.				
AC	P04624;						
DT	13-AUG-1987 (Rel. 05, Created)						
DT	01-FEB-1996 (Rel. 33, Last sequence update)						
DT	15-JUL-1999 (Rel. 38, Last annotation update)						
DE	Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp11)].						
GN	ENV.						
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).						
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.						
OX	NCBI_TaxID=11707;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=85228248; PubMed=298795;						
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;						
RT	"HIV-1 env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";						
RL	Cell 41:979-986(1985).						
CC	-----						
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CC	-----						
DR	EMBL; M14100; AAA44679.1; -						
DR	HIV; M14100; ENVSHXB3.						
DR	InterPro; IPR000328; Env_Gp11.						
DR	InterPro; IPR000777; Gp120.						
DR	Pfam; PF00516; Gp120.1.						
DR	Pfam; PF00517; Gp41.1.						
KW	AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.						
KW	SIGNAL.						
FT	SIGNAL	1	30				
FT	CHAIN	31	511	EXTERIOR MEMBRANE GLYCOPROTEIN.			
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.			
FT	DISULFID	119	205	BY SIMILARITY.			
FT	DISULFID	126	196	BY SIMILARITY.			
FT	DISULFID	131	157	BY SIMILARITY.			
FT	DISULFID	218	247	BY SIMILARITY.			
FT	DISULFID	228	239	BY SIMILARITY.			
FT	DISULFID	296	331	BY SIMILARITY.			
FT	DISULFID	378	445	BY SIMILARITY.			
FT	DISULFID	385	418	BY SIMILARITY.			
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).			

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 97188 MW: 3373688B84C1AFC CRC64:

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Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLSHSLIEESONOQKNEQLELDKMASLWMP 36
DB 638 YTSLSHSLIEESONOQKNEQLELDKMASLWMP 673

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```

RESULT 5
ENV_HVILW STANDARD; PRT: 856 AA.
ID ENV_HVILW STANDARD; PRT: 856 AA.
AC 070626;
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
ENV Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

```

```

OS Human immunodeficiency virus type 1 (HIV2.3 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB).";
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC EMBL, U12055; AAA76690.1;
DR GLYCOSITEDB; 070626;
DR Interpro; IPR000328; Env_GP41.

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DR Interpro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA: 96938 MW: 0C241332CF7E6687 CRC64:

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Query Match 100.0%; Score 195; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.2e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 YTSLSHSLIEESONOQKNEQLELDKMASLWMP 36
DB 638 YTSLSHSLIEESONOQKNEQLELDKMASLWMP 673

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RESULT 6
ENV_HVILW STANDARD; PRT: 861 AA.
ID ENV_HVILW STANDARD; PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
ENV Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

```

```

OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64;

Query Match
Best Local Similarity 98.5%; Score 192; DB 1; Length 853;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHLSIESONQOEKNEOELLELDKKNASLWNF 36
|||||:|||||:|||||:|||||:|||||:
636 YTSLSHLSIESONQOEKNEOELLELDKKNASLWNF 671

RESULT 8
ENV_HV1PV STANDARD: PRT; 856 AA.
ID ENV_HV1PV STANDARD: PRT; 856 AA.
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;
RN [1]
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/Lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
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CC -----
CC EMBL: K02083; AAB59873.1;
DR EMBL: X01762; CA25903.1; ALT_SEQ.
DR PIR: A03974; VCLJVL.
DR HIV: K02083; ENVSPV22.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 54 74 BY SIMILARITY.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.

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FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 856 AA: 97339 MW: 5FCDB1DC3C1209B3 CRC64;

Query Match
Best Local Similarity 95.4%; Score 186; DB 1; Length 856;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 YTSLSHLSIESONQOEKNEOELLELDKKNASLWNF 35
|||||:|||||:|||||:|||||:|||||:
638 YTSLSHLSIESONQOEKNEOELLELDKKNASLWNF 672

RESULT 9
ENV_HV1SC STANDARD: PRT; 856 AA.
ID ENV_HV1SC STANDARD: PRT; 856 AA.
AC P05878;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11702;
RN [1]
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
1984 IN SOUTHERN CALIFORNIA.
CC -----
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DR EMBL: M17450; -; NOT\_ANNOTATED\_CDS.

DR PIR: B28922; VCLJ3C.

DR HIV: M17450; ENV55C.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT SITE 760 760

FT SITE 760 760

FT DISULFID 53 73

FT DISULFID 118 206

FT DISULFID 125 197

FT DISULFID 130 160

FT DISULFID 219 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 439

FT DISULFID 383 412

FT CARBOHYD 87 129

FT CARBOHYD 129 135

FT CARBOHYD 135 135

FT CARBOHYD 140 140

FT CARBOHYD 143 143

FT CARBOHYD 159 159

FT CARBOHYD 163 163

FT CARBOHYD 189 189

FT CARBOHYD 198 198

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 276

FT CARBOHYD 276 276

FT CARBOHYD 295 295

FT CARBOHYD 301 301

FT CARBOHYD 302 302

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 384 384

FT CARBOHYD 394 394

FT CARBOHYD 400 400

FT CARBOHYD 405 405

FT CARBOHYD 442 442

FT CARBOHYD 457 457

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

FT CARBOHYD 674 674

FT CARBOHYD 816 816

SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 95.4%; Score 186; DB 1; Length 856;

Best Local Similarity 94.4%; Pred. No. 4e-15;

Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSIESONQOEKNEOELLELDKWSLWMMF 36

DB 638 YTSLIHSIESONQOEKNEOELLELDKWSLWMMF 673

RESULT 10

ENV\_HV1M1 STANDARD; PRT; 856 AA.

ID ENV\_HV1M1

AC P31872;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)).

GN ENV.

OS Human immunodeficiency virus type 1 (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI\_Taxid=31678;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=66218077; PubMed=2423250.

RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;

RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS."

RT Cell 45:637-648(1986).

RL -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT SIGNAL 1 29

FT CHAIN 30 510

FT CHAIN 511 856

FT DISULFID 53 73

FT DISULFID 118 205

FT DISULFID 125 196

FT DISULFID 130 152

FT DISULFID 218 247

FT DISULFID 228 239

FT DISULFID 296 330

FT DISULFID 376 444

FT DISULFID 383 417

FT CARBOHYD 87 87

FT CARBOHYD 134 134

FT CARBOHYD 140 140

FT CARBOHYD 151 151

FT CARBOHYD 155 155

FT CARBOHYD 183 183

FT CARBOHYD 197 197

FT CARBOHYD 234 234

FT CARBOHYD 241 241

FT CARBOHYD 262 262

FT CARBOHYD 276 276

FT CARBOHYD 289 289

FT CARBOHYD 295 295

FT CARBOHYD 331 331

FT CARBOHYD 338 338

FT CARBOHYD 354 354

FT CARBOHYD 360 360

FT CARBOHYD 390 390

FT CARBOHYD 394 394

FT CARBOHYD 404 404

FT CARBOHYD 447 447

FT CARBOHYD 459 459

FT CARBOHYD 611 611

FT CARBOHYD 616 616

FT CARBOHYD 625 625

FT CARBOHYD 637 637

SO SEQUENCE 856 AA; 97526 MW; DB68D1E94C04D69 CRC64;

Query Match 95.4%; Score 186; DB 1; Length 856;

Best Local Similarity 94.4%; Pred. No. 4e-15;

Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSLIHSIESONQOEKNEOELLELDKWSLWMMF 36

Db 638 YTSLLYTLIESQNOQEKNEQELLEDKWASLWMNF 673

RESULT 11

ENV_HV1S3	STANDARD:	PRT:	852 AA.
AC	P19549;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).		
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11690;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90317906; PubMed=2370688;		
RT	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;		
RT	"Human immunodeficiency virus type 1 cellular host range,"		
RT	replication, and cytopathicity are linked to the envelope region of		
RT	the viral genome."		
RL	J. Virol. 64:4016-4020(1990).		
CC	-----		
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL: M38427; AAA45067.1; -		
DR	HIV: M38427; ENVSSSF33.		
DR	InterPro: IPR000328; Env_GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam: PF00516; GP120; 1.		
DR	Pfam: PF00517; GP41; 1.		
KW	AIDS; Coat protein; Glycoprotein; Transmembrane;		
KW	Signal.		
FT	1 31	BY SIMILARITY.	
FT	32 506	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	33 852	TRANSMEMBRANE GLYCOPROTEIN.	
FT	53 73	BY SIMILARITY.	
FT	DISULFID 118 206	BY SIMILARITY.	
FT	DISULFID 125 197	BY SIMILARITY.	
FT	DISULFID 130 156	BY SIMILARITY.	
FT	DISULFID 219 248	BY SIMILARITY.	
FT	DISULFID 229 240	BY SIMILARITY.	
FT	DISULFID 297 331	BY SIMILARITY.	
FT	DISULFID 377 439	BY SIMILARITY.	
FT	DISULFID 384 412	BY SIMILARITY.	
FT	CARBOHYD 87 87	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 129 129	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 136 136	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 141 141	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 142 142	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 144 142	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 155 155	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 159 159	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 189 189	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 198 198	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 242 242	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 263 263	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 277 277	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 290 290	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 296 296	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 332 332	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 339 339	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 355 355	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 385 385	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 391 391	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 397 397	N-LINKED (GLCNAC. . .) (POTENTIAL).	

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 852 AA; 96663 MW; E57BBF8D23C9910D CRC64;

Query Match 94.4%; Score 184; DB 1; Length 852;

Best Local Similarity 91.7%; Pred. No. 7e-15;

Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLLYTLIESQNOQEKNEQELLEDKWASLWMNF 36

Db 634 YTSLLYTLIESQNOQEKNEQELLEDKWASLWMNF 669

RESULT 12

ENV_HV1S1	STANDARD:	PRT:	847 AA.
AC	P19550;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP41)].		
GN	ENV.		
OS	Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).		
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11691;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90347835; PubMed=2384920;		
RT	Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.		
RT	"Viral determinants of human immunodeficiency virus type 1 T-cell or		
RT	macrophage tropism, cytopathogenicity, and CD4 antigen modulation."		
RT	J. Virol. 64:4390-4398(1990).		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL: M65024; AAA45072.1; -		
DR	HIV: M38428; ENVSSSF162.		
DR	InterPro: IPR000328; Env_GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam: PF00516; GP120; 1.		
DR	Pfam: PF00517; GP41; 1.		
KW	AIDS; Coat protein; Glycoprotein; Transmembrane;		
KW	Signal.		
FT	1 29	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	30 502	TRANSMEMBRANE GLYCOPROTEIN.	
FT	33 847	BY SIMILARITY.	
FT	CHAIN 53 73	BY SIMILARITY.	
FT	DISULFID 118 203	BY SIMILARITY.	
FT	DISULFID 125 194	BY SIMILARITY.	
FT	DISULFID 130 155	BY SIMILARITY.	
FT	DISULFID 216 245	BY SIMILARITY.	
FT	DISULFID 226 237	BY SIMILARITY.	
FT	DISULFID 294 328	BY SIMILARITY.	
FT	DISULFID 374 435	BY SIMILARITY.	
FT	DISULFID 381 408	BY SIMILARITY.	
FT	DISULFID 87 87	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 135 135	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 154 154	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 186 186	N-LINKED (GLCNAC. . .) (POTENTIAL).	

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FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL)
SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

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Query Match 93.8%; Score 183; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 9.2e-15;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTSLHSLIEESONQOEKNEDELKWSLWMP 36
DB 629 YTNLYTLIEESONQOEKNEDELKWSLWMP 664

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RESULT 13
ENV_HV1W2 STANDARD; PRT; 847 AA.
AC P05880:
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RX MEDLINE=86235450; PubMed=3012778;
RP Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or
at risk for AIDS."
RT Science 232:1548-1553(1986).
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
WAS PERINATALLY INFECTED BY HER MOTHER.
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: M12507; AAB12990.1;
CC HIV: M12507; ENV5WJ2.
CC InterPro: IPR000326; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.

```

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FT SIGNAL 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 215 244
FT DISULFID 225 236
FT DISULFID 293 326
FT DISULFID 372 435
FT DISULFID 379 408
FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
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FT CARBOHYD 238 238
FT CARBOHYD 259 259
FT CARBOHYD 273 273
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FT CARBOHYD 327 327
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FT CARBOHYD 386 386
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FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SEQUENCE 847 AA; 96466 MW; C01E33D73AAS5CAE CRC64;

Query Match 92.3%; Score 180; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 2.1e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTSLHSLIEESONQOEKNEDELKWSLWMP 36
DB 629 YTSIISLIEESONQOEKNEDELKWSLWMP 664

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RESULT 14
ENV_HV1J3 STANDARD; PRT; 867 AA.
AC P12489:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11694;
RN [1]
RX MEDLINE=89352108; PubMed=2669897;
RP Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
"Nucleotide sequences of gag and env genes of a Japanese isolate of
HIV-1 and their expression in bacteria."
RT AIDS Res. Hum. Retroviruses 5:411-419(1989).
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FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 626 626 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 856 AA; 97140 MW; D197D809940BE732 CRC64;

Query Match 90.8%; Score 177; DB 1; Length 856;  
 Best Local Similarity 88.9%; Pred. No. 5e-14;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNF 36  
 |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|  
 Db 639 YTSLIYSLEKSOEQEKNEQELLELDKWSLWNF 674

Search completed: May 16, 2003, 11:13:31  
 Job time : 7.0729 secs

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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-536

Perfect score: 195  
Sequence: 1 YTSIHSILIESQNOQEKNEQELLDKWSLWVWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

1 number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*  
23: /SID2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	193	99.0	36	16	DP-178 derived fro
2	193	99.0	36	17	DP178 corresponds
3	193	99.0	36	18	HIV-1 derived pept
4	193	99.0	36	19	SEQ ID NO. 108 fro
5	193	99.0	36	19	SYNTHETIC peptide
6	193	99.0	36	20	HIV-1 LAI gp41 T-2
7	193	99.0	36	21	T20/DP178 peptide
8	193	99.0	36	21	T20/DP178 peptide
9	193	99.0	36	21	T20/DP178 peptide
10	193	99.0	36	21	T20/DP178 peptide

Result No.	Score	Query Match	Length	ID	Description
11	193	99.0	36	21	AA14533
12	193	99.0	36	21	AA188655
13	193	99.0	36	21	AA188729
14	193	99.0	36	21	AA188135
15	193	99.0	36	21	AA188136
16	193	99.0	36	21	AA188242
17	193	99.0	36	21	AA188424
18	193	99.0	36	21	AA188692
19	193	99.0	36	21	AA188735
20	193	99.0	36	21	AA188777
21	193	99.0	36	21	AA188982
22	193	99.0	36	21	AA188983
23	193	99.0	36	21	AA188999
24	193	99.0	36	22	AAU70179
25	193	99.0	36	22	AAU70741
26	193	99.0	36	22	AA188961
27	193	99.0	36	22	AA188703
28	193	99.0	36	22	AA1880024
29	193	99.0	36	22	AA1880087
30	193	99.0	36	22	AA1880088
31	193	99.0	36	22	AA1880494
32	193	99.0	36	22	AA1880495
33	193	99.0	36	22	AA1880600
34	193	99.0	36	22	AA1880626
35	193	99.0	36	22	AA1880627
36	193	99.0	36	22	AA1880628
37	193	99.0	36	22	AA1880832
38	193	99.0	36	22	AA1880100
39	193	99.0	36	22	AA1880143
40	193	99.0	36	22	AA1880185
41	193	99.0	36	22	AA1880191
42	193	99.0	36	22	AA1880192
43	193	99.0	36	22	AA18801414
44	193	99.0	36	22	AA18801488
45	193	99.0	36	22	AA18801970

# ALIGNMENTS

RESULT 1  
AA1884364  
ID AA1884364 standard; Peptide: 36 AA.  
AC AA1884364;  
DE 24-AUG-1995 (first entry)  
XX DP-178 derived from HIV-1 isolate LAI has antiviral activity.  
DE DP-178 derived from HIV-1 isolate LAI has antiviral activity.  
XX antiviral activity: DP-178; DP-107; diagnostic: HIV-1LAI;  
XX human immunodeficiency virus; transmembrane protein; gp41;  
XX alpha helix; leucine zipper; DP-185.  
OS Synthetic.  
XX  
FH Key  
FH Modified-site 1 location/Qualifiers  
FT /note= "optionally has an amino, acetyl,  
FT 9-fluorenylmethoxy-carbonyl, hydrophobic or  
FT macromolecular carrier gp. attached"  
FT Modified-site 38  
FT /note= "optionally has a carboxyl, amido, hydrophobic  
FT or macromolecular carrier gp. attached"

PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Peteway SR, Wild CT;  
 DR WPI: 1995-036105/05.  
 XX  
 XX Computer search generated synthetic peptides - are inhibitors of  
 PT HIV transmission  
 PS  
 CC Claim 11; Page 132; 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-598) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibits transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36  
 RESULT 2  
 ID AAR98398  
 AC AAR98398 standard; peptide: 36 AA.  
 XX  
 AC AAR98398;  
 DT 17-FEB-1997 (first entry)  
 DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
 XX  
 XX Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALMORT15; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM Influenza virus; hepatitis B virus.  
 XX  
 XX Human immunodeficiency virus type 1.  
 PM WO9619495-A1.  
 PD 27-JUN-1996.  
 PS 20-DEC-1995; 95WO-US16733.  
 PF 06-JUN-1995; 95US-0470896.  
 PR 20-DEC-1994; 94US-0360107.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Peteway SR, Wild CT;  
 DR WPI: 1996-309517/31.  
 XX  
 XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALMORT15, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure: Fig 1; 471pp; English.

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALMORT15,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36  
 RESULT 3  
 ID AAM17011  
 AC AAM17011 standard; peptide: 36 AA.  
 XX  
 AC AAM17011;  
 DT 30-JUN-1997 (first entry)  
 DE HIV-1 derived peptide useful for treatment of HIV infection.  
 XX  
 XX HIV, SIV: human, simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 XX  
 OS Human immunodeficiency virus type 1 LAI isolate.  
 XX  
 PN WO9640191-A1.  
 PD 19-DEC-1996.  
 PS 06-JUN-1996; 96WO-US09499.  
 PF 07-JUN-1995; 95US-0481957.  
 PR (TRIM-) TRIMERIS INC.  
 PA Johnson RM, Lambert DM;  
 XX  
 XX WPI: 1997-099886/09.  
 DR  
 XX  
 XX Compns. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 PS Claim 2; Figure 1; 84pp; English.  
 XX  
 CC AAM17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSIHSLSIESQNOEKNEQELLELDKWSLWNMF 36  
 DB 1 YTSLSHSLSIESQNOEKNEQELLELDKWSLWNMF 36

## RESULT 4

AAV22912  
ID AAV22912 standard; Peptide: 36 AA.  
XX  
AC AAV22912;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 108 from WO9820036.  
XX  
XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
XX MO9820036-A1.  
XX  
XX 14-MAY-1998.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Pheian JC, Starovasnik MA;  
PI Wells JA;  
XX  
XX WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa-peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX Disclosure: Page 233-234; 279pp; English.  
XX  
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
XX  
SQ Sequence 36 AA:

Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

YY 1 YTSITHSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSILHSLEESONQOEKNEDELLELDKWSLWNMF 36

## RESULT 5

AAV22805  
ID AAV22805 standard; Peptide: 36 AA.  
XX  
AC AAV22805;  
XX  
DT 19-AUG-1999 (first entry)  
XX  
DE SEQ ID NO. 1 from WO9820036.  
XX  
XX HIV; gp41 protein; constrained helical peptide; HIV infection;  
KM vaccine; antibody; viral membrane fusion; viral infectivity;  
KM ligand affinity purification; protein A replacement;  
KM immunoglobulin purification; epitope mimic.  
XX  
OS Human immunodeficiency virus.  
XX  
XX MO9820036-A1.  
XX  
XX 14-MAY-1998.  
XX  
XX 05-NOV-1997; 97WO-US20069.  
XX  
XX 16-JUN-1997; 97US-0876698.  
PR 06-NOV-1996; 96US-0743698.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
PI Braisted A, Judice JK, McDowell RS, Pheian JC, Starovasnik MA;  
PI Wells JA;  
XX  
XX WPI: 1998-286866/25.  
XX  
XX Production of constrained helical peptide(s) by linking side chains  
PT on termini of octa-peptide - derived from human immunodeficiency  
PT virus gp41 protein, useful in vaccines for treatment and prevention  
PT of infection  
XX  
XX Disclosure: Page 143-144; 279pp; English.  
XX  
XX Peptides AAV22805-Y22917 are derived from Human immunodeficiency virus  
CC (HIV). Specifically, AAV22810-Y22910 are derived from gp41 proteins  
CC of known HIV virus strains (AAV22810, AAV22871, AAV22880, AAV22888 and  
CC AAV22903 represent consensus sequences of various sections of the gp41  
CC protein). Sequences derived from the peptides are used to produce  
CC constrained helical peptides of the invention. The constrained helical  
CC peptide is produced by synthesizing an octapeptide in which both terminal  
CC amino acids have a side-chain that includes a group able to form an amide  
CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
CC residues with a difunctional linker to produce two amide bonds.  
CC The constrained helical peptides are used to treat or prevent HIV  
CC infection, especially as vaccines that generate antibodies that  
CC prevent viral membrane fusion or infectivity. Vaccines may contain  
CC constrained helical peptides derived from several different strains of  
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
CC uses for the constrained helical peptides are in affinity purification  
CC of ligands (particularly where complete binding protein is not readily  
CC available, e.g. replacements for protein A in immunoglobulin  
CC purification); as epitope mimics for antibody production; for isolation  
CC of synthetic antibody clones from phage display libraries, or as stable  
CC forms of "floppy" peptides or proteins.  
XX  
XX  
SQ Sequence 36 AA:

Query Match 99.0%; Score 193; DB 19; Length 36;  
Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

YY 1 YTSITHSLEESONQOEKNEDELLELDKWSLWNMF 36  
DB 1 YTSILHSLEESONQOEKNEDELLELDKWSLWNMF 36

RESULT 6  
 AAY31955  
 ID AAY31955 standard; Peptide: 36 AA.  
 XX  
 AC AAY31955;  
 XX  
 DT 21-DEC-1999 (first entry)  
 XX  
 DE Synthetic peptide T-20 (DP-178).  
 XX  
 KM T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 FH Key  
 FT Modified-site 1 Location/Qualifiers  
 FT Modified-site /note= "N-terminal acetyl"  
 FT Modified-site 36  
 XX Modified-site /note= "C-terminal amide"  
 XX  
 PN WO9948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 XX  
 DR WPI: 1999-591038/50.  
 XX  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides -  
 XX  
 PS Claim 1; Page 102; 120pp; English.  
 XX  
 CC The present sequence represents an N- and C-terminal modified  
 CC peptide, designated T-20 (or DP-178), corresponding to amino acids  
 CC 638-673 of the transmembrane protein gp41 of HIV-1 LAI isolate.  
 CC The invention relates to methods for the synthesis of peptides,  
 CC in particular T-20 and T-20-like peptides. The method involves  
 CC synthesizing specific side-chain protected peptide fragment  
 CC intermediates of T-20 or a T-20-like peptide on a solid support,  
 CC coupling the protected fragments in solution to form a protected  
 CC T-20 or T-20-like peptide, followed by deprotection of the side  
 CC chains to yield the final T-20 or T-20-like peptide. The invention  
 CC also relates to individual peptide fragments (see AAY31956-73) which  
 CC act as intermediates in the synthesis of peptides of interest (e.g.  
 CC T-20), and to particular groups of peptide fragments which act as  
 CC intermediates in the synthesis of the peptide of interest. The  
 CC method allows for the large scale, economical production of high  
 CC purity peptides.  
 XX  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

ID AAY31974 standard; Peptide: 36 AA.  
 XX  
 AC AAY31974;  
 XX  
 DT 21-DEC-1999 (first entry)  
 XX  
 DE HIV-1 LAI gp41 T-20 peptide.  
 XX  
 KM T-20; DP-178; HIV-1 LAI; gp41; peptide synthesis.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO9948513-A1.  
 XX  
 PD 30-SEP-1999.  
 XX  
 PF 22-MAR-1999; 99WO-US06230.  
 XX  
 PR 23-MAR-1998; 98US-0045920.  
 PR 01-MAY-1998; 98US-0071877.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Kang M, Bray B, Lichy M, Mader C, Merutka G;  
 XX  
 DR WPI: 1999-591038/50.  
 XX  
 PT Methods of peptide synthesis, particularly used to produce T-20 or  
 PT T-20 like peptides -  
 XX  
 PS Disclosure: Page 9; 120pp; English.  
 XX  
 CC The present sequence represents a peptide, designated T-20 (or  
 CC DP-178), that corresponds to amino acids 638-673 of the  
 CC transmembrane protein gp41 of HIV-1 LAI isolate. The invention  
 CC relates to methods for the synthesis of peptides, in particular  
 CC C- and N-terminal modified T-20 (see AAY31955) and T-20-like peptides.  
 CC The method involves synthesizing specific side-chain protected  
 CC peptide fragment intermediates (see AAY31956-73) of T-20 or a  
 CC T-20-like peptide on a solid support, coupling the protected  
 CC fragments in solution to form a protected T-20 or T-20-like peptide,  
 CC followed by deprotection of the side chains to yield the final T-20  
 CC or T-20-like peptide. The invention also relates to individual  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC peptides of interest (e.g. T-20), and to particular groups of  
 CC peptide fragments which act as intermediates in the synthesis of  
 CC the peptide of interest. The method allows for the large scale,  
 CC economical production of high purity peptides.  
 XX  
 SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 20; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 AAB52655  
 ID AAB52655 standard; Peptide: 36 AA.  
 XX  
 AC AAB52655;  
 XX  
 DT 23-FEB-2001 (first entry)  
 XX  
 DE T20/DP178 peptide fragment #33.  
 XX  
 KM Antiflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
 KM formyl peptide receptor family; FPR; inflammatory response up-regulation;  
 KM chemottractant.

XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX antagonist is used to modulate inflammation -  
XX Claim 12; Page 24; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLIESONQOEKNEELLELDKWSLWNWF 36  
DB 1 YTSIHSLIESONQOEKNEELLELDKWSLWNWF 36  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide; 36 AA.  
XX AAB52688;  
XX  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #66.  
XX KW Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX KW chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.

XX OS Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 12; Page 25; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.  
XX SQ Sequence 36 AA:  
XX  
XX Query Match 99.0%; Score 193; DB 21; Length 36;  
XX Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
XX Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTSIHSLIESONQOEKNEELLELDKWSLWNWF 36  
DB 1 YTSIHSLIESONQOEKNEELLELDKWSLWNWF 36  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide; 36 AA.  
XX AAB52818;  
XX  
XX DT 23-FEB-2001 (first entry)  
XX DE T20/Dp178 peptide fragment #97.  
XX KW Antiinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
XX KW formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX KW chemoattractant.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200066622-A1.  
XX PD 09-NOV-2000.  
XX PF 05-MAY-2000; 2000WO-US12371.  
XX PR 05-MAY-1999; 99US-0132686.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX DR MPI; 2000-656493/63.  
XX PT Administration of peptide agents with a sequence corresponding to a  
XX PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
XX PT antagonist is used to modulate inflammation -  
XX PS Claim 14; Page 40; 148pp; English.  
XX CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
XX CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
XX CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
XX CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
XX CC interacts with members of the formyl peptide receptor (FPR) family and  
XX CC thereby up-regulates an inflammatory response, and acts as a potent  
XX CC chemoattractant and activator of human peripheral blood phagocytes  
XX CC (but not T cells). The present peptide can be used to modulate an  
XX CC inflammatory response in a subject.

[illegible]

CC	HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to reduce HIV infection of uninfected cells. Antibodies raised against entry-relevant gp1 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry.
XX	
SQ	Sequence 36 AA:
Query Match	99.0% Score 193; DB 21; Length 36;
Best Local Similarity	97.2%; Pred. No. 6 ie-17;
Matches 35; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
OY	1 YTSIIHSLIEESONOEKNEQELLELDKWASLWMNF 36       1 YTSLIHSLIEESONOEKNEQELLELDKWASLWMNF 36
Db	
RESULT 12	
AAY88665	standard; peptide; 36 AA.
AC	AAY88665;
DT	23-MAY-2000 (first entry)
DE	Core polypeptide fragment T No. 20.
XX	
Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1; HIV-2; STV; pharmacokinetic; half-life; growth factor; cytokine; viral; anti-fusogenic; differentiation factor; interleukin; interferon; colony stimulating factor; hormone; angiogenic factor.	
XX	
OS	Unidentified.
XX	
PN	W09593615-A1.
XX	
PD	25-NOV-1999.
XX	
PE	20-MAY-1999; 99WO-US11219.
PR	20-MAY-1998; 98US-0082279.
PA	(TRIM-) TRIMERIS INC.
XX	
PI	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
DR	WPI: 2000-136792/12.
XX	
P7	A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence -
XX	
PS	Disclosure; Page 21; 124pp: English.
XX	
The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and STV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AY88651-Y90055 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.	

XX Sequence 36 AA: 99.0%; Score 193; DB 21; Length 36;  
 Query Match Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
 DB 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

RESULT 13  
 AAY8729  
 ID AAY8729 standard; peptide; 36 AA.  
 AC AAY8729;  
 XX  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 84.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN MO959615-A1.  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PR 20-MAY-1998; 98US-0082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS  
 XX Disclosure; Page 22; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.

SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

DB 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

RESULT 14  
 AAY89135  
 ID AAY89135 standard; peptide; 36 AA.  
 AC AAY89135;  
 XX  
 DT 23-MAY-2000 (first entry)

Core polypeptide fragment T No. 573.

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN MO959615-A1.  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PR 20-MAY-1998; 98US-0082279.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS  
 XX Disclosure; Page 30; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic factor. The peptides of the invention can be used for inhibiting viral infection and can be used in anti-viral and anti-fusogenic treatments. Sequences AAY8651-Y9005 represent core polypeptide fragments that can be used in the invention. Some sequences among those indicated also comprise enhancer fragments at terminal ends and form hybrid polypeptides.

SO Sequence 36 AA:  
 Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6.1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36  
 DB 1 YTSIIHSLIEESONQOEKNEQELLELDKMASLWNMF 36

RESULT 15  
 AAY89136  
 ID AAY89136 standard; peptide; 36 AA.  
 XX

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 574.  
 XX  
 KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9595615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PF 20-MAY-1998; 98US-0082279.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 XX comprises enhancer sequence -  
 XX  
 PS Disclosure; Page 30; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.  
 SU Sequence 36 AA;  
 Query Match 99.0%; Score 193; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 6,1e-17;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTSIIHSLSIESQNOQEKNEQELLELDKVASLWNMF 36  
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 DB 1 YTSIIHSLSIESQNOQEKNEQELLELDKVASLWNMF 36

Search completed: May 16, 2003, 11:12:05  
 Job time : 33.4578 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-535

Perfect score: 197  
Sequence: 1 YTNLIHSLIESONQOEKNEOELLELDKWSLWNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Published\_Applications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubppaa/PCT\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	36	9	US-09-874-475-16
2	192	97.5	36	9	US-10-116-797-1
3	192	97.5	36	9	US-09-493-346-1
4	192	97.5	36	10	US-09-796-202-10
5	192	97.5	36	10	US-09-779-451-5
6	192	97.5	36	10	US-09-834-628-1
7	192	97.5	36	10	US-09-854-816-1
8	192	97.5	36	10	US-09-854-816-108
9	192	97.5	37	9	US-09-848-616-176
10	192	97.5	46	10	US-09-779-451-41
11	192	97.5	56	10	US-09-779-451-4
12	192	97.5	177	9	US-10-040-349B-2
13	192	97.5	221	9	US-10-059-271-84
14	192	97.5	232	9	US-10-059-271-81
15	192	97.5	254	9	US-10-059-271-82
16	192	97.5	256	9	US-10-059-271-97
17	192	97.5	268	10	US-09-854-816-16
18	192	97.5	268	10	US-09-854-816-17
19	192	97.5	268	10	US-09-854-816-18

20	192	97.5	344	9	US-10-040-349B-1	Sequence 1, Appl
21	192	97.5	345	9	US-10-026-741-49	Sequence 49, Appl
22	192	97.5	345	10	US-09-779-451-8	Sequence 8, Appl
23	192	97.5	391	9	US-10-059-271-93	Sequence 93, Appl
24	192	97.5	519	10	US-09-756-551A-8	Sequence 8, Appl
25	192	97.5	853	9	US-10-003-035-33	Sequence 33, Appl
26	192	97.5	856	9	US-09-476-242-1	Sequence 103, App
27	192	97.5	861	9	US-10-026-741-103	Sequence 53, Appl
28	192	97.5	1101	9	US-10-003-035-53	Sequence 55, Appl
29	192	97.5	1186	9	US-10-003-035-55	Sequence 1, Appl
30	189	95.9	36	10	US-09-912-824-1	Sequence 19, Appl
31	189	95.9	268	10	US-09-854-816-19	Sequence 26, Appl
32	188	95.4	268	10	US-09-854-816-26	Sequence 4, Appl
33	188	95.4	619	10	US-09-891-609-4	Sequence 2, Appl
34	188	95.4	646	10	US-09-891-609-2	Sequence 2, Appl
35	188	95.4	847	10	US-09-476-242-2	Sequence 94, Appl
36	186	94.4	1231	9	US-10-059-271-94	Sequence 13, Appl
37	184	93.4	268	10	US-09-854-816-13	Sequence 50, Appl
38	183	92.9	233	10	US-09-854-816-50	Sequence 9, Appl
39	183	92.9	268	10	US-09-854-816-9	Sequence 12, Appl
40	183	92.9	269	10	US-09-854-816-12	Sequence 38, Appl
41	182	92.4	267	10	US-09-854-816-38	Sequence 41, Appl
42	182	92.4	268	10	US-09-854-816-41	Sequence 43, Appl
43	182	92.4	269	10	US-09-854-816-43	Sequence 46, Appl
44	182	92.4	269	10	US-09-854-816-46	Sequence 109, App
45	181	91.9	46	10	US-09-854-816-109	

#### ALIGNMENTS

RESULT 1  
US-09-874-475-16  
; Sequence 16, Application US/09874475  
; Publication No. US20020182592A1  
; GENERAL INFORMATION:  
; APPLICANT: Petropoulos, Christos J.  
; APPLICANT: Parkin, Neil T.  
; APPLICANT: Whitcomb, Jeanette  
; APPLICANT: Huang, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
; FILE REFERENCE: 2793/65166  
; CURRENT APPLICATION NUMBER: US/09/874,475  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 16  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16  
  
Query Match 97.5%; Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTNLIHSLIESONQOEKNEOELLELDKWSLWNMF 36  
DB 1 YTNLIHSLIESONQOEKNEOELLELDKWSLWNMF 36  
  
RESULT 2  
US-10-116-797-1  
; Sequence 1, Application US/10116797  
; Publication No. US20030044411A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen, William C.  
; APPLICANT: Madden, Paul J.  
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
; FILE REFERENCE: 64672-A  
; CURRENT APPLICATION NUMBER: US/10/116,797  
; CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 97.5%; Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKNASLWNMF 36  
1 YTSLSHSLIEESONQOEKNEQELLELDKNASLWNMF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 97.5%; Score 192; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKNASLWNMF 36  
1 YTSLSHSLIEESONQOEKNEQELLELDKNASLWNMF 36

RESULT 4  
US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SOLIDATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 97.5%; Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTNLIHSLIEESONQOEKNEQELLELDKNASLWNMF 36  
1 YTSLSHSLIEESONQOEKNEQELLELDKNASLWNMF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Alleyway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 97.5%; Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKNASLWNMF 36  
1 YTSLSHSLIEESONQOEKNEQELLELDKNASLWNMF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US20020119922A1  
GENERAL INFORMATION:

APPLICANT: YO, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 97.5%; Score 192; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.2e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKNASLWNMF 36  
1 YTSLSHSLIEESONQOEKNEQELLELDKNASLWNMF 36

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RESULT 7
US-09-854-816-1
Sequence 1, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 97.5%; Score 192; DB 10; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
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Db 1 YTSLIHSLIEESQNOQEKNEQELFLDKWASLWNF 36
RESULT 8
US-09-854-816-108
Sequence 108, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
MOLECULE TYPE: DP178
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
9-854-816-1
Query Match 97.5%; Score 192; DB 10; Length 36;
Best Local Similarity 97.2%; Pred. No. 2.2e-16;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
QY 1 YTNLIHSLIEESQNOQEKNEQELFLDKWASLWNF 36
||:|||||
1 YTSLIHSLIEESQNOQEKNEQELFLDKWASLWNF 36
Db 1 YTSLIHSLIEESQNOQEKNEQELFLDKWASLWNF 36

```

Db 2 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNNF 37

RESULT 10

US-09-779-451-41

; Sequence 41, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT FILING DATE: US/09/779,451

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 41

; LENGTH: 46

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 97.5%; Score 192; DB 10; Length 46;

Best Local Similarity 97.2%; Pred. No. 2,9e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESQNOQEKNEQELLELDKWSLWNNF 36

Db 11 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNNF 46

RESULT 11

US-09-779-451-4

; Sequence 4, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT FILING DATE: US/09/779,451

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 56

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 97.5%; Score 192; DB 10; Length 56;

Best Local Similarity 97.2%; Pred. No. 3,5e-16;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESQNOQEKNEQELLELDKWSLWNNF 36

Db 16 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNNF 51

RESULT 12

US-10-040-349B-2

; Sequence 2, Application US/10040349B

; Publication No. US20030082521A1

; GENERAL INFORMATION:

; APPLICANT: Brasseur, Robert

; APPLICANT: Charlotiaux, Benoit

; APPLICANT: Chevallier, Michel

; APPLICANT: El Habib, Raphaelle

; APPLICANT: Krell, Tino

; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

; FILE REFERENCE: 01-078-A

; CURRENT FILING DATE: US/10/040,349B

; CURRENT FILING DATE: 2002-07-09

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 177

; TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: (1)..(177)

; OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 97.5%; Score 192; DB 9; Length 177;

Best Local Similarity 97.2%; Pred. No. 1,2e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESQNOQEKNEQELLELDKWSLWNNF 36

Db 104 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNNF 139

RESULT 13

US-10-059-271-84

; Sequence 84, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDE, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; FILE REFERENCE: ALBRE-22

; CURRENT FILING DATE: US/10/059,271

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: DE 101 06 295

; PRIOR FILING DATE: 2001-02-02

; SOFTWARE: PatentIn Ver. 2.1

; NUMBER OF SEQ ID NOS: 97

; SEQ ID NO 84

; LENGTH: 221

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match

Best Local Similarity 97.5%; Score 192; DB 9; Length 221;

Best Local Similarity 97.2%; Pred. No. 1,5e-15;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESQNOQEKNEQELLELDKWSLWNNF 36

Db 131 YTSLIHSLEESQNOQEKNEQELLELDKWSLWNNF 166

RESULT 14

US-10-059-271-81

; Sequence 81, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDE, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

```

; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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Query Match          97.5%; Score 192; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1 YTNLIHSLSIESONQOEKNEDELLELDKWSLNNWF 36
||:|||||
Db 144 YTSLSHSLSIESONQOEKNEDELLELDKWSLNNWF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKKE, HEINRICH
; APPLICANT: BUDDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match          97.5%; Score 192; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 1.7e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTNLIHSLSIESONQOEKNEDELLELDKWSLNNWF 36
||:|||||
Db 166 YTSLSHSLSIESONQOEKNEDELLELDKWSLNNWF 201

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Search completed: May 16, 2003, 12:10:24  
 Job time : 15.759 secs

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GenCore version 5.1.4-p5.4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-535  
Perfect score: 197  
Sequence: 1 YTNLHSLIESSQNOEKNEDELIDKRWASLWNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
1 number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCtus.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	36	1 US-08-073-028-1	Sequence 1, Appli
2	192	97.5	36	3 US-08-486-099-1	Sequence 1, Appli
3	192	97.5	36	3 US-09-071-877-1	Sequence 1, Appli
4	192	97.5	36	3 US-08-360-107A-1	Sequence 1, Appli
5	192	97.5	36	3 US-08-484-223B-1	Sequence 1, Appli
6	192	97.5	36	3 US-08-919-597-1	Sequence 1, Appli
7	192	97.5	36	3 US-08-475-668A-1	Sequence 1, Appli
8	192	97.5	36	3 US-08-485-551A-1	Sequence 1, Appli
9	192	97.5	36	3 US-08-471-913A-1	Sequence 1, Appli
10	192	97.5	36	4 US-08-554-616-1	Sequence 1, Appli
11	192	97.5	36	4 US-08-485-264A-1	Sequence 1, Appli
12	192	97.5	36	4 US-09-082-279B-15	Sequence 15, Appli
13	192	97.5	36	4 US-09-082-279B-497	Sequence 497, App
14	192	97.5	36	4 US-09-082-279B-498	Sequence 498, App
15	192	97.5	36	4 US-09-082-279B-603	Sequence 603, App
16	192	97.5	36	4 US-09-082-279B-630	Sequence 630, App
17	192	97.5	36	4 US-09-082-279B-631	Sequence 631, App
18	192	97.5	36	4 US-09-082-279B-705	Sequence 705, App
19	192	97.5	36	4 US-09-082-279B-834	Sequence 834, App
20	192	97.5	36	4 US-09-082-279B-1076	Sequence 1076, App
21	192	97.5	36	4 US-09-082-279B-1121	Sequence 1121, App
22	192	97.5	36	4 US-09-082-279B-1161	Sequence 1161, App
23	192	97.5	36	4 US-08-965-056-1	Sequence 1, Appli
24	192	97.5	36	4 US-08-965-056-108	Sequence 108, App
25	192	97.5	36	4 US-09-045-920-1	Sequence 1, Appli
26	192	97.5	36	4 US-08-474-349A-1	Sequence 399, App
27	192	97.5	36	4 US-08-474-349A-399	Sequence 399, App

28	192	97.5	36	4 US-08-474-349A-413	Sequence 413, App
29	192	97.5	36	4 US-09-315-304B-15	Sequence 15, Appli
30	192	97.5	36	4 US-09-315-304B-497	Sequence 497, App
31	192	97.5	36	4 US-09-315-304B-498	Sequence 498, App
32	192	97.5	36	4 US-09-315-304B-603	Sequence 603, App
33	192	97.5	36	4 US-09-315-304B-630	Sequence 630, App
34	192	97.5	36	4 US-09-315-304B-631	Sequence 631, App
35	192	97.5	36	4 US-09-315-304B-705	Sequence 705, App
36	192	97.5	36	4 US-09-315-304B-834	Sequence 834, App
37	192	97.5	36	4 US-09-315-304B-1076	Sequence 1076, App
38	192	97.5	36	4 US-09-315-304B-1121	Sequence 1121, App
39	192	97.5	36	4 US-09-315-304B-1161	Sequence 1161, App
40	192	97.5	36	4 US-09-315-304B-1469	Sequence 1469, App
41	192	97.5	36	4 US-09-315-304B-1470	Sequence 1470, App
42	192	97.5	36	4 US-09-315-304B-1486	Sequence 1486, App
43	192	97.5	36	4 US-08-255-208A-1	Sequence 1, Appli
44	192	97.5	37	4 US-08-082-279B-771	Sequence 771, App
45	192	97.5	37	4 US-09-082-279B-775	Sequence 775, App

ALIGNMENTS

RESULT 1  
US-08-073-028-1  
; Sequence 1, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dant P.  
; APPLICANT: Mathews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-1  
Query Match 97.5%; Score 192; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Y 1 YTNLHSLIESSQNOEKNEDELIDKRWASLWNF 36  
|:|||||||||||||||||||||||||||||

Db 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

RESULT 2

US-08-486-099-1

Sequence 1, Application US/08486099

Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

TITLE OF INVENTION: B VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 209

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,099

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-031

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-486-099-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

Db 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

RESULT 3

US-09-071-877-1

Sequence 1, Application US/09071877

Patent No. 6015881

GENERAL INFORMATION:

APPLICANT: Kang, Myung-Chol

APPLICANT: Bray, Brian

APPLICANT: Lichty, Maynard

APPLICANT: Mader, Catherine

APPLICANT: Merutka, Gene

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PEPTIDE SYNTHESIS

FILE REFERENCE: 7872-050

Db 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

CURRENT APPLICATION NUMBER: US/09/071,877

CURRENT FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 36

TYPE: PRT

ORGANISM: Human Immunodeficiency virus

US-09-071-877-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

Db 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

RESULT 4

US-08-360-107A-1

Sequence 1, Application US/08360107A

Patent No. 6017536

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 149

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/360,107A

FILING DATE: 20-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-013

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-360-107A-1

Query Match 97.5%; Score 192; DB 3; Length 36;

Best Local Similarity 97.2%; Pred. No. 3.4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTNLIHSLIESQNOQEKNEDELLDLKWSLWNNF 36

Db 1 YTNLHSLIEESONOQEKNEQLELIDKWSLWMP 36  
||:|||||

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 97.5%; Score 192; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHSLIEESONOQEKNEQLELIDKWSLWMP 36  
||:|||||

Db 1 YTNLHSLIEESONOQEKNEQLELIDKWSLWMP 36  
||:|||||

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 97.5%; Score 192; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHSLIEESONOQEKNEQLELIDKWSLWMP 36  
||:|||||

Db 1 YTNLHSLIEESONOQEKNEQLELIDKWSLWMP 36  
||:|||||

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESQNOEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESQNOEKNEQELLELDKVASLWNWF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESQNOEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESQNOEKNEQELLELDKVASLWNWF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Daniel P.  
APPLICANT: Mathews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Pellew, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNTE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 97.5% Score 192; DB 3; Length 36;  
Best Local Similarity 97.2% Pred. No. 3.4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESQNOEKNEQELLELDKVASLWNWF 36  
1 YTSLSHSLEESQNOEKNEQELLELDKVASLWNWF 36

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHLSLEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLSHLSLEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHLSLEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLSHLSLEESONOQEKNEDELLEDKWASLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 97.5%; Score 192; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 3,4e-17;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLHLSLEESONOQEKNEDELLEDKWASLWNMF 36  
DB 1 YTSLSHLSLEESONOQEKNEDELLEDKWASLWNMF 36

Db 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

## RESULT 13

US-09-082-279B-497

Sequence 497, Application US/09082279B  
Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

Q ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3,4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide.

US-09-082-279B-498

Query Match 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3,4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

## RESULT 15

US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 97.5%; Score 192; DB 4; Length 36;

Best Local Similarity 97.2%; Pred. No. 3,4e-17;

Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

DB 1 YTNLIHSLIEESQNOQEKNEQELLELDKWSLWNP 36

Search completed: May 16, 2003, 11:22:12  
Job time: 10.1928 secs

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds

(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533A-535

Perfect score: 197

Sequence: 1 YTNLIHSLEESQNOEKNEQELLEDKWASLWNF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	645	15	0993A6 human immun
2	192	97.5	747	15	070607 human immun
3	192	97.5	748	15	070606 human immun
4	192	97.5	752	15	070604 human immun
5	192	97.5	752	15	070605 human immun
6	192	97.5	752	15	070608 human immun
7	192	97.5	851	15	078243 human immun
8	192	97.5	852	15	089797 human immun
9	192	97.5	854	15	085582 human immun
10	192	97.5	854	15	072502 human immun
11	192	97.5	856	15	092877 human immun
12	192	97.5	856	15	074599 human immun
13	192	97.5	856	15	074090 human immun
14	188	95.4	122	15	09YX08 human immun
15	188	95.4	684	15	09IK06 human immun
16	188	95.4	854	15	090178 human immun

17	188	95.4	854	15	078705 human immun
18	188	95.4	855	15	09IK00 human immun
19	188	95.4	860	15	09YP43 human immun
20	188	95.4	860	15	09YP50 human immun
21	188	95.4	861	15	09IK05 human immun
22	188	95.4	861	15	09IK04 human immun
23	188	95.4	861	15	09IK03 human immun
24	188	95.4	863	15	09IJ20 human immun
25	188	95.4	863	15	09IJY9 human immun
26	188	95.4	863	15	09IJY8 human immun
27	188	95.4	863	15	09IJY7 human immun
28	188	95.4	863	15	09MUT4 human immun
29	188	95.4	864	15	09YP48 human immun
30	188	95.4	865	15	09IK11 human immun
31	188	95.4	865	15	09IK10 human immun
32	188	95.4	865	15	09IK09 human immun
33	188	95.4	865	15	09IK08 human immun
34	188	95.4	865	15	09IK07 human immun
35	188	95.4	866	15	09IJ24 human immun
36	187	94.9	856	15	090SM7 human immun
37	187	94.9	858	15	071974 human immun
38	187	94.9	859	15	092937 human immun
39	186	94.4	122	15	09YXM9 human immun
40	186	94.4	616	15	0933B0 human immun
41	186	94.4	618	15	0933B2 human immun
42	186	94.4	757	15	090722 human immun
43	186	94.4	848	15	069990 human immun
44	186	94.4	859	15	080863 human immun
45	185	93.9	122	15	09EA89 human immun

## ALIGNMENTS

RESULT 1	0993A6	PRELIMINARY:	PRT;	645 AA.
AC	0993A6;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Truncated envelope glycoprotein (fragment).			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1007;			
RX	MEDLINE=21192672; PubMed=11287644;			
RA	Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,			
RA	White S.W., Doherty P.C., Hurwitz J.L.;			
RT	"Localization of CD4+ T cell epitope hotspots to exposed strands of			
RT	HIV envelope glycoprotein suggests structural influences on antigen			
RT	processing."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).			
DR	EMBL: AF321563; AAK18810.1;			
DR	InterPro: IPR000328; Env.GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
KW	AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;			
KW	Transmembrane.			
FT	NON_TER			
SQ	SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;			
Query Match	97.5%; Score 192; DB 15; Length 645;			
Best Local Similarity	97.2%; Pred. No. 4,9e-15;			
Matches	35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
OY	1 YTNLIHSLEESQNOEKNEQELLEDKWASLWNF 36			
DB	607 YTNLIHSLEESQNOEKNEQELLEDKWASLWNF 642			

## RESULT 2

Q70607 PRELIMINARY: PRT: 747 AA.  
 AC 070607;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-1;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-1;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12034; AAA76669.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR KMs: Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 747  
 SQ SEQUENCE 747 AA; 84250 MW; 732836A52245B14 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 747;  
 Best Local Similarity 97.2%; Pred. No. 5.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
 DB 633 YTSLSHSLEESONQOEKNEQELLELDKWSLWNMF 668

## RESULT 3

Q70606 PRELIMINARY: PRT: 748 AA.  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW881;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW881;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12032; AAA76668.1; -

DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 748  
 SQ SEQUENCE 748 AA; 84224 MW; 56BEDF186C67994B CRC64;

Query Match 97.5%; Score 192; DB 15; Length 748;  
 Best Local Similarity 97.2%; Pred. No. 5.6e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
 DB 634 YTSLSHSLEESONQOEKNEQELLELDKWSLWNMF 669

## RESULT 4

Q70604 PRELIMINARY: PRT: 752 AA.  
 AC 070604;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW851;  
 RX MEDLINE-95127297; PubMed-7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIIB).";  
 AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW851;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12030; AAA76666.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM Aids; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT NON\_TER 752  
 SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEQELLELDKWSLWNMF 36  
 DB 638 YTSLSHSLEESONQOEKNEQELLELDKWSLWNMF 673

## RESULT 5

Q70605 PRELIMINARY: PRT: 752 AA.  
 AC 070605;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_Taxid=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKMSLWMP 36  
 DB 638 YTSLIHSLEESONOEKNEDELLELDKMSLWMP 673

RESULT 6  
 Q70608 PRELIMINARY; PRT; 752 AA.  
 ID 070608;  
 AC 070608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Vital variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HTLV type IIIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA; 84780 MW; 706872A2DDC0E8F8 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKMSLWMP 36  
 DB 638 YTSLIHSLEESONOEKNEDELLELDKMSLWMP 673

DB 638 YTSLIHSLEESONOEKNEDELLELDKMSLWMP 673

RESULT 7  
 ID 078243 PRELIMINARY; PRT; 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polyprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federico M., Equestre M., Ricci S., Ratti G., Zibai O.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone."  
 RL J. Viral Diseases 14:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate."  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borsetti A., Saglio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone."  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL; Z11530; CAA7628.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 6.4e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONOEKNEDELLELDKMSLWMP 36  
 DB 633 YTSLIHSLEESONOEKNEDELLELDKMSLWMP 668

RESULT 8  
 ID 089797 PRELIMINARY; PRT; 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
 RT "Vital variability and serum antibody response in a laboratory worker."

Matches	35;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	YTNLIHSIIIESQNOOEKNEOELLELDKWSLWNMF	36						
Db	636	YTSLIHSIIIESQNOOEKNEOELLELDKWSLWNMF	671						
RESULT	10								
072502	ID	PRELIMINARY;	PRT;	854	AA.				
AC	072502								
DT	01-NOV-1996	(TREMBLrel. 01, Created)							
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)							
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)							
DE	ENV	polyprotein.							
GN	ENV.								
OS	Human immunodeficiency virus type 1.								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
OX	NCBI_TaxID=11676;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=NL4-3;								
RA	MEDLINE=96036482; PubMed=7483282;								
RA	Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,								
RA	Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;								
RT	"Recovery of virtually full-length HIV-1 provirus of diverse subtypes								
RT	from primary virus cultures using the polymerase chain reaction.";								
RL	Virology 213:80-86(1995).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=NL4-3;								
RX	MEDLINE=86281827; PubMed=3016298;								
RA	Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,								
RA	Martin M.A.;								
RT	"Production of acquired immunodeficiency syndrome-associated								
RT	retrovirus in human and nonhuman cells transfected with an infectious								
RT	molecular clone.";								
RL	J. Virol. 59:284-291(1986).								
DR	EMBL; 026942; AAB60578.1;								
DR	InterPro; IPR000328; Env_Gp41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120; 1.								
KW	Pfam; PF00517; GP41; 1.								
KW	AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.								
FT	CONFILCT 214 214 H -> L (IN REF. 2).								
FT	CONFILCT 530 530 A -> S (IN REF. 2).								
FT	CONFILCT 739 739 G -> D (IN REF. 2).								
SEQ	SEQUENCE 854 AA; 97005 MW; FF2264B3841DD1220 CRC64;								
Query Match		97.5%;	Score 192;	DB 15;	Length 854;				
Best Local Similarity		97.2%;	Pred. No. 6.4e-15;						
Matches	35;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Oy	1	YTNLIHSIIIESQNOOEKNEOELLELDKWSLWNMF	36						
Db	636	YTSLIHSIIIESQNOOEKNEOELLELDKWSLWNMF	671						
RESULT	11								
092877	ID	PRELIMINARY;	PRT;	856	AA.				
AC	092877;								
DT	01-NOV-1998	(TREMBLrel. 08, Created)							
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)							
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)							
DE	Envelope glycoprotein.								
GN	ENV.								
OS	Simian-Human immunodeficiency virus.								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
OX	NCBI_TaxID=57667;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=99089884; PubMed=9882298;								

RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.;  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 responsible for the pathogenicity of a multiply passaged simian-human  
 immunodeficiency virus (SHV-HXBc2).";  
 RT J. Virol. 73:976-984(1999).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF041850; AAD1242.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00517; Gp41; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOLLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOLLELDKWSLWNMF 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOLLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOLLELDKWSLWNMF 673

## RESULT 13

O74090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 RT Virology 174:103-116(1990).  
 RL [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; Gp120.  
 DR Pfam: PF00516; Gp120; 1.  
 DR Pfam: PF00517; Gp41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 97.5%; Score 192; DB 15; Length 856;  
 Best local Similarity 97.2%; Pred. No. 6.5e-15;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOLLELDKWSLWNMF 36  
 DB 638 YTSLIHSLIEESONQOEKNEOLLELDKWSLWNMF 673

## RESULT 14

ID 09YX08 PRELIMINARY; PRT; 122 AA.  
 AC 09YX08;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein immunodominant region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RJ96BRP029;  
 RA Tanui A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
 RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,  
 RA Rayfield M.;  
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";  
 RT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF034045; AAC79297.1;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR Pfam: PF00517; Gp41; 1.  
 KW Transmembrane.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 122 AA; 14767 MW; B0B60F44F72975CB CRC64;

Query Match 95.4%; Score 188; DB 15; Length 122;  
 Best local Similarity 94.4%; Pred. No. 2.7e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLIEESONQOEKNEOLLELDKWSLWNMF 36

Db 78 YTNLIYNLIEESONQOEKNEQELLELDKWSLWNMF 113

RESULT 15

Q9IK06 PRELIMINARY; PRT; 684 AA.  
 AC Q9IK06;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=546HC-86;  
 RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;  
 RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from  
 a patient with HIV dementia: evidence for monocyte trafficking into  
 brain."  
 RL J. Neurovirol. 0:0-0(2000).  
 DR EMBL: AF217161; AAF75503.1; -;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.  
 SQ SEQUENCE 684 AA; 77266 MW; F9E6F3CC6AD32E10 CRC64;

Query Match 95.4%; Score 188; DB 15; Length 684;  
 Best Local Similarity 94.4%; Pred. No. 1.6e-14;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESONQOEKNEQELLELDKWSLWNMF 36  
 Db 643 YTNLIYNLIEESONQOEKNEQELLELDKWSLWNMF 678

Search completed: May 16, 2003, 11:19:47  
 Job time : 26.3124 secs

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FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;

Query Match 89.3%; Score 176; DB 1; Length 867;  
 Best Local Similarity 88.9%; Pred. No. 1.3e-13;  
 Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESQNOQEKNEQELLEDDKXASLWNMF 36  
 ||:|||||  
 Db 649 YTSLIYTLIEESQNOQEKNEQELLEGLDKWASLWNMF 684

Search completed: May 16, 2003, 11:13:35  
 Job time : 7.07229 secs



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FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 852 AA; 9663 MW; EETBBF8D23C9910D CRC64;

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Query Match          91.9%; Score 181; DB 1; Length 852;
Best Local Similarity 88.9%; Pred. No. 3,3e-14;
Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 1 YTNLIHSLEESONQOEKNEOELELDKWSLWNF 36
   ||:::|||||
Db 634 YTSLLTYLLEESONQOEKNEOELELDKWSLWNF 669

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RESULT 13
ENV_HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11685;
RN [1]
RP MEDLINE=85090453; PubMed=2578227;
   Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
   Stempelin M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
   Levy J.A., Dina D., Luciw P.A.;
   "Nucleotide sequence and expression of an AIDS-associated retrovirus
   (ARV-2).";
   Science 227:484-492(1985).
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CC -----
CC EMBL: K02007; AAB59882.1; -
CC PIR: A03976; VCLJAJ2.
CC HIV: K02007; ENVSEF2.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120.1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29

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FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
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FT DISULFID 118 208 BY SIMILARITY.
FT DISULFID 125 199 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 221 250 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 299 333 BY SIMILARITY.
FT DISULFID 380 442 BY SIMILARITY.
FT DISULFID 387 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573ACADIA2 CRC64;

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Query Match          91.9%; Score 181; DB 1; Length 855;
Best Local Similarity 88.9%; Pred. No. 3,3e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YTNLIHSLEESONQOEKNEOELELDKWSLWNF 36
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Db 637 YTNLYTLEESONQOEKNEOELELDKWSLWNF 672

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RESULT 14
ENV_HV1W2 STANDARD; PRT; 847 AA.
AC P05880;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WM2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11705;
RN [1]
RP MEDLINE=86235450; PubMed=3012778;
   Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
   RA Hahn B.H., Shaw G.M., Taylor M.E., Taylor M.E., Parks W.P.,
   RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks W.P.,
   RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
   at risk for AIDS.";

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FT	DISULFID	383	417	BY SIMILARITY.	
FT	CARBOHYD	87		N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	134	134	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	140	140	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	151	151	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	155	155	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	183	183	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	197	197	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	234	234	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	241	241	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	262	262	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	276	276	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	289	289	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	295	295	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	331	331	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	338	338	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	354	354	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	360	360	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	394	394	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	404	404	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	447	447	N-LINKED	(GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	459	459	N-LINKED	(GLCNAC. .) (POTENTIAL)

DR	Pfam: PF00517; GP41; 1.
KM	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
RV	Signal.
FT	SIGNAL.
FT	CHAIN 1 31 BY SIMILARITY.
FT	CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID 53 73 BY SIMILARITY.
FT	DISULFID 118 206 BY SIMILARITY.
FT	DISULFID 125 197 BY SIMILARITY.
FT	DISULFID 130 156 BY SIMILARITY.
FT	DISULFID 219 248 BY SIMILARITY.
FT	DISULFID 229 331 BY SIMILARITY.
FT	DISULFID 297 240 BY SIMILARITY.
FT	DISULFID 377 439 BY SIMILARITY.
FT	DISULFID 384 412 BY SIMILARITY.
FT	CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL.)
FT	CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL.)

DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 FT SIGNAL  
 FT CHAIN 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
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 FT DISULFID 131 157  
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 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
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 FT CARBOHYD 463 463  
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 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MW; 5FCD81DC3C1209B3 CRC64;

Query Match 92.9%; Score 183; DB 1; Length 856;  
 Best Local Similarity 94.3%; Pred. No. 1.9e-14;  
 Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKREDELLEDKWASLMMN 35  
 DB 638 YTSLIHSLEESONOEKREDELLEDKWASLMMN 672

RESULT 10  
 ENV\_HVISC STANDARD; PRT: 856 AA.  
 AC P05878;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP120 precursor [Contains: Exterior membrane  
 glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OC NCBI\_TaxID=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates";  
 RL Virology 164:531-536(1988)  
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
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 CC -----  
 CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; ENV\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 FT SIGNAL  
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 FT CHAIN 30 510  
 FT CHAIN 511 856  
 FT STYPE 760 760  
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 FT DISULFID 118 206  
 FT DISULFID 125 197  
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 FT CARBOHYD 338 338  
 FT CARBOHYD 354 354  
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 FT CARBOHYD 384 384  
 FT CARBOHYD 394 394  
 FT CARBOHYD 400 400  
 FT CARBOHYD 405 405  
 FT CARBOHYD 442 442  
 FT CARBOHYD 457 457  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 92.9%; Score 183; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 1.9e-14;

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 96912 MW; 337789386F22ABA CRC64;

Query Match
Best Local Similarity 94.4%; Score 189; DB 1; Length 853;
Pred. No. 3.6e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTNLHSLIEESONOQEKNEQELLELDKWSLMMNF 36
11:|||||:|||||:|||||:|||||:|||||:
636 YTNLHSLIEESONOQEKNEQELLELDKWSLMMNF 671

RESULT 8
ENV_HV1S1 STANDARD: PRT; 847 AA.
ID ENV_HV1S1
AC P19550;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 38, Last annotation update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
RT macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RT J. Virol. 64:4390-4398(1990).
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CC -----
CC EMBL: M65024; AAA5072.1; -
CC HIV; M38428; ENV5SP162.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120; 1.
CC DR Pfam: PF00517; GP41; 1.
CC KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
CC KW STGNAL.
FT CHAIN 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.

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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96135 MW; 0A901317FD7FE2AB CRC64;

Query Match
Best Local Similarity 94.4%; Score 188; DB 1; Length 847;
Pred. No. 4.7e-15;
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 YTNLHSLIEESONOQEKNEQELLELDKWSLMMNF 36
11:|||||:|||||:|||||:|||||:|||||:
629 YTNLHSLIEESONOQEKNEQELLELDKWSLMMNF 664

RESULT 9
ENV_HV1PV STANDARD: PRT; 856 AA.
ID ENV_HV1PV
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2962104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RT Nature 313:450-458(1985).
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CC -----
CC EMBL: K02083; AAB59873.1; -
CC HIV; A03874; VCLJYL.
CC DR PIR; A03874; VCLJYL.
CC DR HIV; K02083; ENV5PV22.
CC DR InterPro: IPR000328; Env_GP41.
CC DR InterPro: IPR000777; GP120.
CC DR Pfam: PF00516; GP120; 1.

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 836 AA; 97188 MW; 3373C68B84C1AFC CRC64;

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Query Match          97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLHSLIESQNOOEKNEQLLELDKWSLWNP 36
Db 638 YTNLHSLIESQNOOEKNEQLLELDKWSLWNP 673

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RESULT 5
ENV_HV11W STANDARD; PRT: 856 AA.
ID ENV_HV11W STANDARD; PRT: 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB)."
RL Aids Res. Hum. Retroviruses 10:1143-1155(1994).

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CC EMBL: U12055; AAA76690.1;
CC GlycoSuiteDB: Q70626;
DR InterPro: IPR000328; Env_GP41.
DR
RN [1]

```

```

DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 836 AA; 96938 MW; 0C241332CF7E687 CRC64;

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Query Match          97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 YTNLHSLIESQNOOEKNEQLLELDKWSLWNP 36
Db 638 YTNLHSLIESQNOOEKNEQLLELDKWSLWNP 673

```

```

RESULT 6
ENV_HV11R STANDARD; PRT: 861 AA.
ID ENV_HV11R STANDARD; PRT: 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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[illegible]

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

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Query Match 97.5%; Score 192; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 YTNLIHSLEESONOENKNEOELLELDKVASLWNPF 36
Db 633 YTSLIHSLEESONOENKNEOELLELDKVASLWNPF 668

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RESULT 2
ENV_HV1B1 STANDARD: PRT; 856 AA.
ID ENV_HV1B1 STANDARD: PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_TaxID=11678;
NCBI_TaxID=11678;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patara R., Lyvak K.J., Starich B.R.,
Joseph S.F., Doran E.R., Katsalski J.A., Whitehorn E.A.,
Baumeyer K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
Laurenberger J.A., Pappas T.S., Ghayee J., Chang N.T., Gallo R.C.,
Wong-Staal F.;
"Complete nucleotide sequence of the AIDS virus, HTLV-III."
RT Nature 313:277-284(1985).
RN [2]
DI DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
Gregory T.J.;
"Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells."
RT J. Biol. Chem. 265:10373-10382(1990).
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CC EMBL; M15654; AAA44205.1;
CC PIR; A03973; VCLJH3.
CC HIV; M15654; ENVSBH102.
CC InterPro; IPR000328; ENV GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Glycoprotein; Transmembrane;
CC Signal.
CC CHAIN 1 30
CC CHAIN 512 856
CC DISULFID 54 74
CC DISULFID 119 205
CC DISULFID 126 196
CC DISULFID 131 157
CC DISULFID 218 247
CC DISULFID 228 239
CC DISULFID 296 331
CC DISULFID 378 445
CC DISULFID 385 418
CC CARBOHYD 88 88
CC CARBOHYD 136 136
CC CARBOHYD 141 141
CC CARBOHYD 156 156
CC CARBOHYD 160 160
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CC CARBOHYD 197 197
CC CARBOHYD 230 230
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CC CARBOHYD 301 301
CC CARBOHYD 332 332
CC CARBOHYD 339 339
CC CARBOHYD 356 356
CC CARBOHYD 386 386
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CC CARBOHYD 448 448
CC CARBOHYD 463 463
CC CARBOHYD 611 611
CC CARBOHYD 616 616
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CC CARBOHYD 637 637
CC CARBOHYD 674 674
CC CARBOHYD 750 750
CC CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

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Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 1.6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 YTNLIHSLEESONOENKNEOELLELDKVASLWNPF 36
Db 638 YTSLIHSLEESONOENKNEOELLELDKVASLWNPF 673

```

```

RESULT 3
ENV_HV1H2 STANDARD: PRT; 856 AA.
ID ENV_HV1H2 STANDARD: PRT; 856 AA.
AC P04578; 009779;

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GenCore version 5.1.4-p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533A-535

Perfect score: 197

Sequence: 1 YTNLIHSLEESQNOEKNEQELLELDKWSLWMP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	192	97.5	851	1 ENV_HV1B8	P04582 human immun
2	192	97.5	856	1 ENV_HV1B1	P03375 human immun
3	192	97.5	856	1 ENV_HV1B2	P04578 human immun
4	192	97.5	856	1 ENV_HV1B3	P04624 human immun
5	192	97.5	856	1 ENV_HV1B4	P07626 human immun
6	192	97.5	856	1 ENV_HV1B5	P03377 human immun
7	189	95.9	853	1 ENV_HV1B6	P19550 human immun
8	188	95.4	847	1 ENV_HV1B7	P19550 human immun
9	183	92.9	856	1 ENV_HV1B8	P03376 human immun
10	183	92.9	856	1 ENV_HV1B9	P03376 human immun
11	183	92.9	856	1 ENV_HV1B10	P03376 human immun
12	181	91.9	852	1 ENV_HV1B11	P03376 human immun
13	181	91.9	852	1 ENV_HV1B12	P03376 human immun
14	177	89.8	847	1 ENV_HV1B13	P05880 human immun
15	176	89.3	867	1 ENV_HV1B14	P12489 human immun
16	175	88.8	843	1 ENV_HV1B15	P35961 human immun
17	175	88.8	852	1 ENV_HV1B16	P12488 human immun
18	175	88.8	853	1 ENV_HV1B17	P04581 human immun
19	175	88.8	865	1 ENV_HV1B18	P04579 human immun
20	174	88.3	848	1 ENV_HV1B19	P20871 human immun
21	174	88.3	853	1 ENV_HV1B20	P12487 human immun
22	174	88.3	855	1 ENV_HV1B21	P20888 human immun
23	174	88.3	855	1 ENV_HV1B22	P04580 human immun
24	174	88.3	856	1 ENV_HV1B23	P05877 human immun
25	173	87.8	861	1 ENV_HV1B24	P31819 human immun
26	172	87.3	846	1 ENV_HV1B25	P18799 human immun
27	167	84.8	859	1 ENV_HV1B26	P04583 human immun
28	165	83.8	868	1 ENV_HV1B27	P05879 human immun
29	162	82.2	854	1 ENV_HV1B28	P05882 human immun
30	151	76.6	854	1 ENV_HV1B29	P17281 chimpanzee
31	149	75.6	856	1 ENV_HV1B30	P05881 human immun
32	90	45.7	854	1 ENV_HV1B31	O02837 simian immun
33	86	43.7	881	1 ENV_HV1B32	P05884 simian immun

34	86	43.7	882	1 ENV_HV1B33	P05885 simian immun
35	85	43.1	885	1 ENV_HV1B34	P12492 simian immun
36	84.5	42.9	860	1 ENV_HV1B35	P18094 human immun
37	84	42.6	859	1 ENV_HV1B36	P15831 human immun
38	82.5	41.9	889	1 ENV_HV1B37	P19503 simian immun
39	82	41.6	880	1 ENV_HV1B38	P1267 simian immun
40	80.5	40.9	859	1 ENV_HV1B39	P24105 human immun
41	77.5	39.3	846	1 ENV_HV1B40	P12449 human immun
42	77.5	39.3	851	1 ENV_HV1B41	P17755 human immun
43	77.5	39.3	851	1 ENV_HV1B42	P18040 human immun
44	77.5	39.3	857	1 ENV_HV1B43	O74126 human immun
45	77.5	39.3	859	1 ENV_HV1B44	P20872 human immun

## ALIGNMENTS

RESULT 1	ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582;				
DT	13-AUG-1987 (Rel. 05, Created)				
DT	13-AUG-1987 (Rel. 05, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OC	Viruses; Retroviridae; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; PubMed=2578615;				
RA	Ratner L., Hesselberg W., Patarca R., Liyak K.J., Starcich B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peltway S.R., Pearson M.L., Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	"Complete nucleotide sequence of the AIDS virus, HTLV-III.";				
RL	Nature 313:277-284(1985).				
CC	-----				
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CC	EMBL, K02011; AAA44661.1; -.				
DR	HIV; K02011; ENVSBB8.				
DR	Glycosylated; P04582; -.				
DR	InterPro: IPR000328; Env GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
DR	Pfam: PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	506		
FT	CHAIN	507	851		
FT	DISULFID	54	74		
FT	DISULFID	119	205		
FT	DISULFID	126	196		
FT	DISULFID	131	157		
FT	DISULFID	218	247		
FT	DISULFID	228	239		
FT	DISULFID	296	331		
FT	DISULFID	378	440		
FT	DISULFID	385	413		
FT	CARBOHYD	88	88		
FT	CARBOHYD	136	136		
FT	CARBOHYD	141	141		

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 32.4578 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533a-535  
Perfect score: 197  
Sequence: 1 YTNLIHSLIESQNOQEKNEQELDLKQASIMNMF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : A.Geneseq\_101002:\*\*  
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21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	97.5	36	16	DP-178 derived from AAR64364
2	192	97.5	36	17	DP178 corresponds to HIV-1 derived pept
3	192	97.5	36	18	AAW17011
4	192	97.5	36	19	AAV22812
5	192	97.5	36	19	AAV22805
6	192	97.5	36	20	AAV31955
7	192	97.5	36	20	AAV31974
8	192	97.5	36	21	AAV52655
9	192	97.5	36	21	AAV52688
10	192	97.5	36	21	AAV52818

Result No.	Score	Query Match	Length	ID	Description
11	192	97.5	36	21	AAV14533
12	192	97.5	36	21	AAV88665
13	192	97.5	36	21	AAV88729
14	192	97.5	36	21	AAV89135
15	192	97.5	36	21	AAV89136
16	192	97.5	36	21	AAV89242
17	192	97.5	36	21	AAV89424
18	192	97.5	36	21	AAV89622
19	192	97.5	36	21	AAV89735
20	192	97.5	36	21	AAV89777
21	192	97.5	36	21	AAV89982
22	192	97.5	36	21	AAV89983
23	192	97.5	36	21	AAV89999
24	192	97.5	36	22	AAU70179
25	192	97.5	36	22	AAU70741
26	192	97.5	36	22	AAV82961
27	192	97.5	36	22	AAV82961
28	192	97.5	36	22	AAV82961
29	192	97.5	36	22	AAV82961
30	192	97.5	36	22	AAV82961
31	192	97.5	36	22	AAV82961
32	192	97.5	36	22	AAV82961
33	192	97.5	36	22	AAV82961
34	192	97.5	36	22	AAV82961
35	192	97.5	36	22	AAV82961
36	192	97.5	36	22	AAV82961
37	192	97.5	36	22	AAV82961
38	192	97.5	36	22	AAV82961
39	192	97.5	36	22	AAV82961
40	192	97.5	36	22	AAV82961
41	192	97.5	36	22	AAV82961
42	192	97.5	36	22	AAV82961
43	192	97.5	36	22	AAV82961
44	192	97.5	36	22	AAV82961
45	192	97.5	36	22	AAV82961

## ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	192	97.5	36	21	AAV14533
2	192	97.5	36	21	AAV88665
3	192	97.5	36	21	AAV88729
4	192	97.5	36	21	AAV89135
5	192	97.5	36	21	AAV89136
6	192	97.5	36	21	AAV89242
7	192	97.5	36	21	AAV89424
8	192	97.5	36	21	AAV89622
9	192	97.5	36	21	AAV89735
10	192	97.5	36	21	AAV89777
11	192	97.5	36	21	AAV89982
12	192	97.5	36	21	AAV89983
13	192	97.5	36	21	AAV89999
14	192	97.5	36	22	AAU70179
15	192	97.5	36	22	AAU70741
16	192	97.5	36	22	AAV82961
17	192	97.5	36	22	AAV82961
18	192	97.5	36	22	AAV82961
19	192	97.5	36	22	AAV82961
20	192	97.5	36	22	AAV82961
21	192	97.5	36	22	AAV82961
22	192	97.5	36	22	AAV82961
23	192	97.5	36	22	AAV82961
24	192	97.5	36	22	AAV82961
25	192	97.5	36	22	AAV82961
26	192	97.5	36	22	AAV82961
27	192	97.5	36	22	AAV82961
28	192	97.5	36	22	AAV82961
29	192	97.5	36	22	AAV82961
30	192	97.5	36	22	AAV82961
31	192	97.5	36	22	AAV82961
32	192	97.5	36	22	AAV82961
33	192	97.5	36	22	AAV82961
34	192	97.5	36	22	AAV82961
35	192	97.5	36	22	AAV82961
36	192	97.5	36	22	AAV82961
37	192	97.5	36	22	AAV82961
38	192	97.5	36	22	AAV82961
39	192	97.5	36	22	AAV82961
40	192	97.5	36	22	AAV82961
41	192	97.5	36	22	AAV82961
42	192	97.5	36	22	AAV82961
43	192	97.5	36	22	AAV82961
44	192	97.5	36	22	AAV82961
45	192	97.5	36	22	AAV82961

PA (UYDU-) UNIV DUKE.  
 XX  
 XX Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
 PI Petterway SR, Wild CT;  
 XX  
 XX WPI: 1995-036105/05.  
 DR  
 XX  
 PT Computer search generated synthetic peptides - are inhibitors of  
 HIV transmission  
 XX  
 PS Claim 11; Page 132; 182pp; English.  
 CC AAR64364 is designated DP-178, and corresponds to amino acids  
 CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
 CC forms a putative alpha helix at the C-terminal end of the gp41  
 CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
 CC 558-595) which contains a leucine zipper motif. The peptides complex  
 CC via non-covalent protein-protein interactions, and possess anti-viral  
 CC activity. Homologues of these peptides were identified by a computer  
 CC assisted peptide sequence search. The peptides inhibit transmission to  
 CC uninfected cells, and can also be used as type and/or subtype specific  
 CC diagnostic tools.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 Query Match 97.5%; Score 192; DB 16; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNLHSLIEESONQOEKNEDELELDKWSLWNMF 36  
 DB 1 YTSLSHLSIESONQOEKNEDELELDKWSLWNMF 36  
 RESULT 2  
 AAR98398  
 ID AAR98398 standard; peptide: 36 AA.  
 XX  
 AC AAR98398;  
 XX  
 DT 17-FEB-1997 (first entry)  
 XX  
 DE DP178 corresponds to residues 638-673 of HIV-1(LAI) gp41.  
 XX  
 XX Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KM ALUMOTIS; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KM Influenza virus; hepatitis B virus.  
 XX  
 XX Human immunodeficiency virus type 1.  
 PN WO9619495-A1;  
 XX  
 PD 27-JUN-1996.  
 XX  
 PF 20-DEC-1995; 95WO-US16733.  
 XX  
 PR 06-JUN-1995; 95US-0470896.  
 PR 20-DEC-1994; 94US-0360107.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PA (UYDU-) UNIV DUKE.  
 PI Barney SO, Bolognesi DP, Lambert DM, Langlois AJ;  
 PI Matthews TJ, Petterway SR, Wild CT;  
 XX  
 DR WPI: 1996-309517/31.  
 XX  
 PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALUMOTIS, 107x178x4 or PLZIP  
 PT sequence search motif  
 XX  
 PS Disclosure; Fig 1; 471pp; English.  
 XX

CC The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALUMOTIS,  
 CC 107x178x4 and PLZIP search motifs. These peptides may be used to  
 CC inhibit the transmission of a virus, pref. HIV, Influenza virus, or  
 CC hepatitis B virus, to a cell.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 Query Match 97.5%; Score 192; DB 17; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNLHSLIEESONQOEKNEDELELDKWSLWNMF 36  
 DB 1 YTSLSHLSIESONQOEKNEDELELDKWSLWNMF 36  
 RESULT 3  
 AAM17011  
 ID AAM17011 standard; peptide: 36 AA.  
 XX  
 AC AAM17011;  
 XX  
 DT 30-JUN-1997 (first entry)  
 XX  
 DE HIV-1 derived peptide useful for treatment of HIV infection.  
 XX  
 XX HIV; HIV: human; simian immunodeficiency virus; glycoprotein 41;  
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KM replication; transmission.  
 XX  
 OS Human immunodeficiency virus type 1 LAI isolate.  
 XX  
 PN WO9640191-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PF 06-JUN-1996; 96WO-US09499.  
 XX  
 PR 07-JUN-1995; 95US-0481957.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 PI Johnson RM, Lambert DM;  
 XX  
 DR WPI: 1997-099886/09.  
 XX  
 XX Compens. contg. DP-178 or DP-107 in combination with other  
 PT therapeutic agent - useful for treatment of HIV infection, esp. by  
 PT inhibiting replication or transmission of HIV.  
 XX  
 PS Claim 2; Figure 1; 84pp; English.  
 XX  
 CC AAM17011 represents a peptide designated DP-178, a peptide derived  
 CC from HIV type 1 glycoprotein 41 (gp41) transmembrane protein. The  
 CC peptide corresponds to residues 638-673 of gp41. DP-178 and its  
 CC derivatives are used in combination with a therapeutic agent, e.g. a  
 CC reverse transcriptase, viral protease, cytokine, glycosylation or viral  
 CC mRNA processing inhibitor or a nucleoside inhibitor. The peptides work  
 CC by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection.  
 XX  
 SQ Sequence 36 AA;  
 XX  
 Query Match 97.5%; Score 192; DB 18; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTNLHSLIEESONQOEKNEDELELDKWSLWNMF 36  
 DB 1 YTSLSHLSIESONQOEKNEDELELDKWSLWNMF 36

RESULT 4  
 AAY22912  
 ID AAY22912 standard; Peptide: 36 AA.  
 AC AAY22912;  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 108 from WO9820036.  
 XX  
 KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PD WO9820036-A1.  
 PD 14-MAY-1998.  
 PE 05-NOV-1997; 97WO-US20069.  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI: 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termin of octa:peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Disclosure; Page 233-234; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 XX  
 SO Sequence 36 AA;  
 Query Match 97.5%; Score 192; DB 19; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTNLIHSIIIESQNOQEKNEOELLELDKWSLWMWF 36  
 DB 1 YTSLIHSIIIESQNOQEKNEOELLELDKWSLWMWF 36

RESULT 5  
 AAY22805  
 ID AAY22805 standard; Peptide: 36 AA.  
 AC AAY22805;  
 DT 19-AUG-1999 (first entry)  
 DE SEQ ID NO. 1 from WO9820036.  
 XX  
 KW HIV; gp41 protein; constrained helical peptide; HIV infection;  
 KW vaccine; antibody; viral membrane fusion; viral infectivity;  
 KW ligand affinity purification; protein A replacement;  
 KW immunoglobulin purification; epitope mimic.  
 XX  
 OS Human immunodeficiency virus.  
 XX  
 PD WO9820036-A1.  
 PD 14-MAY-1998.  
 PE 05-NOV-1997; 97WO-US20069.  
 PR 16-JUN-1997; 97US-0876698.  
 PR 06-NOV-1996; 96US-0743698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Braisted A, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;  
 PI Wells JA;  
 DR WPI: 1998-286866/25.  
 XX  
 PT Production of constrained helical peptide(s) by linking side chains  
 PT on termin of octa:peptide - derived from human immunodeficiency  
 PT virus gp41 protein, useful in vaccines for treatment and prevention  
 PT of infection  
 XX  
 PS Disclosure; Page 143-144; 279pp; English.  
 XX  
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus  
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins  
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and  
 CC AAY22903 represent consensus sequences of various sections of the gp41  
 CC protein). Sequences derived from the peptides are used to produce  
 CC constrained helical peptides of the invention. The constrained helical  
 CC peptide is produced by synthesizing an octapeptide in which both terminal  
 CC amino acids have a side-chain that includes a group able to form an amide  
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain  
 CC residues with a difunctional linker to produce two amide bonds.  
 CC The constrained helical peptides are used to treat or prevent HIV  
 CC infection, especially as vaccines that generate antibodies that  
 CC prevent viral membrane fusion or infectivity. Vaccines may contain  
 CC constrained helical peptides derived from several different strains of  
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other  
 CC uses for the constrained helical peptides are in affinity purification  
 CC of ligands (particularly where complete binding protein is not readily  
 CC available, e.g. replacements for protein A in immunoglobulin  
 CC purification); as epitope mimics for antibody production; for isolation  
 CC of synthetic antibody clones from phage display libraries, or as stable  
 CC forms of "floppy" peptides or proteins.  
 CC  
 XX  
 SO Sequence 36 AA;  
 Query Match 97.5%; Score 192; DB 19; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 YTNLIHSIIIESQNOQEKNEOELLELDKWSLWMWF 36  
 DB 1 YTSLIHSIIIESQNOQEKNEOELLELDKWSLWMWF 36



XX Human immunodeficiency virus type 1.  
OS  
XX WO20006622-A1.  
PN  
XX  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
DR WPI; 2000-656493/63.  
XX  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
antagonist is used to modulate inflammation -  
XX  
SQ Claim 12; Page 24; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
SQ Sequence 36 AA:  
XX  
Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTNLIHSLSIESONQOEKNEDELIDKWSLWNMF 36  
DB 1 YTSLSHSLSIESONQOEKNEDELIDKWSLWNMF 36  
XX  
RESULT 9  
AAB52688  
ID AAB52688 standard; Peptide: 36 AA.  
XX  
AAB52688;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE T20/Dp178 peptide fragment #66.  
XX  
KM Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KM chemoattractant.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO20006622-A1.  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX WPI; 2000-656493/63.  
DR

XX Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
SQ Claim 12; Page 25; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
SQ Sequence 36 AA:  
XX  
Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTNLIHSLSIESONQOEKNEDELIDKWSLWNMF 36  
DB 1 YTSLSHSLSIESONQOEKNEDELIDKWSLWNMF 36  
XX  
RESULT 10  
AAB52818  
ID AAB52818 standard; Peptide: 36 AA.  
XX  
AC AAB52818;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE T20/Dp178 peptide fragment #97.  
XX  
KM Antinflammatory; T20/Dp178; gp41 ectodomain; HIV-1 fusion;  
KM formyl peptide receptor family; FPR; inflammatory response up-regulation;  
KM chemoattractant.  
XX  
OS Human immunodeficiency virus type 1.  
XX  
PN WO20006622-A1.  
PD 09-NOV-2000.  
XX  
PF 05-MAY-2000; 2000WO-US12371.  
XX  
PR 05-MAY-1999; 99US-0132686.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
DR WPI; 2000-656493/63.  
XX  
PT Administration of peptide agents with a sequence corresponding to a  
PT partial-length T20/Dp178 or T21/Dp107 formyl peptide receptor  
PT antagonist is used to modulate inflammation -  
XX  
SQ Claim 14; Page 40; 148pp; English.  
XX  
CC The present sequence is a peptide fragment of T20/Dp178. T20/Dp178 is a  
CC helical segment of the ectodomain of HIV-1 protein gp41. T20/Dp178 is  
CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/Dp178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemoattractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.

XX Sequence 36 AA;  
 SQ Query Match 97.5%; Score 192; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1,3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEOELLELDKMASLWNMF 36  
 1 YTSLSHSLSIESONQOEKNEOELLELDKMASLWNMF 36  
 Db

RESULT 11  
 AAB14533 standard; peptide; 36 AA.  
 ID AAB14533;  
 XX AAB14533;  
 XX 24-NOV-2000 (first entry)  
 DT

HIV-1 isolate LAI gp41 C-helical domain residues 643-678 (peptide P-18).

KM HIV-1: gp41 C-helical domain;  
 KM gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KM core 6-helix bundle; viral entry inhibition; immunogenic;  
 KM antibody; humoral response; broad spectrum vaccine; anti-HIV-  
 KM envelope glycoprotein; prophylaxis; therapy.  
 XX  
 OS Human immunodeficiency virus type 1.  
 PN WO200040616-A1.  
 XX 13-JUL-2000.  
 PD  
 XX 10-JAN-2000; 2000MO-US00456.  
 PF  
 XX 08-JAN-1999; 99US-0115404.  
 PR 07-JAN-2000; 2000US-0480336.  
 PR  
 XX (WILD/) WILD C T.  
 PA (WEIS/) WEISS C D.  
 XX  
 PI Wild CT, Weiss CD;  
 XX  
 DR WPI: 2000-465959/40.  
 XX  
 PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -  
 PS Claim 13; Page 12; 97pp; English.

XX Sequences AAB14532-B14534 and AAB14569-B14602 represent specifically  
 CC claimed peptides derived from the C-helical domain of the gp41  
 CC envelope glycoprotein from a variety of HIV-1 isolates. The invention  
 CC relates to raising a neutralizing antibody response to a broad spectrum  
 CC of HIV (human immunodeficiency virus) strains and isolates, comprising  
 CC the administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the process  
 CC of viral entry into host cells. Such peptides can correspond to or  
 CC mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly a  
 CC combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can  
 CC be alternately linked together to form a peptide which mimics the  
 CC core 6-helix bundle. Administration of the peptide(s) generates a  
 CC humoral response, with the production of antibodies against gp41  
 CC structures involved in viral entry. As these portions of gp41 are well  
 CC conserved, such antibodies may be effective against a broad range of

CC HIV strains and isolates. The peptide compositions may be administered  
 CC as a prophylactic or therapeutic vaccine to generate antibodies which  
 CC reduce or inhibit the ability of HIV to infect uninfected cells. A  
 CC composition comprising polyclonal or monoclonal antibodies can be  
 CC administered to reduce HIV infection of uninfected cells. Antibodies  
 CC raised against entry-relevant gp41 structures may also be used  
 CC therapeutically and as tools to further elucidate the mechanism of HIV  
 CC cell entry.  
 CC  
 XX Sequence 36 AA;  
 SQ Query Match 97.5%; Score 192; DB 21; Length 36;  
 Best Local Similarity 97.2%; Pred. No. 1,3e-16;  
 Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEOELLELDKMASLWNMF 36  
 1 YTSLSHSLSIESONQOEKNEOELLELDKMASLWNMF 36  
 Db

RESULT 12  
 AAY88665 standard; peptide; 36 AA.  
 ID AAY88665;  
 AC AAY88665;  
 XX 23-MAY-2000 (first entry)  
 DT

Core polypeptide fragment T No. 20.

DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KM anti-fusogenic; differentiation factor; interleukin; interferon;  
 KM colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9959615-A1.  
 XX 25-NOV-1999.  
 PD  
 XX 20-MAY-1999; 99MO-US11219.  
 PF  
 XX 20-MAY-1998; 98US-0082279.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI: 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 PS Disclosure; Page 21; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX Sequence 36 AA: 97.5%; Score 192; DB 21; Length 36;  
Query Match Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 13  
ID AAY88729 standard; peptide: 36 AA.  
XX AAY88729;  
XX  
XX 23-MAY-2000 (first entry)  
DT  
XX Core polypeptide fragment T No. 84.

XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX anti-fusogenic; differentiation factor; interleukin; interferon;  
XX colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
XX  
XX WO959615-A1.  
XX  
XX 25-NOV-1999.  
XX  
XX 20-MAY-1999; 99WO-US11219.  
XX  
XX 20-MAY-1998; 98US-0082279.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI: 2000-136792/12.  
XX  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
XX  
XX Disclosure: Page 22; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,  
XX interleukin, interferon, colony stimulating factor, hormone or  
XX angiogenic factor. The peptides of the invention can be used for  
XX inhibiting viral infection and can be used in anti-viral and  
XX anti-fusogenic treatments. Sequences AAY88729-190055 represent core  
XX polypeptide fragments that can be used in the invention. Some sequences  
XX among those indicated also comprise enhancer fragments at terminal ends  
XX and form hybrid polypeptides.

XX  
XX Sequence 36 AA:  
SQ

Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 14  
ID AAY89135 standard; peptide: 36 AA.  
XX AAY89135;  
XX  
XX 23-MAY-2000 (first entry)  
DT  
XX Core polypeptide fragment T No. 573.

XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX anti-fusogenic; differentiation factor; interleukin; interferon;  
XX colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
XX  
XX WO959615-A1.  
XX  
XX 25-NOV-1999.  
XX  
XX 20-MAY-1999; 99WO-US11219.  
XX  
XX 20-MAY-1998; 98US-0082279.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI: 2000-136792/12.  
XX  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence -  
XX  
XX  
XX Disclosure: Page 30; 124pp; English.

XX The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,  
XX interleukin, interferon, colony stimulating factor, hormone or  
XX angiogenic factor. The peptides of the invention can be used for  
XX inhibiting viral infection and can be used in anti-viral and  
XX anti-fusogenic treatments. Sequences AAY88729-190055 represent core  
XX polypeptide fragments that can be used in the invention. Some sequences  
XX among those indicated also comprise enhancer fragments at terminal ends  
XX and form hybrid polypeptides.

XX  
XX Sequence 36 AA:  
SQ

Query Match 97.5%; Score 192; DB 21; Length 36;  
Best Local Similarity 97.2%; Pred. No. 1.3e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLSIESONQOEKNEQELLELDKWSLWNMF 36  
||:|||||  
1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLSHSLSIESONQOEKNEQELLELDKWSLWNMF 36

RESULT 15  
ID AAY89136 standard; peptide: 36 AA.  
XX

AC AAY89136;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Core polypeptide fragment T No. 574.  
 XX  
 KW Retrovirus: hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX  
 OS Unidentified.  
 XX  
 PN WO9959615-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 20-MAY-1999; 99WO-US11219.  
 XX  
 PR 20-MAY-1998; 980S-0082279.  
 XX  
 (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX  
 DR WPI; 2000-136792/12.  
 XX  
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX  
 PS Disclosure; Page 30; 124pp; English.  
 XX  
 CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.  
 CC  
 CC Sequence 36 AA;  
 CC  
 CC Query Match 97.5%; Score 192; DB 21; Length 36;  
 CC Best Local Similarity 97.2%; Pred. No. 1,3e-16;  
 CC Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 YTNLIHSLSIESQNOQEKNEQLLELDKWSLWNMF 36  
 CC 11:|||||  
 CC Db 1 YTSLSHSLSIESQNOQEKNEQLLELDKWSLWNMF 36

Search completed: May 16, 2003, 11:12:04  
 Job time : 32.4578 secs

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; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-81

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Query Match          97.0%; Score 191; DB 9; Length 232;
Best Local Similarity 97.2%; Pred. No. 6.5e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 YTGILHSLEESONQOEKNEQELLELDKWSLWNMF 36
|||
Db 144 YTGILHSLEESONQOEKNEQELLELDKWSLWNMF 179

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RESULT 15
US-10-059-271-82
; Sequence 82, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPKE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match          97.0%; Score 191; DB 9; Length 254;
Best Local Similarity 97.2%; Pred. No. 7.2e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 YTGILHSLEESONQOEKNEQELLELDKWSLWNMF 36
|||
Db 166 YTGILHSLEESONQOEKNEQELLELDKWSLWNMF 201

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Search completed: May 16, 2003, 12:10:24  
Job time : 15.759 secs

Db 2 YTSLIHSLIEESONQOEKNEDELLELDKNASLWNMF 37

RESULT 10

US-09-779-451-41

; Sequence 41, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match

Best Local Similarity 97.0%; Score 191; DB 10; Length 46;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLIHSLIEESONQOEKNEDELLELDKNASLWNMF 36

Db 11 YTSLIHSLIEESONQOEKNEDELLELDKNASLWNMF 46

RESULT 11

US-09-779-451-4

; Sequence 4, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match

Best Local Similarity 97.0%; Score 191; DB 10; Length 56;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLIHSLIEESONQOEKNEDELLELDKNASLWNMF 36

Db 16 YTSLIHSLIEESONQOEKNEDELLELDKNASLWNMF 51

RESULT 12

US-10-040-349B-2

; Sequence 2, Application US/10040349B

; Publication No. US20030082521A1

; GENERAL INFORMATION:

; APPLICANT: Brasseur, Robert

; APPLICANT: Charlotaux, Benoit

; APPLICANT: Chevalier, Michel

; APPLICANT: El Habib, Raphaelle

; APPLICANT: Krell, Tino

; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

; FILE REFERENCE: 01-078-A

; CURRENT APPLICATION NUMBER: US/10/040,349B

; CURRENT FILING DATE: 2002-07-09

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

; OTHER INFORMATION: polypeptide derived from gp41 LAI

US-10-040-349B-2

Query Match

Best Local Similarity 97.0%; Score 191; DB 9; Length 177;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLIHSLIEESONQOEKNEDELLELDKNASLWNMF 36

Db 104 YTSLIHSLIEESONQOEKNEDELLELDKNASLWNMF 139

RESULT 13

US-10-059-271-84

; Sequence 84, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDDER, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; FILE REFERENCE: ALBRE-22

; CURRENT APPLICATION NUMBER: US/10/059,271

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: DE 101 06 295

; PRIOR FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

; ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match

Best Local Similarity 97.0%; Score 191; DB 9; Length 221;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGLIHSLIEESONQOEKNEDELLELDKNASLWNMF 36

Db 131 YTSLIHSLIEESONQOEKNEDELLELDKNASLWNMF 166

RESULT 14

US-10-059-271-81

; Sequence 81, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDDER, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

RESULT 7  
US-09-854-816-1  
Sequence 1, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
MOLECULE TYPE: DP178  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLEDKWASLWNMF 36  
DB 1 YTSLHSLEESONOQEKNEQELLEDKWASLWNMF 36  
RESULT 8  
US-09-854-816-108  
Sequence 108, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLEDKWASLWNMF 36  
DB 1 YTSLHSLEESONOQEKNEQELLEDKWASLWNMF 36  
RESULT 9  
US-09-848-616-176  
Sequence 176, Application US/09848616  
Publication No. US20030054010A1  
GENERAL INFORMATION:  
APPLICANT: Seibel, Peter  
APPLICANT: Dunant, Nicolas  
APPLICANT: Bachmann, Martin  
APPLICANT: Tissot, Alain  
APPLICANT: Lechner, Franziska  
TITLE OF INVENTION: Molecular Antigen Array  
FILE REFERENCE: 1700.0180002  
CURRENT APPLICATION NUMBER: US/09/848,616  
CURRENT FILING DATE: 2001-05-05  
NUMBER OF SEQ ID NOS: 186  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 176  
LENGTH: 37  
TYPE: PPT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 97.0%; Score 191; DB 9; Length 37;  
Best Local Similarity 97.2%; Pred. No. 9,4e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
CY 1 YTGILHSLEESONOQEKNEQELLEDKWASLWNMF 36  
DB 1 YTGILHSLEESONOQEKNEQELLEDKWASLWNMF 36

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match 97.0%; Score 191; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNF 36  
1 YTSLSHSLEESQNOQEKNEDELLELDKWSLWNF 36

RESULT 3  
US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO: 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match 97.0%; Score 191; DB 9; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNF 36  
1 YTSLSHSLEESQNOQEKNEDELLELDKWSLWNF 36

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US20020068813A1  
GENERAL INFORMATION:

APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNF 36  
1 YTSLSHSLEESQNOQEKNEDELLELDKWSLWNF 36

RESULT 5  
US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US20020094521A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900 0300003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO: 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNF 36  
1 YTSLSHSLEESQNOQEKNEDELLELDKWSLWNF 36

RESULT 6  
US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, KEY-SUN  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match 97.0%; Score 191; DB 10; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.2e-17;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEDELLELDKWSLWNF 36  
1 YTSLSHSLEESQNOQEKNEDELLELDKWSLWNF 36

GenCore version 5.1.4\_p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 15.759 Seconds  
(without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-534  
Perfect score: 197  
Sequence: 1 YTGILHSLEESQNOEKNEDELELDKXWASLWNNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

1 number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : PublishedApplications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PC1\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	97.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	191	97.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	191	97.0	36	9 US-09-493-346-1	Sequence 1, Appl
4	191	97.0	36	10 US-09-796-202-10	Sequence 10, Appl
5	191	97.0	36	10 US-09-779-451-5	Sequence 5, Appl
6	191	97.0	36	10 US-09-834-628-1	Sequence 1, Appl
7	191	97.0	36	10 US-09-854-816-1	Sequence 1, Appl
8	191	97.0	36	10 US-09-854-816-108	Sequence 108, App
9	191	97.0	37	9 US-09-848-616-176	Sequence 176, App
10	191	97.0	46	10 US-09-779-451-41	Sequence 41, Appl
11	191	97.0	56	10 US-09-779-451-4	Sequence 4, Appl
12	191	97.0	177	9 US-10-040-349B-2	Sequence 2, Appl
13	191	97.0	221	9 US-10-059-271-84	Sequence 84, Appl
14	191	97.0	232	9 US-10-059-271-81	Sequence 81, Appl
15	191	97.0	234	9 US-10-059-271-82	Sequence 82, Appl
16	191	97.0	256	9 US-10-059-271-97	Sequence 97, Appl
17	191	97.0	268	10 US-09-854-816-16	Sequence 16, Appl
18	191	97.0	268	10 US-09-854-816-17	Sequence 17, Appl
19	191	97.0	268	10 US-09-854-816-18	Sequence 18, Appl

20	191	97.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	191	97.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	191	97.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	191	97.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	191	97.0	519	10 US-09-756-551A-8	Sequence 8, Appl
25	191	97.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	191	97.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	191	97.0	861	9 US-10-026-741-103	Sequence 103, App
28	191	97.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	191	97.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	188	95.4	36	10 US-09-912-824-1	Sequence 1, Appl
31	188	95.4	267	10 US-09-854-816-38	Sequence 38, Appl
32	188	95.4	268	10 US-09-854-816-19	Sequence 19, Appl
33	188	95.4	268	10 US-09-854-816-41	Sequence 41, Appl
34	188	95.4	269	10 US-09-854-816-43	Sequence 43, Appl
35	185	93.9	1231	9 US-10-059-271-94	Sequence 94, Appl
36	183	92.9	268	10 US-09-854-816-13	Sequence 13, Appl
37	182	92.4	233	10 US-09-854-816-50	Sequence 50, Appl
38	182	92.4	268	10 US-09-854-816-9	Sequence 9, Appl
39	182	92.4	268	10 US-09-854-816-26	Sequence 26, Appl
40	182	92.4	269	10 US-09-854-816-12	Sequence 12, Appl
41	182	92.4	619	10 US-09-891-609-4	Sequence 4, Appl
42	182	92.4	646	10 US-09-891-609-2	Sequence 2, Appl
43	182	92.4	847	10 US-09-476-242-2	Sequence 2, Appl
44	181	91.9	46	10 US-09-854-816-109	Sequence 109, App
45	181	91.9	269	10 US-09-854-816-6	Sequence 6, Appl

## ALIGNMENTS

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RESULT 1
US-09-874-475-16
; Sequence 16, Application US/09874475
; Publication No. US20020182592A1
GENERAL INFORMATION:
; APPLICANT: Petropoulos, Christos J.
; APPLICANT: Parkin, Neil T.
; APPLICANT: Whitcomb, Jeanette
; APPLICANT: Huang, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
; FILE REFERENCE: 2793/65166
; CURRENT APPLICATION NUMBER: US/09/874,475
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match          97.0%  Score 191; DB 9; Length 36;
Best Local Similarity 97.2%  Pred. No. 9.2e-17;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YTGILHSLEESQNOEKNEDELELDKXWASLWNNF 36
|||||||
DB      1 YTGILHSLEESQNOEKNEDELELDKXWASLWNNF 36

RESULT 2
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US2003004411A1
GENERAL INFORMATION:
; APPLICANT: Olesen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; CURRENT FILING DATE: 2002-10-15

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Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWVNF 36

## RESULT 13

Sequence 497, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 497

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-497

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLSIESQNOEKNEQELLELDKWSLWVNF 36

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWVNF 36

## RESULT 14

US-09-082-279B-498

Sequence 498, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 498

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-498

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLSIESQNOEKNEQELLELDKWSLWVNF 36

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWVNF 36

RESULT 15  
US-09-082-279B-603

Sequence 603, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 603

LENGTH: 36

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-603

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLSIESQNOEKNEQELLELDKWSLWVNF 36

Db 1 YTSLIHSLIEESQNOEKNEQELLELDKWSLWVNF 36

Search completed: May 16, 2003, 11:22:12  
Job time: 10.1928 secs

RESULT 10  
US-08-554-616-1  
Sequence 1, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-1  
Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36  
RESULT 11  
US-08-485-264A-1  
Sequence 1, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Felleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-264A-1

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 12  
US-09-082-279B-15  
Sequence 15, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-15

Query Match 97.0%; Score 191; DB 4; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 8  
US-08-485-551A-1  
Sequence 1, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A.  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36

RESULT 9  
US-08-471-913A-1  
Sequence 1, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9,3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWNMF 36  
DB 1 YTSLSHSLEESQNOEKNEQELLELDKWSLWNMF 36

Db 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 5  
US-08-484-223B-1  
Sequence 1, Application US/08484223B  
Patent No. 6020459

GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 6  
US-08-919-597-1  
Sequence 1, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-1

Query Match 97.0%; Score 191; DB 3; Length 36;  
Best Local Similarity 97.2%; Pred. No. 9.3e-18;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLSIESQNOQEKNEQELLELDKWSLWNMF 36  
Db 1 YTSLIHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 7  
US-08-475-668A-1  
Sequence 1, Application US/08475668A  
Patent No. 6060065  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Peteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

QY 1 YTGLIHSLIEESQÑQÑEKNQELLEDKWSLWNWF 36

GenCore version 5.1.4\_P5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 10.1928 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197

Sequence: 1 YTGILHSIESONQOEKNEQELLELDKWSIWMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2.6/ptodata/1/1aa/PCUTS.COMB.pep:\*  
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	97.0	36	1 US-08-073-028-1	Sequence 1, Appli
2	191	97.0	36	3 US-08-486-099-1	Sequence 1, Appli
3	191	97.0	36	3 US-09-071-877-1	Sequence 1, Appli
4	191	97.0	36	3 US-08-360-107A-1	Sequence 1, Appli
5	191	97.0	36	3 US-08-484-223B-1	Sequence 1, Appli
6	191	97.0	36	3 US-08-919-597-1	Sequence 1, Appli
7	191	97.0	36	3 US-08-475-668A-1	Sequence 1, Appli
8	191	97.0	36	3 US-08-485-551A-1	Sequence 1, Appli
9	191	97.0	36	3 US-08-471-913A-1	Sequence 1, Appli
10	191	97.0	36	4 US-08-554-616-1	Sequence 1, Appli
11	191	97.0	36	4 US-08-485-264A-1	Sequence 1, Appli
12	191	97.0	36	4 US-09-082-279B-15	Sequence 15, Appli
13	191	97.0	36	4 US-09-082-279B-497	Sequence 497, App
14	191	97.0	36	4 US-09-082-279B-498	Sequence 498, App
15	191	97.0	36	4 US-09-082-279B-603	Sequence 603, App
16	191	97.0	36	4 US-09-082-279B-630	Sequence 630, App
17	191	97.0	36	4 US-09-082-279B-631	Sequence 631, App
18	191	97.0	36	4 US-09-082-279B-705	Sequence 705, App
19	191	97.0	36	4 US-09-082-279B-834	Sequence 834, App
20	191	97.0	36	4 US-09-082-279B-1076	Sequence 1076, Ap
21	191	97.0	36	4 US-09-082-279B-1121	Sequence 1121, Ap
22	191	97.0	36	4 US-09-082-279B-1161	Sequence 1161, Ap
23	191	97.0	36	4 US-08-965-056-1	Sequence 1, Appli
24	191	97.0	36	4 US-08-965-056-108	Sequence 108, App
25	191	97.0	36	4 US-09-045-920-1	Sequence 1, Appli
26	191	97.0	36	4 US-08-474-349A-1	Sequence 1, Appli
27	191	97.0	36	4 US-08-474-349A-399	Sequence 399, App

28	191	97.0	36	4 US-08-474-349A-413	Sequence 413, App
29	191	97.0	36	4 US-09-315-304B-15	Sequence 15, Appli
30	191	97.0	36	4 US-09-315-304B-497	Sequence 497, App
31	191	97.0	36	4 US-09-315-304B-498	Sequence 498, App
32	191	97.0	36	4 US-09-315-304B-603	Sequence 603, App
33	191	97.0	36	4 US-09-315-304B-630	Sequence 630, App
34	191	97.0	36	4 US-09-315-304B-631	Sequence 631, App
35	191	97.0	36	4 US-09-315-304B-705	Sequence 705, App
36	191	97.0	36	4 US-09-315-304B-834	Sequence 834, App
37	191	97.0	36	4 US-09-315-304B-834	Sequence 834, App
38	191	97.0	36	4 US-09-315-304B-1121	Sequence 1121, Ap
39	191	97.0	36	4 US-09-315-304B-1161	Sequence 1161, Ap
40	191	97.0	36	4 US-09-315-304B-1469	Sequence 1469, Ap
41	191	97.0	36	4 US-09-315-304B-1470	Sequence 1470, Ap
42	191	97.0	36	4 US-09-315-304B-1486	Sequence 1486, Ap
43	191	97.0	36	4 US-09-315-304B-1520	Sequence 1520, Ap
44	191	97.0	36	4 US-08-255-208A-1	Sequence 1, Appli
45	191	97.0	37	4 US-09-082-279B-771	Sequence 771, App

## ALIGNMENTS

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RESULT 1
US-08-073-028-1
; Sequence 1, Application US/08073028
; Patent No. 5464933
;
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,028
FILING DATE: 07-JUN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-073-028-1
Query Match 97.0%; Score 191; DB 1; Length 36;
Best Local Similarity 97.2%; Pred. No. 9.3e-18;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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E:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.9%; Score 181; DB 1; Length 855;

Best Local Similarity 88.9%; Pred. No. 1,1e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEOELLELDKMASLWNMF 36  
 DB 637 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 672

# RESULT 12

S21998 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 28

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

Submitted to the EMBL Data Library, July 1991

A:Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR

A:Reference number: S21990

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MID:92144209; PMID:1736940

A:Accession: S70425

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222, 'X', 224-358 <STE2>

A:Cross-references: EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:G60183

C:Superfamily: type E retrovirus env polyprotein

Query Match 91.4%; Score 180; DB 2; Length 358;

Best Local Similarity 88.9%; Pred. No. 5,6e-14;

Matches 32; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEOELLELDKMASLWNMF 36  
 DB 140 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 175

# RESULT 13

S22004 envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 4B

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

Submitted to the EMBL Data Library, July 1991

A:Title: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 <STE1>

A:Cross-references: EMBL:X61353; NID:G60188; PIDN:CAA43618.1; PID:G60189

R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid

A:Reference number: S70417; MID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292, 'X', 294-357 <STE2>

A:Cross-references: EMBL:X61353; NID:G60188

C:Superfamily: type E retrovirus env polyprotein

Query Match 89.8%; Score 177; DB 2; Length 357;

Best Local Similarity 88.9%; Pred. No. 1,3e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEOELLELDKMASLWNMF 36  
 DB 139 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 174

# RESULT 14

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

Submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:G1465777; PID:G1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 89.3%; Score 176; DB 2; Length 847;

Best Local Similarity 88.9%; Pred. No. 4,4e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEOELLELDKMASLWNMF 36  
 DB 629 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 664

# RESULT 15

S13289

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack,

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MID:91043044; PMID:2172833

A:Accession: S13289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBK>

C:Superfamily: type E retrovirus env polyprotein

Query Match 89.3%; Score 176; DB 2; Length 847;

Best Local Similarity 88.9%; Pred. No. 4,4e-13;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTNLIHSLEESONQOEKNEOELLELDKMASLWNMF 36  
 DB 629 YTNLIYTLIEESONQOEKNEOELLELDKMASLWNMF 664

Search completed: May 16, 2003, 11:25:09  
 Job time: 12.1446 secs

C:Accession: A24774  
 R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STAN>  
 A:Cross-references: GB:K03455; GB:M38432; NID:91906382  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.9%; Score 183; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 6, 6e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESQNOEKNEDELLEDKWASLWNMF 36  
 ||:|||||  
 Db 638 YTSLYTLIEESQNOEKNEDELLEDKWASLWNMF 673

RESULT 8  
 VCLJ2C  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 92.9%; Score 183; DB 1; Length 861;  
 Best Local Similarity 91.7%; Pred. No. 6, 6e-14;  
 Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESQNOEKNEDELLEDKWASLWNMF 36  
 ||:|||||  
 Db 643 YTSLYTLIEESQNOEKNEDELLEDKWASLWNMF 678

RESULT 9  
 S21994  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 278  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAAA3622.1; PID:960180  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STEE2>  
 A:Cross-references: EMBL:X61355; NID:960179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.4%; Score 182; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 3, 2e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESQNOEKNEDELLEDKWASLWNMF 36  
 ||:|||||  
 Db 139 YTLTYTLIEESQNOEKNEDELLEDKWASLWNMF 174

RESULT 10  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70422  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-357 <ST2>  
 A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAAA3624.1; PID:91067129  
 A:Experimental source: patient 27L  
 A:Note: submitted to the EMBL Data Library, July 1991  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 92.4%; Score 182; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 3, 2e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTNLHSLIEESQNOEKNEDELLEDKWASLWNMF 36  
 ||:|||||  
 Db 139 YTLTYTLIEESQNOEKNEDELLEDKWASLWNMF 174

RESULT 11  
 VCLJ22  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown  
 Science 227, 484-492, 1985  
 A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
 A:Reference number: A04003; MUID:85090453; PMID:2578227  
 A:Accession: A03976  
 A:Molecule type: DNA  
 A:Residues: 1-855 <SAN>  
 A:Cross-references: GB:K02007; NID:9328658; PIDN:AA59882.1; PID:9328666  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; poly  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:510-855/Product: transmembrane glycoprotein #status predicted <TM>  
 F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,

```

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran,
R.; Berger, J.A.; Papas, T.S.; Ghrayedji, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:2-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.5%; Score 192; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 638 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 673

RESULT 4
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hodson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 97.5%; Score 192; DB 1; Length 861;
Best Local Similarity 97.2%; Pred. No. 5,6e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 643 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 678

RESULT 5
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein

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```

N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: CA1621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Glibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: CA1621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
Query Match 92.9%; Score 183; DB 2; Length 443;
Best Local Similarity 91.7%; Pred. No. 3,1e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 36
DB 378 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 413

RESULT 6
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUE>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <STIC>
F:1-51/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMN>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 92.9%; Score 183; DB 1; Length 856;
Best Local Similarity 94.3%; Pred. No. 6,6e-14;
Matches 33; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTNLIHSLEESONOEKNEOELLELDKASLWNMF 35
DB 638 YTSLIHSLEESONOEKNEOELLELDKASLWNMF 672

RESULT 7
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WM1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997

```

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-535

Perfect score: 197  
Sequence: 1 YTNLIHSLIEESQNOOEKNEDELLELDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	97.5	851	2 S33985	env polyprotein -
2	192	97.5	854	2 S13288	env protein - huma
3	192	97.5	856	1 VCLJH3	env polyprotein pr
4	192	97.5	861	1 VCLJLV	env polyprotein pr
5	183	92.9	443	2 C41621	env polyprotein p
6	183	92.9	856	1 VCLJLV	env polyprotein pr
7	183	92.9	856	1 VCLJ3W	env polyprotein pr
8	183	92.9	861	1 VCLJSC	env polyprotein pr
9	182	92.4	357	2 S21994	env polyprotein pr
10	182	92.4	357	2 S21996	env polyprotein g
11	181	91.9	855	1 VCLJAJ	env polyprotein pr
12	180	91.4	358	2 S21998	env polyprotein pr
13	176	89.8	357	2 S22004	env polyprotein g
14	176	89.3	847	2 T09448	env polyprotein g
15	176	89.3	847	2 S13289	env protein - huma
16	175	88.8	357	2 S21992	env polyprotein g
17	175	88.8	445	2 A41621	env polyprotein M
18	175	88.8	843	1 H44001	env polyprotein pr
19	175	88.8	852	1 VCLJBR	env polyprotein -
20	174	88.3	357	2 S22006	env polyprotein g
21	174	88.3	358	2 S22002	env polyprotein g
22	174	88.3	358	2 S22000	env polyprotein g
23	174	88.3	358	2 S70417	env polyprotein g
24	174	88.3	352	2 T12016	env polyprotein g
25	174	88.3	853	2 S54384	env polyprotein g
26	174	88.3	855	2 VCLJZR	env polyprotein pr
27	174	88.3	859	1 VCLJMN	env polyprotein pr
28	173	87.8	729	1 VCLJXK	env polyprotein pr
29	173	87.8	861	1 VCLJKB	env polyprotein pr

30	172	87.3	846	1 VCLJND	env polyprotein pr
31	167	84.8	859	2 T01672	env polyprotein pr
32	165	83.8	136	2 J00266	env polyprotein pr
33	165	83.8	136	2 J00954	env polyprotein pr
34	165	83.8	156	2 B41621	env polyprotein pr
35	165	83.8	868	1 VCLJH4	env polyprotein -
36	151	76.6	854	1 VCLJSI	env polyprotein pr
37	149	75.6	856	1 A44963	env polyprotein pr
38	144	73.1	357	2 S21990	env polyprotein pr
39	133	67.5	877	2 S49197	env polyprotein p
40	116	58.9	863	2 A53034	env polyprotein -
41	86	43.7	881	1 VCLJG3	env polyprotein -
42	86	43.7	881	2 S03068	env protein - huma
43	86	43.7	889	1 VCLJG5	env polyprotein -
44	85	43.1	151	2 S30448	env protein - huma
45	85	43.1	151	2 S30452	env protein - huma

## ALIGNMENTS

## RESULT 1

S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985

R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991

A:Reference number: S33979  
A:Accession: S33985

A>Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA7628.1; PID:g60199

C:Superfamily: type E retrovirus env polyprotein

Query Match 97.5%; Score 192; DB 2; Length 851;  
Best local similarity 97.2%; Pred. No. 5.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOOEKNEDELLELDKWSLWMP 36  
DB 633 YTNLIHSLIEESQNOOEKNEDELLELDKWSLWMP 668

## RESULT 2

S13288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match 97.5%; Score 192; DB 2; Length 854;  
Best local similarity 97.2%; Pred. No. 5.6e-15;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNLIHSLIEESQNOOEKNEDELLELDKWSLWMP 36  
DB 636 YTNLIHSLIEESQNOOEKNEDELLELDKWSLWMP 671

## RESULT 3

VCLJH3

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## RESULT 12

VCLJZR

env polypotein precursor - human immunodeficiency virus Zr-6  
N:Alternate names: coat polypotein

C:Species: human immunodeficiency virus Zr-6

C&gt;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 16-Jul-1999

C:Accession: D26192

R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feolino, P.; Schuchtmann, G.; Cu

Gene 52, 71-82, 1987

A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot

A:Reference number: A26192; MUID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 &lt;SRT&gt;

A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-29/Domain: signal sequence #status predicted &lt;Sig&gt;

F:20-855/Product: env polypotein #status predicted &lt;Mat&gt;

F:502-520/Product: exterior membrane glycoprotein #status predicted &lt;EXT&gt;

F:501-855/Product: transmembrane glycoprotein #status predicted &lt;TM&gt;

F:87,129,140,145,154,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

F:87,129,140,145,154,158,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match

Best Local Similarity 91.4%; Score 180; DB 1; Length 855;

Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

## RESULT 13

S21998

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 28

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S21998; S70425

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determ

A:Reference number: S21998

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 &lt;STEL&gt;

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70425

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222, 'X', 224-358 &lt;STEL&gt;

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polypotein

Query Match

Best Local Similarity 90.9%; Score 179; DB 2; Length 358;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

## RESULT 14

VCLJND

env polypotein precursor - human immunodeficiency virus type 1 (isolate NDK)

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C&gt;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C:Accession: J00066

R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,

Gene 81, 275-284, 1989

A:Title: Nucleotide sequence of HIV-1-NK: a highly cytopathic strain of the human imm

A:Reference number: J00065; MUID:90034200; PMID:2806517

A:Accession: J00066

A:Molecule type: DNA

A:Residues: 1-846 &lt;SPI&gt;

A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA4873.1; PID:g328162

A:Note: the authors translated the codon GCG for residue 523 as Arg

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polypotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-29/Domain: signal sequence #status predicted &lt;Sig&gt;

F:30-501/Product: coat protein gp120 #status predicted &lt;CPI&gt;

F:502-846/Product: coat protein gp41 #status predicted &lt;CP2&gt;

F:502-520/Domain: transmembrane #status predicted &lt;TM1&gt;

F:674-692/Domain: transmembrane #status predicted &lt;TM2&gt;

F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

Query Match

Best Local Similarity 90.4%; Score 178; DB 1; Length 846;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

S22004

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: isolate 4B

C&gt;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 &lt;STEL&gt;

A:Cross-references: EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PID:g60189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70419; MUID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292, 'X', 294-357 &lt;STEL&gt;

A:Cross-references: EMBL:X61353; NID:g60188

C:Superfamily: type E retrovirus env polypotein

Query Match

Best Local Similarity 88.8%; Score 175; DB 2; Length 357;

Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Search completed: May 16, 2003, 11:25:09

Job time: 13.1446 secs

A:Molecule type: DNA  
 A:Residues: 1-856 <MUE>  
 A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:g328559  
 C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
 F:1-30/Domain: signal sequence #status predicted <SIG>  
 F:31-51/Product: exterior membrane glycoprotein #status predicted <TM>  
 F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
 F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
 F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 92.4%; Score 182; DB 1; Length 856;  
 Best Local Similarity 94.3%; Pred. No. 4.9e-14;

Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNMF 35  
 638 YTSILYLRLEESONQOEKNEDELLELDKWSLWNMF 672

## RESULT 8

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
 N:Contains: coat protein gp120; coat protein gp41  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
 C:Accession: A24774  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M88432; NID:g1906382  
 C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:30-50/Product: coat protein gp120 #status predicted <GP2>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 92.4%; Score 182; DB 1; Length 856;  
 Best Local Similarity 91.7%; Pred. No. 4.9e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNMF 36  
 638 YTSILYLRLEESONQOEKNEDELLELDKWSLWNMF 673

## RESULT 9

env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A>Note: host Homo sapiens (man)  
 C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Guirao, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-861/Product: env polyprotein #status predicted <EPP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

Query Match 92.4%; Score 182; DB 1; Length 861;  
 Best Local Similarity 91.7%; Pred. No. 5e-14;  
 Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNMF 36  
 643 YTSILYLRLEESONQOEKNEDELLELDKWSLWNMF 678

## RESULT 10

env polyprotein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variety: isolate 27B  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21994; S70421  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21994  
 A:Molecule type: DNA  
 A:Residues: 1-357 <STP1>

A:Cross-references: EMBL:X61355; NID:g60179; PIDN:CAA43622.1; PID:g60180  
 R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940  
 A:Accession: S70421  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A:Cross-references: EMBL:X61355; NID:g60179  
 C:Superfamily: type E retrovirus env polyprotein

Query Match 91.4%; Score 180; DB 2; Length 357;  
 Best Local Similarity 91.7%; Pred. No. 3.2e-14;

Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNMF 36  
 139 YTSILYLRLEESONQOEKNEDELLELDKWSLWNMF 174

## RESULT 11

env polyprotein - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 26-Aug-1999  
 C:Accession: S54384  
 R:Theodore, T.; Buckler-White, A.J.  
 submitted to the EMBL Data Library, July 1989  
 A:Reference number: S54377  
 A:Accession: S54384  
 A>Status: preliminary  
 A:Molecule type: genomic RNA  
 A:Residues: 1-853 <RHE>  
 A:Cross-references: EMBL:M22639; NID:g329377; PIDN:AAA45370.1; PID:g329385  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: polyprotein

Query Match 91.4%; Score 180; DB 2; Length 853;  
 Best Local Similarity 91.7%; Pred. No. 8.6e-14;  
 Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNMF 36  
 635 YTSILYLRLEESONQOEKNEDELLELDKWSLWNMF 670

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03973  
R:Ratner, L.; Papas, T.S.; Chirgub, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2576615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAAA42  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:1-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:2-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 97.0%; Score 191; DB 1; Length 856;  
Best Local Similarity 97.2%; Pred. No. 4e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03975  
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allzon, M.  
Cell 40, 9-17, 1985  
A:Title: Nucleotide sequence of the AIDS virus, LAV.  
A:Reference number: A90866; MUID:85099333; PMID:2981635  
A:Accession: A03975  
A:Molecule type: DNA  
A:Residues: 1-861 <WAI>  
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB5951.1; PID:9326424  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:1-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,197,202,230,234,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (asn) (covalent) #status predic  
Query Match 97.0%; Score 191; DB 1; Length 861;  
Best Local Similarity 97.2%; Pred. No. 4.1e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 5  
env polyprotein precursor - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CA443624.1; PID:91067129  
A:Experimental source: patient 27L  
A:Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein  
Query Match 95.4%; Score 188; DB 2; Length 357;  
Best Local Similarity 94.4%; Pred. No. 3.5e-15;  
Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
env polyprotein P - human immunodeficiency virus type 1 (fragment)  
C:Accession: C41621  
N:Alternate names: coat polyprotein  
M:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 26-Aug-1999  
C:Accession: C41621  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi  
A:Reference number: A41621; MUID:92107924; PMID:1765038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BUR>  
A:Cross-references: GB:M77230; NID:9328631; PIDN:AAB03792.1; PID:9555015  
A:Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:  
Query Match 92.4%; Score 182; DB 2; Length 443;  
Best Local Similarity 91.7%; Pred. No. 2.3e-14;  
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 7  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
C:Accession: A03974  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974

GenCore version 5.1.4-p5-A578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 12.1446 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533A-534

Perfect score: 197  
Sequence: 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	97.0	851	2	env polypeptide - huma
2	191	97.0	854	2	env polypeptide - huma
3	191	97.0	856	1	env polypeptide - huma
4	191	97.0	861	1	env polypeptide - huma
5	188	95.4	357	2	env polypeptide - huma
6	182	92.4	443	2	env polypeptide - huma
7	182	92.4	456	1	env polypeptide - huma
8	182	92.4	856	1	env polypeptide - huma
9	182	92.4	861	1	env polypeptide - huma
10	180	91.4	357	2	env polypeptide - huma
11	180	91.4	855	1	env polypeptide - huma
12	180	91.4	855	1	env polypeptide - huma
13	179	90.9	358	1	env polypeptide - huma
14	178	90.4	846	1	env polypeptide - huma
15	175	88.8	357	2	env polypeptide - huma
16	175	88.8	847	2	env polypeptide - huma
17	175	88.8	847	2	env polypeptide - huma
18	175	88.8	847	2	env polypeptide - huma
19	174	88.3	445	1	env polypeptide - huma
20	174	88.3	445	1	env polypeptide - huma
21	173	87.8	358	2	env polypeptide - huma
22	173	87.8	358	2	env polypeptide - huma
23	173	87.8	358	2	env polypeptide - huma
24	173	87.8	852	1	env polypeptide - huma
25	173	87.8	852	1	env polypeptide - huma
26	172	87.3	357	2	env polypeptide - huma
27	172	87.3	843	1	env polypeptide - huma
28	169	85.8	357	2	env polypeptide - huma
29	169	85.8	852	1	env polypeptide - huma

30	167	84.8	729	1	VCLJKB	env polypeptide - huma
31	167	84.8	861	1	VCLJKB	env polypeptide - huma
32	163	82.7	454	2	B41621	env polypeptide - huma
33	162	82.2	868	1	VCLJH4	env polypeptide - huma
34	159	80.7	136	2	JT0954	env polypeptide - huma
35	159	80.7	136	2	JT0954	env polypeptide - huma
36	157	79.7	854	1	VCLJST	env polypeptide - huma
37	147	74.6	856	1	A44963	env polypeptide - huma
38	143	72.6	357	2	S21990	env polypeptide - huma
39	132	67.0	877	2	S49197	env polypeptide - huma
40	115	58.4	863	2	A53034	env polypeptide - huma
41	86	43.7	881	1	VCLJG3	env polypeptide - huma
42	86	43.7	881	1	S03068	env polypeptide - huma
43	86	43.7	889	1	VCLJG5	env polypeptide - huma
44	85	43.1	151	2	S30448	env polypeptide - huma
45	85	43.1	151	2	S30452	env polypeptide - huma

## ALIGNMENTS

## RESULT 1

S33985  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:211530; NID:g60192; PIDN:CAA77628.1; PID:g60199  
C:Superfamily: type E retrovirus env polypeptide

Query Match 97.0%; Score 191; DB 2; Length 851;  
Best Local Similarity 97.2%; Pred. No. 4e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36  
DB 633 YTSILHSLEESQNOQEKNEQELLELDKWSLMMNF 668

## RESULT 2

S13288  
env polypeptide - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,  
Nature 348, 69-73, 1990  
A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypeptide

Query Match 97.0%; Score 191; DB 2; Length 854;  
Best Local Similarity 97.2%; Pred. No. 4e-15;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILHSLEESQNOQEKNEQELLELDKWSLMMNF 36  
DB 636 YTSILHSLEESQNOQEKNEQELLELDKWSLMMNF 671

## RESULT 3

VCLJH3

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FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA; 97043 MW; 849B0B8CBAFF7008 CRC64;

Query Match 91.4%; Score 180; DB 1; Length 853;  
 Best Local Similarity 91.7%; Pred. No. 1.5e-14;

Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YTGILHSITFEESQNOOEKNEOELELDKWSLWME 36  
 Db 635 YTGILIRLIESQTOOEKNEOELELDKWSLWME 670

Search completed: May 16, 2003, 11:13:34  
 Job time : 6.07229 secs

"Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome." J. Virol. 64:4016-4020(1990).

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CC -----

DR EMBL: M38427; AAA45067.1; -

DR HIV: M38427; ENV52639.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

Signal.

FT CHAIN 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 467 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 852 AA: 96663 MW: EE7BFB8D23C9910D CXC64.

SEQUENCE

Query Match 91.4%; Score 180; DB 1; Length 852;

Best Local Similarity 88.9%; Pred. No. 1.5e-14;

Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

1 YVGLHSITIEEONOENKNELELDKASIMNMF 36

DB 634 YTSLYTTLIESONOENKNELELDKASIMNMF 669

RESULT 15

ENV\_HV122

ID ENV\_HV122

AC P12487

DT 01-OCT-1989

DT 01-OCT-1989

DT 16-OCT-2001

DE Envelope glycoprotein gp160 precursor [containing: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

DE ENV.

OS Human immunodeficiency virus type 1 (Z2/CDC-234 isolate) (HIV-1).

OC Viruses; Retroviridae; Lentivirus.

OC NCBI\_TaxID=11683;

OX [1]

RP SEQUENCE FROM N.A.

RA Theodore T. Buckler-White A.

RL Submitted (NOV-1988) to the HIV data bank.

CC -----

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CC -----

DR EMBL: M22639; AAA45370.1; -

DR HIV: M22639; ENV52266.

DR InterPro: IPR000328; Env\_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;

Signal.

FT CHAIN 1 31 BY SIMILARITY.

FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 154 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 330 BY SIMILARITY.

FT DISULFID 376 442 BY SIMILARITY.

FT DISULFID 383 415 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA: 96721 MW: F9CD864DAD0D7A5 CRC64;

Query Match 91.9%; Score 181; DB 1; Length 853;
Best Local Similarity 91.7%; Pred. No. 1,2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 36
Db 635 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 670

RESULT 13
ENV_HV1RH STANDARD: PRT: 865 AA.
ID ENV_HV1RH STANDARD: PRT: 865 AA.
AC P04579;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11701;
PN [1]
SEQUENCE FROM N.A.
MEDLINE=66218077; PubMed=2423250;
RA Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,
Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
RT "Identification and characterization of conserved and variable of
regions in the envelope gene of HTLV-III/LAV, the retrovirus of
RT AIDS";
RT Cell 45:637-648(1986).
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CC EMBL: M17451; AAA45057.1; -
CC HIV: M17451; ENVSRF.
CC InterPro: IPR000328; ENV_GP41.
CC InterPro: IPR000777; GP120.
CC Pfam: PF00516; GP120; 1.
CC Pfam: PF00517; GP41; 1.
CC AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.

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FT SIGNAL 1 29
FT CHAIN 30 519
FT CHAIN 520 865
FT DISULFID 53 73
FT DISULFID 118 218
FT DISULFID 125 209
FT DISULFID 130 157
FT DISULFID 231 260
FT DISULFID 241 252
FT DISULFID 309 343
FT DISULFID 389 452
FT DISULFID 396 425
FT DISULFID 87 87
FT CARBOHYD 129 129
FT CARBOHYD 136 136
FT CARBOHYD 139 139
FT CARBOHYD 156 156
FT CARBOHYD 193 193
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FT CARBOHYD 198 198
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FT CARBOHYD 407 407
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FT CARBOHYD 418 418
FT CARBOHYD 455 455
FT CARBOHYD 471 471
FT CARBOHYD 620 620
FT CARBOHYD 625 625
FT CARBOHYD 634 634
FT CARBOHYD 646 646
FT CARBOHYD 825 825
SQ SEQUENCE 865 AA: 97809 MW: 28828BC2314ADCAC CRC64;

Query Match 91.9%; Score 181; DB 1; Length 865;
Best Local Similarity 86.18%; Pred. No. 1,2e-14;
Matches 31; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 36
Db 647 YTGILHSILIESONOQEKNEQELLELDKWSLWNMF 682

RESULT 14
ENV_HV1S3 STANDARD: PRT: 852 AA.
ID ENV_HV1S3 STANDARD: PRT: 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
ON NCBI_TaxID=11690;
PN [1]
SEQUENCE FROM N.A.
MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

```



DR Pfam: PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 FT SIGNAL 1 30  
 FT CHAIN 512 856  
 FT DISULFID 34 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 236 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
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 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
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 FT CARBOHYD 366 366  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
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 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MW; 5FCBIDLC3C1209B3 CRC64;

Query Match  
 Best Local Similarity 92.4%; Score 182; DB 1; Length 856;  
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGILSLIEESONOEKNEDELLEDKANSLMNM 35  
 DB 638 YTSLSLIEESONOEKNEDELLEDKANSLMNM 672

RESULT 10  
 ENV\_HVISC STANDARD; PRT; 856 AA.  
 AC P05678;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.,  
 RL "Envelope sequences of two new United States HIV-1 isolates";  
 CC Virology 164:531-536(1988).  
 CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
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 CC -----  
 CC DR PIR: M17450; NOT\_ANNOTATED\_CDS.  
 CC DR PIR: B28922; VCLJSC.  
 DR HIV; M17450; ENV5SC.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
 FT SIGNAL 1 29  
 FT CHAIN 30 510  
 FT SITE 511 856  
 FT SITE 760 760  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 160  
 FT DISULFID 219 247  
 FT DISULFID 228 239  
 FT DISULFID 236 330  
 FT DISULFID 376 439  
 FT DISULFID 383 412  
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 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97055 MW; DAF4DA600DBA7A08 CRC64;

Query Match  
 Best Local Similarity 91.7%; Score 182; DB 1; Length 856;  
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 853 AA; 96912 MW; 3377B93B6F22ABA CRC64;

Query Match 95.4%; Score 188; DB 1; Length 853;
Best Local Similarity 94.4%; Pred. No. 1,6e-15;
Matches 34; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESONQOEKNEDELLELDKWSLMMNF 36
|||||:|||||:|||||:|||||:|||||:
636 YTSILHSLEESONQOEKNEDELLELDKWSLMMNF 671

RESULT 8
ENV_HV1S1 STANDARD; PRT; 847 AA.
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11691;
RN [1]
RP MEDLINE=90347835; PubMed=2384920;
RX Cheng-Mayer C., Outroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
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CC -----
CC EMBL M55024; AAA45072.1;
DR HIV; M38428; ENV5SFI62;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.

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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 0A901317ED7FE2AB CRC64;

Query Match 92.4%; Score 182; DB 1; Length 847;
Best Local Similarity 91.7%; Pred. No. 8,6e-15;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESONQOEKNEDELLELDKWSLMMNF 36
|||||:|||||:|||||:|||||:|||||:
629 YTNILYTLIEESONQOEKNEDELLELDKWSLMMNF 664

RESULT 9
ENV_HV1PV STANDARD; PRT; 856 AA.
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11700;
RN [1]
RP MEDLINE=85111157; PubMed=2982104;
RX Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
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CC -----
CC EMBL K02083; AAB59873.1;
DR EMBL; X01762; CA25903.1; ALT_SEQ.
DR PIR; A03974; VCLPV2.
DR HIV; K02083; ENVSPV22.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

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Query Match          97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6.8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 YTGILHSLEESQNOEKNEDELIDKWSLIMNF 36
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DB 638 YTSILHSLEESQNOEKNEDELIDKWSLIMNF 673

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RESULT 5
ENV_HVILW STANDARD; PRT; 856 AA.
ID ENV_HVILW
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OC Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OX Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=82834;

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RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
   Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
   infected with HIV type 1 (HIV type IIIB)."
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

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CC -----
CC EMBL: U12055; AAA76690.1;
DR GLYCOsuiteDB: Q70626;
DR InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
   Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match          97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6.8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

OY 1 YTGILHSLEESQNOEKNEDELIDKWSLIMNF 36
    ||||||||||||||||||||||||||||
DB 638 YTSILHSLEESQNOEKNEDELIDKWSLIMNF 673

```

```

RESULT 6
ENV_HVILW STANDARD; PRT; 861 AA.
ID ENV_HVILW
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
   glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OC Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OX Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN NCBI_TaxID=11686;

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[illegible]

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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 851 AA; 96644 MW; D16A3C9085785F1 CRC64;

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Query Match 97.0%; Score 191; DB 1; Length 851;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNF 36
Db 633 YTSILHSLEESONQOEKNEDELLELDKWSLWNF 668

```

```

RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
ID ENV_HV1B1
AC P03375;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
NCBI_TaxID=11678;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; Pubmed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
Baumleister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
Lautenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
Wong-Staal F.;
"Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Nature 313:277-284 (1985).
RL Nature 313:277-284 (1985).
RN [12]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; Pubmed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
Gregory T.J.;
"Assignment of intrachain disulfide bonds and characterization of
potential glycosylation sites of the type 1 recombinant human
immunodeficiency virus envelope glycoprotein (gp120) expressed in
Chinese hamster ovary cells.";
J. Biol. Chem. 265:10373-10382 (1990).
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```

CC EMBL: M15654; AAA44205.1; -.
DR PIR: A03973; VCLJH3.
DR HIV: M15654; ENV5BH102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
Signal.
FT SIGNAL 1 30
FT CHAIN 512 856
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 366 366
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 625 625
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFPB1A8931BB27 CRC64;

```

```

Query Match 97.0%; Score 191; DB 1; Length 856;
Best Local Similarity 97.2%; Pred. No. 6,8e-16;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 YTGILHSLEESONQOEKNEDELLELDKWSLWNF 36
Db 638 YTSILHSLEESONQOEKNEDELLELDKWSLWNF 673

```

```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
ID ENV_HV1H2
AC P04578; 009779;

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GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:39 ; Search time 6.07229 Seconds

(without alignments)  
245.895 Million cell updates/sec

Title: US-09-623-533a-534

Perfect score: 197  
Sequence: 1 YTGIIHSLIEESQNOEKNEQELLEDRKWSLIMWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	191	97.0	851	1	ENV_HV1B8
2	191	97.0	856	1	ENV_HV1B1
3	191	97.0	856	1	ENV_HV1H2
4	191	97.0	856	1	ENV_HV1H3
5	191	97.0	856	1	ENV_HV1LW
6	191	97.0	861	1	ENV_HV1BR
7	188	95.4	853	1	ENV_HV1MF
8	182	92.4	847	1	ENV_HV1SL
9	182	92.4	856	1	ENV_HV1PV
10	182	92.4	856	1	ENV_HV1SC
11	182	92.4	856	1	ENV_HV1W1
12	181	91.9	853	1	ENV_HV1EL
13	181	91.9	865	1	ENV_HV1RH
14	180	91.4	852	1	ENV_HV1S3
15	180	91.4	853	1	ENV_HV1Z2
16	180	91.4	855	1	ENV_HV1Z6
17	178	90.4	846	1	ENV_HV1ND
18	176	89.3	847	1	ENV_HV1W2
19	175	88.8	855	1	ENV_HV1A2
20	175	88.8	867	1	ENV_HV1J3
21	173	87.8	856	1	ENV_HV1M1
22	173	87.8	859	1	ENV_HV1M2
23	172	87.3	843	1	ENV_HV1M4
24	171	86.8	855	1	ENV_HV1OY
25	169	85.8	852	1	ENV_HV1BN
26	168	85.3	848	1	ENV_HV1JR
27	168	85.3	863	1	ENV_HV1Z8
28	167	84.8	861	1	ENV_HV1KB
29	162	82.2	868	1	ENV_HV1C4
30	157	79.7	854	1	ENV_HV1C2
31	147	74.6	856	1	ENV_HV1ZH
32	93	47.2	854	1	ENV_HV1AT
33	86	43.7	881	1	ENV_HV1MK

34	86	43.7	882	1	ENV_HV1M1	P05885 simian immu
35	85	43.1	885	1	ENV_HV1S4	P12492 simian immu
36	84	42.6	859	1	ENV_HV2D2	P15831 human immu
37	84	42.6	860	1	ENV_HV2BE	P18094 human immu
38	82	41.6	880	1	ENV_HV1ML	P11267 simian immu
39	80	40.6	859	1	ENV_HV2CA	P24105 human immu
40	80	40.6	889	1	ENV_HV2SP	P19503 simian immu
41	79	40.1	768	1	ENV_HV1A1	P27957 simian immu
42	78	39.6	877	1	ENV_HV1AG	P27977 simian immu
43	77	39.1	846	1	ENV_HV2SB	P12449 human immu
44	77	39.1	851	1	ENV_HV2D1	P17755 human immu
45	77	39.1	851	1	ENV_HV2G1	P18040 human immu

## ALIGNMENTS

RESULT 1	ID	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582;				
DT	13-AUG-1987 (rel. 05, Created)				
DT	13-AUG-1987 (rel. 05, Last sequence update)				
DT	15-JUL-1999 (rel. 38, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
DE	ENV.				
GN	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).				
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.				
OX	NCBI_TaxID=11684;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8511123; Pubmed=2578615;				
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starich B.R., Josephs S.F., Doran F.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff U., Pettey S.R., Pearson M.L., Lautenberger J.A., Papas T.S., Ghayab S.J., Chang N.T., Gallo R.C., Wong-Staal F.;				
RA	*Complete nucleotide sequence of the AIDS virus, HTLV-III.*;				
RT	Nature 313:277-284(1985).				
RL	-----				
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CC	-----				
DR	EMBL: K02011; AAA44661.1; -				
DR	HIV: K02011; ENV5B8.				
DR	GLCOSUitedB: P04582; -				
DR	InterPro: IPR000328; Env-GP41.				
DR	InterPro: IPR000777; GP120.				
DR	Pfam: PF00516; GP120; 1.				
DR	Pfam: PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	506		EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	507	851			TRANSMEMBRANE GLYCOPROTEIN.
FT	CHAIN	507	851		
FT	DISULFID	54	74		BY SIMILARITY.
FT	DISULFID	119	205		BY SIMILARITY.
FT	DISULFID	126	196		BY SIMILARITY.
FT	DISULFID	131	157		BY SIMILARITY.
FT	DISULFID	218	247		BY SIMILARITY.
FT	DISULFID	228	239		BY SIMILARITY.
FT	DISULFID	296	331		BY SIMILARITY.
FT	DISULFID	378	440		BY SIMILARITY.
FT	DISULFID	385	413		BY SIMILARITY.
FT	CARBOHYD	88	88		N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	136	136		N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT	CARBOHYD	141	141		N-LINKED (GLCNAC. . . ) (POTENTIAL).

Db 78 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 113

RESULT 15

ID O9QIWO PRELIMINARY: PRT: 122 AA.  
 AC O9QIWO;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses: Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GP41ERRJ1;  
 RC Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,  
 Machado E., de Sa C.A.M., Eyer W., Passioni L.F.C., Menezes J.A.,  
 Calzans A.R., Tanuri A.;  
 RT "Genotyping and phenotyping analysis of B and non-B Human  
 immunodeficiency virus type 1 subtypes from patients under HAART";  
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF165544; AAF08489.1; -  
 DR InterPro: IPR000328; Env\_GP41.  
 DR pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 122  
 SO SEQUENCE 122 AA; 14716 MW; CB39CE85DADE28FE CRC64;  
  
 Query Match 95.9%; Score 189; DB 15; Length 122;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 36  
 Db 78 YTGIIYSLEESQNOEKNEQELLELDKWSLWNMF 113

Search completed: May 16, 2003, 11:19:47  
 Job time : 27.3124 secs

RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 RA Sodroski J.G.:  
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 RT responsible for the pathogenicity of a multiply passaged simian-human  
 RT immunodeficiency virus (SHV-HXB2)."  
 RL J. Virol. 73:976-984(1999).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.:  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF041850; AAD12142.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73639 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSHLSIESONOEKNEDELLELDKWSLWMP 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.:  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates."  
 RT Virology 174:103-116(1990).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MCK1;  
 RA Iwatani Y.:  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSHLSIESONOEKNEDELLELDKWSLWMP 673

## RESULT 13

O74090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RX MEDLINE=90101366; PubMed=1688473;  
 RA Cloyd M.W., Moore B.E.:  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 RT (HIV-1) Isolates."  
 RT Virology 174:103-116(1990).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PM213;  
 RA Iwatani Y.:  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 97.0%; Score 191; DB 15; Length 856;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEDELLELDKWSLWMP 36  
 DB 638 YTSLSHLSIESONOEKNEDELLELDKWSLWMP 673

## RESULT 14

ID 09YXR6 PRELIMINARY; PRT; 122 AA.  
 AC 09YXR6;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE Envelope glycoprotein immunodominant region (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RJ96BRP004;  
 RA Tanuri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,  
 RA Costa L.J., Telles J.G., Brindeiro R., Schable C., Plenzazek D.,  
 RA Rayfield M.:  
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."  
 RT Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF034037; AAC79289.1; -  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP41; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW Transmembrane.  
 FT NON\_TER 1 1  
 FT NON\_TER 122 122  
 SQ SEQUENCE 122 AA; 14702 MW; 873C9A28AE14BA78 CRC64;

Query Match 95.9%; Score 189; DB 15; Length 122;  
 Best Local Similarity 94.4%; Pred. No. 1.1e-15;  
 Matches 34; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEDELLELDKWSLWMP 36

RT Infected with HIV type 1 (HTLV type IIB).";  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LM90-2;  
 RA Mulder K.E.;  
 RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U12053; AAA7665.1;  
 DR EMBL: U12036; AAA7667.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
 KW Transmembrane.  
 SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;

Query Match 97.0%; Score 191; DB 15; Length 852;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESONQOEKNEQLLELDKASLWNMF 36  
 634 YTSILHSLEESONQOEKNEQLLELDKASLWNMF 669

RESULT 9  
 ID 085582 PRELIMINARY; PRT; 854 AA.  
 AC 085582;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope polypeptide.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 RA Martin M.A.;  
 RA "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone.";  
 RT J. Virol. 59:284-291(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;  
 RA Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Buckler C.E.;  
 RA Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92219406; PubMed=1373204;  
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T  
 RT lymphocytes.";  
 RT J. Virol. 66:3151-3154(1992).  
 DR EMBL: M19921; AAA44992.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 KW SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 97.0%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;

Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESONQOEKNEQLLELDKASLWNMF 36  
 636 YTSILHSLEESONQOEKNEQLLELDKASLWNMF 671

RESULT 10  
 ID 072502 PRELIMINARY; PRT; 854 AA.  
 AC 072502;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE ENV polypeptide.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NL4-3;  
 RC MEDLINE=96036482; PubMed=7483282;  
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
 RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
 RT from primary virus cultures using the polymerase chain reaction.";  
 RT J. Virol. 69:80-86(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NL4-3;  
 RC MEDLINE=86281827; PubMed=3016298;  
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
 RA Martin M.A.;  
 RA "Production of acquired immunodeficiency syndrome-associated  
 RT retrovirus in human and nonhuman cells transfected with an infectious  
 RT molecular clone.";  
 RT J. Virol. 59:284-291(1986).  
 DR EMBL: U26942; AAB60578.1;  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 FT CONFLICT 214 H -> L (IN REF. 2).  
 FT CONFLICT 530 A -> S (IN REF. 2).  
 FT CONFLICT 739 G -> D (IN REF. 2).  
 SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 854;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 YTGILHSLEESONQOEKNEQLLELDKASLWNMF 36  
 636 YTSILHSLEESONQOEKNEQLLELDKASLWNMF 671

RESULT 11  
 ID 092877 PRELIMINARY; PRT; 856 AA.  
 AC 092877;  
 DT 01-NOV-1998 (TRENBLREL. 08, Created)  
 DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Simian-human immunodeficiency virus.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=57667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99098984; PubMed=9882298;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW852;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12031; AAA76667.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA: 84894 MW: 8830AB94013B45A CRC64:  
 Query Match 97.0%; Score 191; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 36  
 DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMP 673

RESULT 6  
 ID 070608 PRELIMINARY: PRT: 752 AA.  
 AC 070608;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW87-2;  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 752  
 SEQUENCE 752 AA: 84780 MW: 708672A2D0C0E8F8 CRC64:

Query Match 97.0%; Score 191; DB 15; Length 752;  
 Best Local Similarity 97.2%; Pred. No. 4e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 36  
 DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMP 673

DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMP 673

RESULT 7  
 ID 078243 PRELIMINARY: PRT: 851 AA.  
 AC 078243;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Env polypotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,  
 RA Verani P., Rossi G.B.;  
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
 chronically infected HUT-78 cellular clone."  
 RL J. Viral Diseases 1:40-55(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89352106; PubMed=2765297;  
 RA Federic M., Tilti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Macchi B., Mangiano N., Verani P., Rossi G.;  
 RT "Biological and molecular characterization of producer and non  
 producer clones from HUT-78 infected with a patient HIV isolate."  
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Tilti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
 RA Borselli A., Saggio I., Verani P., Rossi G.;  
 RT "Variability of HIV-1 virus: characteristics of an infected but not  
 productive clone."  
 RL Int. J. Immunopharmacol. 3:17-23(1990).  
 DR EMBL: Z11530; CAA77628.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 851  
 SEQUENCE 851 AA: 96630 MW: 1A3767B9B7E98027 CRC64:

Query Match 97.0%; Score 191; DB 15; Length 851;  
 Best Local Similarity 97.2%; Pred. No. 4.5e-15;  
 Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 36  
 DB 638 YTSILHSLEESQNOEKNEQELLELDKWSLWMP 668

RESULT 8  
 ID 089797 PRELIMINARY: PRT: 852 AA.  
 AC 089797;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LW90-2;  
 RX MEDLINE=95127297; PubMed=7826699;  
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
 RT "Viral variability and serum antibody response in a laboratory worker  
 infected with HIV type 1 (HIV type IIB)."  
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Mulder K.E.;  
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U12035; AAA76670.1;  
 DR InterPro: IPR000328; Env\_GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
 NON\_TER 852  
 SEQUENCE 852 AA: 96630 MW: 1A3767B9B7E98027 CRC64:

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RESULT 2
O70607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DR 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RX MEDLINE-95127297; PubMed-7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RX Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12034; AAA76669.1;
DR InterPro: IPR000328; Env-GP41.
DR Pfam: PF00516; GP120.1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64;

Query Match 97.0%; Score 191; DB 15; Length 747;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEOELLELDKWSLWNMF 36
DB 633 YTSLSHSLEESONOEKNEOELLELDKWSLWNMF 668

RESULT 3
O70606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DR 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RX MEDLINE-95127297; PubMed-7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM881;
RX Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12032; AAA76668.1;

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DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
RW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA: 84224 MW: 56BEDF186C67694B CRC64;

Query Match 97.0%; Score 191; DB 15; Length 748;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEOELLELDKWSLWNMF 36
DB 634 YTSLSHSLEESONOEKNEOELLELDKWSLWNMF 669

RESULT 4
O70604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DR 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RX MEDLINE-95127297; PubMed-7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
  Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
  "Viral variability and serum antibody response in a laboratory worker
  infected with HIV type 1 (HIV type IIB).";
  AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RX Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12030; AAA76666.1;
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
RW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64;

Query Match 97.0%; Score 191; DB 15; Length 752;
Best Local Similarity 97.2%; Pred. No. 4e-15;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YTGILHSLEESONOEKNEOELLELDKWSLWNMF 36
DB 638 YTSLSHSLEESONOEKNEOELLELDKWSLWNMF 673

RESULT 5
O70605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DR 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
ENV Envelope glycoprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 26.241 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-534

Perfect score: 197  
Sequence: 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	97.0	645	15	0993A6 human immun
2	191	97.0	747	15	070607 human immun
3	191	97.0	748	15	070606 human immun
4	191	97.0	752	15	070604 human immun
5	191	97.0	752	15	070605 human immun
6	191	97.0	752	15	070608 human immun
7	191	97.0	851	15	078243 human immun
8	191	97.0	852	15	089797 human immun
9	191	97.0	854	15	085582 human immun
10	191	97.0	854	15	072502 human immun
11	191	97.0	856	15	092877 simian-huma
12	191	97.0	856	15	074599 human immun
13	191	97.0	856	15	074090 human immun
14	189	95.9	122	15	09YXR6 human immun
15	189	95.9	122	15	09Q1W0 human immun
16	188	95.4	122	15	09YXR2 human immun

17	188	95.4	122	15	09YXP0 human immun
18	188	95.4	122	15	091JR0 human immun
19	188	95.4	122	15	091JO3 human immun
20	188	95.4	122	15	091JP2 human immun
21	188	95.4	357	15	078119 human immun
22	188	95.4	843	15	070008 human immun
23	188	95.4	847	15	069996 human immun
24	188	95.4	854	15	040222 human immun
25	188	95.4	855	15	080367 human immun
26	188	95.4	859	15	097013 human immun
27	187	94.9	851	15	0994B6 human immun
28	187	94.9	854	15	090178 human immun
29	187	94.9	854	15	078705 human immun
30	186	94.4	122	15	09YXP1 human immun
31	186	94.4	122	15	091JN5 human immun
32	186	94.4	123	15	09EAA3 human immun
33	186	94.4	727	15	090KJ3 human immun
34	186	94.4	789	15	090KJ4 human immun
35	186	94.4	837	15	090KJ5 human immun
36	186	94.4	837	15	090KJ5 human immun
37	186	94.4	852	15	092761 human immun
38	186	94.4	852	15	073303 human immun
39	186	94.4	854	15	065566 human immun
40	186	94.4	856	15	090SM7 human immun
41	186	94.4	861	15	056109 human immun
42	185	93.9	122	15	0901V1 human immun
43	185	93.9	122	15	091JN6 human immun
44	185	93.9	127	15	09YXX0 human immun
45	185	93.9	129	15	09YXZ5 human immun

## ALIGNMENTS

Result 1	0993A6	PRELIMINARY:	PRT:	645 AA.
ID	0993A6			
AC	0993A6			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Truncated envelope glycoprotein (fragment).			
GN	ENV.			
OS	Human immunodeficiency virus type 1.			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11676;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=1007;			
RX	MEDLINE=21192672; PubMed=11287644;			
RA	Suman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,			
RA	White S.W., Doherty P.C., Hurwitz J.L.;			
RT	"Localization of CD4+ T cell epitope hotspots to exposed strands of			
RT	HIV envelope glycoprotein suggests structural influences on antigen			
RT	processing."			
RT	Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).			
RL	EMBL: AF321563; AAK18810.1;			
DR	InterPro: IPR000328; Env-GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
KW	AIDS; Coat protein; Envelope protein; glycoprotein; Polypeptide;			
KW	Transmembrane.			
FT	NON_TER			
FT	SEQUENCE 1 1			
FT	645 AA: 72485 MW: B076514BE93362EC CRC64:			
Query Match	97.0%;	Score 191;	DB 15;	Length 645;
Best Local Similarity	97.2%;	Pred. No. 3.4e-15;		
Matches	35;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

QY 1 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 36  
DB 607 YTGILHSLEESQNOEKNEQELLELDKWSLWMP 642

GenCore version 5.1.4.p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 10:53:24 ; Search time 29.753 Seconds  
(without alignments)  
147.792 Million cell updates/sec

Title: US-09-623-533A-119  
Perfect score: 179  
Sequence: 1 LHSLEESQNOEKNEQELLEDKWASLWNMF 33

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	179	100.0	33	16 AAR64395	DP-178 homologue 6
2	179	100.0	33	21 AAB52685	T20/DP178 peptide
3	179	100.0	33	21 AAB52819	T716 peptide fragm
4	179	100.0	33	21 AAB14658	HIV-1 isolate LAI
5	179	100.0	33	21 AAY8710	Core polypeptide f
6	179	100.0	33	21 AAY8390	Core polypeptide f
7	179	100.0	33	22 ABB00069	Viral DP178/107-11
8	179	100.0	33	22 ABB00635	Viral DP178/107-11
9	179	100.0	33	22 ABB00798	Viral DP178/107-11
10	179	100.0	33	22 ABB01534	Viral core polypep

11	179	100.0	33	22 ABB02112	Viral core polypep
12	179	100.0	33	22 ABB02274	Viral core polypep
13	179	100.0	33	22 AAU12618	DP178-11ke/DP107-1
14	179	100.0	33	22 AAU13183	DP178-11ke/DP107-1
15	179	100.0	33	22 AAU13344	DP178-11ke/DP107-1
16	179	100.0	33	22 AAB77065	Core polypeptide T
17	179	100.0	33	22 AAB77630	Core polypeptide T
18	179	100.0	33	22 AAB77791	Core polypeptide T
19	179	100.0	33	22 AAB54932	Anti-HIV peptide D
20	179	100.0	34	16 AAR64396	DP-178 homologue 6
21	179	100.0	34	21 AAB52686	T20/DP178 peptide
22	179	100.0	34	21 AAB14659	HIV-1 isolate LAI
23	179	100.0	34	21 AAY8389	Core polypeptide f
24	179	100.0	34	22 ABB00797	Viral DP178/107-11
25	179	100.0	34	22 ABB02273	Viral core polypep
26	179	100.0	34	22 AAU13343	DP178-11ke/DP107-1
27	179	100.0	34	22 AAB77790	Core polypeptide T
28	179	100.0	34	22 AAB54933	Anti-HIV peptide D
29	179	100.0	35	16 AAR64397	DP-178 homologue 6
30	179	100.0	35	21 AAB52687	T20/DP178 peptide
31	179	100.0	35	21 AAB14670	HIV-1 isolate LAI
32	179	100.0	35	21 AAY8388	Core polypeptide f
33	179	100.0	35	22 ABB00634	Viral DP178/107-11
34	179	100.0	35	22 ABB00796	Viral DP178/107-11
35	179	100.0	35	22 ABB02111	Viral core polypep
36	179	100.0	35	22 ABB02272	Viral core polypep
37	179	100.0	35	22 AAU13382	DP178-11ke/DP107-1
38	179	100.0	35	22 AAU13342	DP178-11ke/DP107-1
39	179	100.0	35	22 AAB77629	Core polypeptide T
40	179	100.0	35	22 AAB77789	Core polypeptide T
41	179	100.0	35	22 AAB54934	Anti-HIV peptide T
42	179	100.0	35	16 AAR64364	DP-178 derived fro
43	179	100.0	35	17 AAR8338	DP178 corresponds
44	179	100.0	36	18 AAU17011	HIV-1 derived pept
45	179	100.0	36	19 AAT22912	SEQ ID NO. 108 fro

#### ALIGNMENTS

RESULT 1  
AAR64395 standard; Peptide: 33 AA.

ID	Score	Query Match	Length DB	ID	Description
1	179	100.0	33	16 AAR64395	DP-178 homologue 64 derived from HIV-1 has antiviral activity.
2	179	100.0	33	21 AAB52685	antiviral activity: DP-178: DP-107: diagnostic: HIV-1LAI:
3	179	100.0	33	21 AAB52819	human immunodeficiency virus: transmembrane protein; gp41;
4	179	100.0	33	21 AAB14658	alpha helix; leucine zipper; DP-185.
5	179	100.0	33	21 AAY8710	Synthetic.
6	179	100.0	33	21 AAY8390	Key
7	179	100.0	33	22 ABB00069	Modified-site
8	179	100.0	33	22 ABB00635	Modified-site
9	179	100.0	33	22 ABB00798	Modified-site
10	179	100.0	33	22 ABB01534	Modified-site

Location/Qualifiers  
/note- "optionally has an amino, acetyl, 9-fluorenylmethoxy-carbonyl, hydrophobic or macromolecular carrier gp. attached"

Modified-site 33 /note- "optionally has a carboxyl, amido, hydrophobic or macromolecular carrier gp. attached"

W09428920-A.  
22-DEC-1994.  
07-JUN-1994; 94WO-US05739.  
07-JUN-1993; 93US-0073028.

PA (UYDU-) UNIV DUKE.  
XX  
PI Barney SO, Bolognesi DP, Lambert DM, Matthews TJ;  
PI Peteway SR, Wild CT;  
XX  
DR WPI: 1995-036105/05.  
XX  
PT Computer search generated synthetic peptides - are inhibitors of  
PT HIV transmission  
XX  
PS Claim 11; Page 133; 182pp; English.  
XX  
CC AAB64365-97 are peptide derivs. of DP-178 (AAR64364) which have been  
CC truncated at the amino terminus. DP-178 corresponds to amino acids  
CC 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It  
CC forms a putative alpha helix at the C-terminal end of the gp41  
CC ectodomain, and complexes with DP-107 (corresponds to amino acids  
CC 538-593) which contains a leucine zipper motif. The peptides complex  
CC via non-covalent protein-protein interactions, and possess anti-viral  
CC activity. The peptide derivs. were identified by a computer assisted  
CC peptide sequence search. The peptides inhibit transmission to  
CC uninfected cells, and can also be used as type and/or subtype  
CC specific diagnostic tools.  
XX  
SQ Sequence 33 AA;  
XX  
Query Match 100.0%; Score 179; DB 16; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
DB 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
XX  
RESULT 2  
AAB52685  
ID AAB52685 standard; Peptide: 33 AA.  
XX  
AC AAB52685;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE T20/DP178 peptide fragment #63.  
XX  
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemottractant.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX WO20006622-A1.  
XX  
XX 09-NOV-2000.  
XX  
XX 05-MAY-2000; 2000WO-US12371.  
XX  
XX 05-MAY-1999; 99US-0132686.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX WPI: 2000-656493/63.  
XX  
XX Administration of peptide agents with a sequence corresponding to a  
XX partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
XX antagonist is used to modulate inflammation -  
XX  
XX Claim 12; Page 25; 148pp; English.  
XX  
XX The present sequence is a peptide fragment of T20/DP178. T20/DP178 is a  
XX helical segment of the ectodomain of HIV-1 protein gp41. T20/DP178 is

CC located in the carboxyl terminus of the gp41 ectodomain. gp41 plays a  
CC critical role in the fusion of HIV-1 and host cell membranes. T20/DP178  
CC interacts with members of the formyl peptide receptor (FPR) family and  
CC thereby up-regulates an inflammatory response, and acts as a potent  
CC chemottractant and activator of human peripheral blood phagocytes  
CC (but not T cells). The present peptide can be used to modulate an  
CC inflammatory response in a subject.  
XX  
SQ Sequence 33 AA;  
XX  
Query Match 100.0%; Score 179; DB 21; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
DB 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
XX  
RESULT 3  
AAB52819  
ID AAB52819 standard; Peptide: 33 AA.  
XX  
AC AAB52819;  
XX  
DT 23-FEB-2001 (first entry)  
XX  
DE T716 peptide fragment.  
XX  
XX Antinflammatory; T20/DP178; gp41 ectodomain; HIV-1 fusion; T21/DP107;  
XX formyl peptide receptor family; FPR; inflammatory response up-regulation;  
XX chemottractant.  
XX  
XX Human immunodeficiency virus type 1.  
XX  
XX WO20006622-A1.  
XX  
XX 09-NOV-2000.  
XX  
XX 05-MAY-2000; 2000WO-US12371.  
XX  
XX 05-MAY-1999; 99US-0132686.  
XX  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Wang JM, Oppenheim JJ, Su S, Gong W, Gao J, Murphy PM;  
XX WPI: 2000-656493/63.  
XX  
XX Administration of peptide agents with a sequence corresponding to a  
XX partial-length T20/DP178 or T21/DP107 formyl peptide receptor  
XX antagonist is used to modulate inflammation -  
XX  
XX Example 1; Page 40; 148pp; English.  
XX  
XX The present invention relates to peptide fragments of T20/DP178 and  
XX T21/DP107 (see AAB52623-B52818 and AAB52823-B52824). T20/DP178 and  
XX CC T21/DP107 are helical segments of the ectodomain of HIV-1 protein gp41.  
XX gp41 plays a critical role in the fusion of HIV-1 and host cell  
XX membranes. T20/DP178 and T21/DP107 interact with members of the formyl  
XX peptide receptor (FPR) family and thereby up-regulate an inflammatory  
XX response, and act as potent chemottractants and activators of human  
XX peripheral blood phagocytes (but not T cells). The peptides of the  
XX present invention can be used to modulate an inflammatory response in a  
XX subject. The present sequence is a peptide isolated in the present  
XX invention.  
XX  
SQ Sequence 33 AA;  
XX  
Query Match 100.0%; Score 179; DB 21; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEQELLELDKWSLWNMF 33  
 |||||||  
 DB 1 LHSLSIESONQOEKNEQELLELDKWSLWNMF 33

RESULT 4  
 AAB14668  
 ID AAB14668 standard; peptide; 33 AA.  
 XX  
 AC AAB14668;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX

DE HIV-1 isolate LAI gp41 C-helical domain peptide P-18, fragment #62.  
 XX

KW HIV-1; gp41 C-helical domain;  
 KW gp41 transmembrane-proximal amphipathic alpha-helical segment;  
 KW core 6-helix bundle; viral entry inhibition; immunogenic;  
 KW antibody; humoral response; broad spectrum vaccine; anti-HIV;  
 KW envelope glycoprotein; prophylaxis; therapy; group M; subtype B;  
 isolate LAI.

OS Human immunodeficiency virus type 1.  
 XX

PN WO200040616-A1.  
 XX

PD 13-JUL-2000.  
 XX

PE 10-JAN-2000; 2000WO-US00456.  
 XX

PR 08-JAN-1999; 9905-0115404.  
 XX

PR 07-JAN-2000; 2000US-0480336.  
 XX

PPA (WILD/) WILD C.F.  
 XX (WEISS/) WEISS C.D.

PI Wild CT, Weiss CD;  
 XX

DR WPI; 2000-465959/40.  
 XX

PT Raising neutralizing antibody response to human immunodeficiency virus,  
 PT comprises administering a polypeptide capable of forming a stable  
 PT coiled-coil solution structure -  
 XX

PS Disclosure: Page 33; 97pp; English.  
 XX

CC Sequences AAB14604-B14606 and AAB14607-B14670 represent peptides derived  
 CC from the C-helical domain of the gp41 envelope glycoprotein from  
 CC HIV-1 group M, subtype B, isolate LAI. The invention relates to raising  
 CC a neutralising antibody response to a broad spectrum of HIV (human  
 CC immunodeficiency virus) strains and isolates, comprising the  
 CC administration of a peptide which corresponds to or mimics highly  
 CC conserved portions of gp41 which are important in mediating the  
 CC process of viral entry into host cells. Such peptides can correspond  
 CC to or mimic the coiled coil solution structure of the N-helical domain  
 CC (the heptad repeat region), or can correspond or mimic the C-helical  
 CC domain (the transmembrane-proximal amphipathic alpha-helical segment),  
 CC or the gp41 core 6-helix bundle, which is formed by the interaction  
 CC of the N- and C-helical domains of three gp41 proteins. The peptides  
 CC can be administered either singly or as a combination (particularly  
 CC a combination of N-helical and C-helical peptides), and can be  
 CC multimerised. For example, N- and C-helical domain peptides can be  
 CC alternately linked together to form a peptide which mimics the core  
 CC 6-helix bundle. Administration of the peptide(s) generates a humoral  
 CC response, with the production of antibodies against gp41 structures  
 CC involved in viral entry. As these portions of gp41 are well conserved,  
 CC such antibodies may be effective against a broad range of HIV strains  
 CC and isolates. The peptide compositions may be administered as a  
 CC prophylactic or therapeutic vaccine to generate antibodies which reduce  
 CC or inhibit the ability of HIV to infect uninfected cells. A composition  
 CC comprising polyclonal or monoclonal antibodies can be administered to  
 CC reduce HIV infection of uninfected cells. Antibodies raised against  
 CC entry-relevant gp41 structures may also be used therapeutically and as

CC tools to further elucidate the mechanism of HIV cell entry.  
 XX  
 SQ Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1,66-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEQELLELDKWSLWNMF 33  
 |||||||  
 DB 1 LHSLSIESONQOEKNEQELLELDKWSLWNMF 33

RESULT 5  
 AAY88710  
 ID AAY88710 standard; peptide; 33 AA.  
 XX  
 AC AAY88710;  
 XX  
 DT 23-MAY-2000 (first entry)  
 XX

DE Core polypeptide fragment T No. 65.  
 XX

KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.  
 XX

OS Unidentified.  
 XX

PN WO9959615-A1.  
 XX

PD 25-NOV-1999.  
 XX

PE 20-MAY-1999; 99WO-US11219.  
 XX

PR 20-MAY-1998; 98US-0082279.  
 XX

PPA (TRIM-) TRIMERIS INC.  
 XX

PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX

DR WPI; 2000-136792/12.  
 XX

PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -  
 XX

PS Disclosure: Page 22; 124pp; English.  
 XX

CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY88651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.  
 CC  
 XX Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1,66-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33  
 |||||||  
 Db 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 6  
 AAY89390  
 ID AAY89390 standard; peptide: 33 AA.

XX AC AAY89390;

XX DT 23-MAY-2000 (first entry)

XX DE Core polypeptide fragment T NO. 925.

XX KW Retrovirus: hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
 KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
 KW anti-fusogenic; differentiation factor; interleukin; interferon;  
 KW colony stimulating factor; hormone; angiogenic factor.

XX Unidentified.

XX PN WO9959615-A1.

XX PD 25-NOV-1999.

XX PF 20-MAY-1999; 99WO-US11219.

XX PR 20-MAY-1998; 98US-0082279.

XX PA (TRIM-) TRIMERIS INC.

XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX DR WPI: 2000-136792/12.

XX PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
 PT comprises enhancer sequence -

XX PS Disclosure; Page 35; 124pp; English.

XX CC The invention relates to hybrid polypeptides comprising enhancer peptide  
 CC sequence linked to core polypeptides. The enhancer polypeptides are  
 CC derived from various retroviral envelope (gp41) protein sequences,  
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
 CC pharmacokinetic properties such as increasing the half-life of any core  
 CC polypeptide that they are linked to. The core polypeptides are any  
 CC polypeptide that may be introduced into a living system and that can  
 CC function as a pharmacologically useful peptide for the treatment or  
 CC prevention of a disease. The core polypeptides are bioactive peptides  
 CC selected from a growth factor, cytokine, differentiation factor,  
 CC interleukin, interferon, colony stimulating factor, hormone or  
 CC angiogenic factor. The peptides of the invention can be used for  
 CC inhibiting viral infection and can be used in anti-viral and  
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core  
 CC polypeptide fragments that can be used in the invention. Some sequences  
 CC among those indicated also comprise enhancer fragments at terminal ends  
 CC and form hybrid polypeptides.

XX SQ Sequence 33 AA:

Query Match 100.0%; Score 179; DB 21; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33  
 |||||||  
 Db 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 7  
 ABB00069  
 ID ABB00069 standard; peptide: 33 AA.

XX ABB00069;

XX DT 03-JAN-2002 (first entry)

XX DE Viral DP178/107-like region peptide T65.

XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW viricide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX OS Viridiae.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal is substituted by Ac"

FT Modified-site 33 /note= "C-terminal amide"

XX PN WO200164013-A2.

XX PD 07-SEP-2001.

XX PF 07-FEB-2001; 2001WO-US03988.

XX PR 29-FEB-2000; 2000US-0515965.

XX PA (TRIM-) TRIMERIS INC.

XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX DR WPI: 2001-514829/56.

XX PT Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection -

XX PS Disclosure; Page 34; 587pp; English.

XX CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
 CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
 CC HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1  
 CC and HR2 regions of proteins interact non-covalently with each other  
 CC and/or with peptides derived from them. This interaction is required for  
 CC normal infectivity of viruses such as RSV and HIV. The heptad  
 CC repeat region peptide analogues may be used to inhibit respiratory  
 CC syncytial virus (RSV) infection in a cell. They may also be used to  
 CC inhibit HIV infection. The present sequence is a peptide provided in  
 CC the specification.

XX SQ Sequence 33 AA:

Query Match 100.0%; Score 179; DB 22; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33  
 |||||||  
 Db 1 LIHSLEESQNOQEKNEQELLELDKWSLWNMF 33

RESULT 8  
 ABB00635  
 ID ABB00635 standard; peptide: 33 AA.

XX AC ABB00635;  
 XX DT 03-JUN-2002 (first entry)

XX DE Viral DP178/107-like region peptide T716.

XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;

KM	vtruncide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
RW	infection.
XX	
OS	Virididae.
FH	Key
FT	Modified-site
FT	1 Location/Qualifiers
FT	/note= "N-terminal is substituted by Ac"
FT	33
FT	/note= "C-terminal amide"
XX	
PN	WO200164013-A2.
PD	
XX	07-SEP-2001.
XX	
PE	07-FEB-2001; 2001WO-US03988.
XX	
PR	29-FEB-2000; 2000US-0515965.
XX	
XX	(TRIM-) TRIMERIS INC.
XX	
DR	Aniczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX	
XX	WPI: 2001-514829/56.
PT	
PT	Heptad repeat region peptide analogs useful for inhibiting virus/cells
PT	fusion, useful for treating HIV and Respiratory Syncytial Virus
PT	infection -
PS	
PS	Disclosure: Page 45; 587pp; English.
XX	
CC	The invention relates to isolated analogues of the heptad repeat region
CC	peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
CC	638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
CC	HRI) respectively, of HIV-1/tat transmembrane protein gp41. The HRI
CC	and HR2 regions of proteins interact non-covalently with each other
CC	and/or with peptides derived from them. This interaction is required for
CC	normal infectivity of viruses such as RSV and HIV. The heptad
CC	repeat region peptide analogues may be used to inhibit respiratory
CC	syncytial virus (RSV) infection in a cell. They may also be used to
CC	inhibit HIV infection. The present sequence is a peptide provided in
CC	the specification.
XX	
SO	Sequence 33 AA:
Query Match	100.0%; Score 179; DB 22; Length 33;
Best Local Similarity	100.0%; Pred. No. 1.6e-15;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
1 LIHSLIESONQEKNEDELLDLKWSLWNMF 33	
1 LIHSLIESONQEKNEDELLDLKWSLWNMF 33	
Db	
RESULT 9	
ABB00798	
ID	ABB00798 standard; Peptide: 33 AA.
XX	
AC	ABB00798;
XX	
DT	03-JAN-2002 (first entry)
XX	
DE	Viral DP178/107-like region peptide T925.
XX	
KW	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW	vtruncide; heptad repeat region; transmembrane protein; gp41; HRI; HR2;
XX	infection.
XX	
OS	Virididae.
XX	
XX	
FT	Key
FT	Modified-site
FT	33 Location/Qualifiers
FT	/note= "C-terminal amide"

```

XX  WO200164013-A2.
PN
XX  07-SEP-2001.
PD
XX  07-FEB-2001; 2001WO-US039988.
PE
XX  29-FEB-2000; 2000US-0515965.
PR
XX  (TRIM-) TRIMERIS INC.
PA
XX  Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
PI
XX  WPI; 2001-514829/56.
DR
XX  HepIad repeat region peptide analogs useful for inhibiting virus/cells
PT  fusion, useful for treating HIV and Respiratory Syncytial Virus
PT  infection -
XX
XX  Disclosure: Page 49; 587pp; English.
PS
XX
XX  The invention relates to isolated analogues of the heptad repeat region
CC  peptides DP178 and DP107. DP178 and DP107 correspond to amino acids
CC  638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region
CC  HR1) respectively, of HIV-1LAI transmembrane protein gp41. The HR1
CC  and HR2 regions of proteins interact non-covalently with each other
CC  and/or with peptides derived from them. This interaction is required for
CC  normal infectivity of viruses such as RSV and HIV. The heptad
CC  repeat region peptide analogues may be used to inhibit respiratory
CC  syncytial virus (RSV) infection in a cell. They may also be used to
CC  inhibit HIV infection. The present sequence is a peptide provided in
CC  the specification.
XX
XX  Sequence 33 AA:
SQ
XX
XX  Query Match 100.0%; Score 179; DB 22; Length 33;
XX  Best Local Similarity 100.0%; Pred. No. 1.0e-15;
XX  Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LIHSLSIESQNOEKNEQELLEDKMASLMMNF 33
DB 1 LIHSLSIESQNOEKNEQELLEDKMASLMMNF 33
XX
XX  RESULT 10
XX  ABB01534
XX  ID ABB01534 standard; Peptide: 33 AA.
XX
XX  ABB01534;
XX
XX  03-JAN-2002 (first entry)
XX
XX  Viral core polypeptide, SEQ ID NO: 61.
DE
XX
XX  Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
KW  vitucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX  infection.
XX
XX  Virididae.
XX  OS
XX  WO200164013-A2.
XX
XX  07-SEP-2001.
XX
XX  07-FEB-2001; 2001WO-US039988.
XX
XX  29-FEB-2000; 2000US-0515965.
XX
XX  (TRIM-) TRIMERIS INC.
XX
XX  Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX  WPI; 2001-514829/56.
XX

```

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
PS Disclosure; Page 182; 587pp; English.  
XX  
CC The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
SQ Sequence 33 AA:  
XX  
Query Match 100.0%; Score 179; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33  
DB 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33  
RESULT 11  
AB02112  
ID AB02112 standard; Peptide: 33 AA.  
XX  
AC ABB02112;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
XX Viral core polypeptide, SEQ ID NO: 639.  
DE  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KM virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KM infection.  
XX  
OS Viridiae.  
XX  
XX WO200164013-A2.  
XX  
XX 07-SEP-2001.  
XX  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
PI  
XX MPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
PS Disclosure; Page 336; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.

CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
SQ Sequence 33 AA:  
XX  
Query Match 100.0%; Score 179; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33  
DB 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33  
RESULT 12  
AB02274  
ID AB02274 standard; Peptide: 33 AA.  
XX  
AC ABB02274;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
XX Viral core polypeptide, SEQ ID NO: 801.  
DE  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KM virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KM infection.  
XX  
OS Viridiae.  
XX  
XX WO200164013-A2.  
XX  
XX 07-SEP-2001.  
XX  
XX 07-FEB-2001; 2001WO-US03988.  
XX  
XX 29-FEB-2000; 2000US-0515965.  
XX  
XX (TRIM-) TRIMERS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
PI  
XX MPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection -  
XX  
PS Disclosure; Page 380; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids  
CC 638-673 (heptad repeat region HR2) and 558-595 (heptad repeat region  
CC HR1) respectively, of HIV-1/IIAI transmembrane protein gp41. The HR1  
CC and HR2 regions of proteins interact non-covalently with each other  
CC and/or with peptides derived from them. This interaction is required for  
CC normal infectivity of viruses such as RSV and HIV. The heptad  
CC repeat region peptide analogues may be used to inhibit respiratory  
CC syncytial virus (RSV) infection in a cell. They may also be used to  
CC inhibit HIV infection. The present sequence is a peptide provided in  
CC the specification.  
XX  
SQ Sequence 33 AA:  
XX  
Query Match 100.0%; Score 179; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33  
DB 1 LHSLIEESONQOEKNEQLELDKWSLWMPF 33



XX	AAU13344 standard; Peptide: 33 AA.
XX	AAU13344;
DT	21-NOV-2001 (first entry)
DE	DP178-1like/DP107-1like peptide T-925.
KM	Anti-retroviral; DP178-1like; DP107-1like; transmembrane protein gp41;
XX	antifusogenic; antiviral; HIV transmission; mutant; mutcin.
OS	Human immunodeficiency virus 1 isolate LAI.
FT	Synthetic.
FT	Key Location/Qualifiers
FT	Modified-site 33 /note= "C-terminal amide"
WO	2000151673-A2.
PD	19-JUL-2001.
PF	05-JUL-2000; 2000WO-US35727.
PR	09-JUL-1999; 99US-0350841.
PA	(TRIM-) TRIMERIS INC.
PI	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
DR	WPI: 2001-442157/47.
PT	Identifying a compound that inhibits the formation of or disrupts a
PT	DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT	or intracellular modulatory activity, by detecting the formation of a
PT	DP107/DP178 complex -
PS	Disclosure: Page 68; 259pp; English.
XX	The present invention relates to peptides which exhibit anti-retroviral
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC	DP178-1like and DP107-1like peptides. The DP178 peptide corresponds
CC	to amino acids 639-673 of the transmembrane protein gp41 from human
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC	corresponds to amino acids 558-596 of gp41 from HIV-1LAI. The invention
CC	also relates to a method of identifying compounds that inhibit the
CC	formation of or disrupts a DP107/DP178 complex. The method comprises
CC	detecting the formation of a DP107/DP178 complex, both in the presence
CC	or absence of a test compound, in a reaction mixture containing DP107
CC	and DP178 peptides. The method is useful for identifying compounds,
CC	including small molecule compounds, which may themselves exhibit
CC	antifusogenic, antiviral or intracellular modulatory activity. The
CC	DP178-1like/DP107-1like peptides are useful to inhibit human and non-human
CC	retroviral, particularly HIV, transmission to uninfected cells. The
CC	present sequence represents one of the DP178-1like/DP107-1like peptides
XX	of the invention.
XX	Sequence 33 AA:
QY	Query Match 100.0%; Score 179; DB 22; Length 33;
DB	Best Local Similarity 100.0%; Pred. No. 1.6e-15;
DB	Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1	LHSLIEESONOEKNEOELLELDKWASIMNMF 33
1	LHSLIEESONOEKNEOELLELDKWASIMNMF 33

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:04:54 ; Search time 11.1325 Seconds  
(without alignments)  
284.970 Million cell updates/sec

Title: US-09-623-533a-119  
Perfect score: 179  
Sequence: 1 LIHSLIEESQNOEKNEQELLELDKWSLMMNF 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
All number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	851	2 S33985	env polypeptin -
2	179	100.0	854	2 S13288	env polypeptin - huma
3	179	100.0	856	1 VCLJH3	env polypeptin pr
4	179	100.0	861	1 VCLJLV	env polypeptin pr
5	170	95.0	357	2 S21994	env polypeptin g
6	170	95.0	357	2 S21996	env polypeptin g
7	170	95.0	443	2 C41621	env polypeptin p
8	170	95.0	856	1 VCLJVL	env polypeptin pr
9	170	95.0	861	1 VCLJW	env polypeptin pr
10	170	95.0	861	1 VCLJSC	env polypeptin pr
11	167	93.3	358	2 S21998	env polypeptin pr
12	166	92.7	847	2 T09448	env polypeptin g
13	166	92.7	847	2 S13289	env polypeptin g
14	164	91.6	357	2 S22004	env polypeptin - huma
15	164	91.6	855	1 VCLJAJ	env polypeptin g
16	162	90.5	445	2 A41621	env polypeptin pr
17	162	90.5	843	1 H44001	env polypeptin M
18	162	90.5	853	1 S54384	env polypeptin pr
19	162	89.5	855	1 VCLJZR	env polypeptin pr
20	161	89.9	357	2 S22005	env polypeptin pr
21	161	89.9	358	2 S22002	env polypeptin g
22	161	88.9	358	2 S22000	env polypeptin g
23	161	88.9	358	2 S70417	env polypeptin g
24	161	89.9	852	2 T12016	env polypeptin g
25	161	89.9	859	1 VCLJMN	env polypeptin pr
26	160	89.4	846	1 VCLJND	env polypeptin pr
27	157	87.7	357	2 S21992	env polypeptin g
28	157	87.7	852	1 VCLJBR	env polypeptin g
29	155	86.6	729	1 VCLJHX	env polypeptin pr

30	155	86.6	859	2 T01672	envelope polypeptin
31	155	86.6	861	1 VCLJKB	env polypeptin pr
32	154	86.0	454	2 B41621	env polypeptin D
33	152	84.9	868	1 VCLJH4	env polypeptin -
34	147	82.1	136	2 J00266	env polypeptin -
35	147	82.1	136	2 J00266	env polypeptin -
36	141	78.8	854	1 VCLJST	env polypeptin pr
37	137	76.5	856	1 A44963	env polypeptin pr
38	131	73.2	357	2 S21990	env polypeptin pr
39	131	73.2	877	2 S49197	envelope protein g
40	115	64.2	863	2 A53034	envelope protein p
41	86	48.0	881	1 VCLJG3	env polypeptin -
42	86	48.0	881	2 S03068	env polypeptin - huma
43	86	48.0	889	1 VCLJG5	env polypeptin - huma
44	85	47.5	151	2 S30448	env polypeptin - huma
45	85	47.5	151	2 S30452	env polypeptin - huma

## ALIGNMENTS

RESULT 1  
S33985  
env polypeptin - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S33985  
R:Carlini, F.  
Submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199  
C:Superfamily: type E retrovirus env polypeptin

Query Match 100.0%; Score 179; DB 2; Length 851;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHSLIEESQNOEKNEQELLELDKWSLMMNF 33  
Db 636 LIHSLIEESQNOEKNEQELLELDKWSLMMNF 668

RESULT 2  
S13288  
env polypeptin - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
C:Superfamily: type E retrovirus env polypeptin

Query Match 100.0%; Score 179; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIHSLIEESQNOEKNEQELLELDKWSLMMNF 33  
Db 639 LIHSLIEESQNOEKNEQELLELDKWSLMMNF 671

RESULT 3  
VCLJH3

```
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran
berger, J.A.; Papas, T.S.; Ghreby, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2576615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
E:1-30/Domain: signal sequence #status predicted <SIG>
E:1-511/Product: exterior membrane glycoprotein #status predicted <TM>
E:1-856/Product: transmembrane glycoprotein #status predicted <TM>
F:18,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,366,392,397,406
F:611,616,623,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESONOEKNEOELELDKWSLWMP 33
DB 641 LHSLSIESONOEKNEOELELDKWSLWMP 673
RESULT 4
VCLUTV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran
berger, J.A.; Papas, T.S.; Ghreby, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2576615
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
E:1-30/Domain: signal sequence #status predicted <SIG>
E:1-316/Product: exterior membrane glycoprotein #status predicted <EXT>
E:1-861/Product: transmembrane glycoprotein #status predicted <TM>
F:18,136,141,156,161,165,191,202,233,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 100.0%; Score 179; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESONOEKNEOELELDKWSLWMP 33
DB 646 LHSLSIESONOEKNEOELELDKWSLWMP 678
RESULT 5
S21994
env polyprotein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
```

```
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994; S70421
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140,'X',142-312,'X',314-357 <STEL>
A:Cross-references: EMBL:X61355; NID:960179
C:Superfamily: type E retrovirus env polyprotein
Query Match 95.0%; Score 170; DB 2; Length 357;
Best Local Similarity 93.9%; Pred. No. 4.7e-13;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESONOEKNEOELELDKWSLWMP 33
DB 142 LVTTLIESONOEKNEOELELDKWSLWMP 174
RESULT 6
S21996
env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:91067129
A:Experimental source: patient 27L
A>Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein
Query Match 95.0%; Score 170; DB 2; Length 357;
Best Local Similarity 93.9%; Pred. No. 4.7e-13;
Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 LHSLSIESONOEKNEOELELDKWSLWMP 33
DB 142 LVTTLIESONOEKNEOELELDKWSLWMP 174
RESULT 7
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polyprotein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
```

A:Molecule type: DNA  
 A:Residues: 1-443 <BUR>  
 A:Cross-references: GB:M77230; NID:g328631; PIDN:AAB03792.1; PID:g555015  
 A:Note: this virus was isolated from the mother's sexual partner  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
 F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>  
 F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>  
 F:424-443/Domain: transmembrane #status predicted <TM>  
 F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match 95.0%; Score 170; DB 1; Length 443;  
 Best Local Similarity 93.9%; Pred. No. 6e-13;  
 Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
 381 LHSLEESONQOEKNEDELLEDKNASLWNMF 413

RESULT 8  
 VCLJVL  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999  
 C:Accession: A03974  
 R:Wensing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
 Nature 313, 450-458, 1985  
 A:Title: Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrov  
 A:Reference number: A93355; MUID:85111157; PMID:2982104  
 A:Accession: A03974  
 A:Molecule type: DNA  
 A:Residues: 1-856 <MUR>  
 A:Cross-references: GB:K02083; NID:g555008; PIDN:AAB59873.1; PID:g328559  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
 F:1-30/Domain: signal sequence #status predicted <Sig>  
 F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
 F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
 F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
 F:611,616,625,637,674,750,816/Binding site: carbohydrate (asn) (covalent) #status predic

Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 96.9%; Pred. No. 1.2e-12;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 32  
 641 LHSLEESONQOEKNEDELLEDKNASLWNMF 672

RESULT 9  
 VCLJ3W  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
 N:Contains: coat protein gp120; coat protein gp41  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 07-Nov-1997  
 C:Accession: A24774  
 R:Starich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
 Cell 45, 637-648, 1986  
 A:Title: Identification and characterization of conserved and variable regions in the en  
 A:Reference number: A24774; MUID:86218077; PMID:2423250  
 A:Accession: A24774  
 A:Molecule type: DNA  
 A:Residues: 1-856 <STA>  
 A:Cross-references: GB:K03455; GB:M38432; NID:g1906382  
 C:Genetics:

A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-501/Product: coat protein gp120 #status predicted <GP1>  
 F:502-847/Product: coat protein gp41 #status predicted <GP2>  
 F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,

Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 93.9%; Pred. No. 1.2e-12;  
 Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
 641 LHSLEESONQOEKNEDELLEDKNASLWNMF 673

RESULT 10  
 VCLJSC  
 env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
 N:Alternate names: coat polyprotein  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Note: host Homo sapiens (man)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
 C:Accession: B28922  
 R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-  
 Virology 164, 531-536, 1988  
 A:Title: Envelope sequences of two new United States HIV-1 isolates.  
 A:Reference number: A28922; MUID:88219542; PMID:3369091  
 A:Accession: B28922  
 A:Molecule type: DNA  
 A:Residues: 1-861 <GUR>  
 C:Genetics:  
 A:Gene: env  
 C:Superfamily: type E retrovirus env polyprotein  
 C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr  
 F:1-29/Domain: signal sequence #status predicted <Sig>  
 F:30-861/Product: env polyprotein #status predicted <EP>  
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,

Query Match 95.0%; Score 170; DB 1; Length 861;  
 Best Local Similarity 93.9%; Pred. No. 1.2e-12;  
 Matches 31; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLEDKNASLWNMF 33  
 646 LHSLEESONQOEKNEDELLEDKNASLWNMF 678

RESULT 11  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C:Species: human immunodeficiency virus type 1, HIV-1  
 A:Variate: Isolate 28  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000  
 C:Accession: S21998; S70425  
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL data library, July 1991  
 A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete  
 A:Reference number: S21990  
 A:Accession: S21998  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STE1>  
 A:Cross-references: EMBL:K61359; NID:g60182; PIDN:CAA43630.1; PID:g60183  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer  
 A:Reference number: S70417; MUID:92144209; PMID:1736940.  
 A:Accession: S70425  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-222, X', 224-358 <STE2>  
 A:Cross-references: EMBL:K61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polypeptide

Query Match 93.3%; Score 167; DB 2; Length 358;

Best Local Similarity 90.9%; Pred. No. 1, 1e-12;

Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLELDKMSLWNF 33

DB 143 LITLIESONQOEKNEDELLELDKMSLWNF 175

RESULT 12

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JFEL)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999

C:Accession: T09448

R:Panig, S.; Vinters, H.V.; Akshat, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:q1465777; PID:q1465781

C:Gene: env

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.7%; Score 166; DB 2; Length 847;

Best Local Similarity 93.8%; Pred. No. 3, 7e-12;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHSLEESONQOEKNEDELLELDKMSLWNF 33

DB 633 IYTLIESONQOEKNEDELLELDKMSLWNF 664

RESULT 13

S13289

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13289; PMID:2172833

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match 92.7%; Score 166; DB 2; Length 847;

Best Local Similarity 93.8%; Pred. No. 3, 7e-12;

Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHSLEESONQOEKNEDELLELDKMSLWNF 33

DB 633 IYTLIESONQOEKNEDELLELDKMSLWNF 664

RESULT 14

S22004

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variety: Isolate 4B

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 01-Dec-2000

C:Accession: S22004; S70419

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi

A:Reference number: S21990

A:Accession: S22004

A:Molecule type: DNA

A:Residues: 1-357 <STEL>

A:Cross-references: EMBL:X61353; NID:q60188; PID:CAA43618.1; PID:q60189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; PMID:92144209; PMID:1736940

A:Accession: S70419

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-292, 'X', 294-357 <STEL>

A:Cross-references: EMBL:X61353; NID:q60188

C:Superfamily: type E retrovirus env polypeptide

Query Match 91.6%; Score 164; DB 2; Length 357;

Best Local Similarity 90.9%; Pred. No. 2, 5e-12;

Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSLEESONQOEKNEDELLELDKMSLWNF 33

DB 142 LITLIESONQOEKNEDELLELDKMSLWNF 174

RESULT 15

VCLJ42

env polypeptide precursor - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: Host Homo sapiens (man)

C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 16-Jul-1999

C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; PMID:85090453; PMID:2578227

A:Accession: A03976

A:Molecule type: DNA

A:Residues: 1-855 <SAN>

A:Cross-references: GB:K02007; NID:q328658; PIDN:AAB59882.1; PID:q328666

C:Gene: env

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; immunodeficiency; poly

F:1-30/Domain: signal sequence #status predicted <Sig>

F:31-509/Product: exterior membrane glycoprotein #status predicted <TM>

F:510-855/Product: transmembrane glycoprotein #status predicted <TM>

F:87,129,140,158,184,190,200,244,265,298,304,334,341,358,364,388,394,400,408,445,

F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.6%; Score 164; DB 1; Length 855;

Best Local Similarity 90.6%; Pred. No. 6, 5e-12;

Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHSLEESONQOEKNEDELLELDKMSLWNF 33

DB 641 IYTLIESONQOEKNEDELLELDKMSLWNF 672

Search completed: May 16, 2003, 11:25:08

Job time: 11.1325 secs



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FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
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SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CR64;

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Query Match 100.0%; Score 179; DB 1; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LHSLSIESQNOOEKNEQELLEDKWSLSLWNP 33
DB 636 LHSLSIESQNOOEKNEQELLEDKWSLSLWNP 668

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```

RESULT 2
ENV_HV1B1 STANDARD; PRT; 856 AA.
AC P03375;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
  glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV
OS Human immunodeficiency virus type 1 (H1D isolate) (HIV-1).
   Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11678;
RA MEDLINE=8511123; PubMed=257815;
RA Ratter L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
  Josephs S.F., Doran P.R., Ratafski J.A., Whitehorn E.A.,
  Baumesister K., Ivanoff L., Peteway S.R. Jr, Pearson M.L.,
  LaTenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
  Wong-Staal F.;
RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284 (1985).
RN [2]
RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=90285159; PubMed=2355006;
RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
  Gregory T.J.;
RT Assignment of intrachain disulfide bonds and characterization of
  potential glycosylation sites of the type 1 recombinant human
  immunodeficiency virus envelope glycoprotein (gp120) expressed in
  Chinese hamster ovary cells.";
RT J. Biol. Chem. 265:10373-10382 (1990).
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```

CC EMBL: M15654; AAA44205.1; -.
DR PIR: A03973; VCL03.
DR HIV: M15654; ENV5BH102.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120_1.
DR Pfam: PF00517; GP41_1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
  Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
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FT DISULFID 385 418
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FT CARBOHYD 637 637
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FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931B827 CR64;

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EXTERIOR MEMBRANE GLYCOPROTEIN.  
TRANSMEMBRANE GLYCOPROTEIN.

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Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1 LHSLSIESQNOOEKNEQELLEDKWSLSLWNP 33
DB 641 LHSLSIESQNOOEKNEQELLEDKWSLSLWNP 673

```

```

RESULT 3
ENV_HV1H2 STANDARD; PRT; 856 AA.
AC P04578; 009779;

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DT	13-AUG-1987	(Rel. 05, Created)	
DT	15-JUL-1999	(Rel. 38, Last sequence update)	
DT	30-MAY-2000	(Rel. 39, Last annotation update)	
DE	Envelope polyprotein	GPI60 precursor [Contains: Exterior membrane glycoprotein (GPI20), Transmembrane glycoprotein (GP41)].	
DE	glycoprotein (GPI20),	Transmembrane glycoprotein (GP41)].	
GN	ENV.		
OS	Human immunodeficiency virus type 1 (Hx2 isolate) (HIV-1).		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_Taxid=11706;		
RL	AIDS Res. Hum. Retroviruses 3:57-69(1987).		
RL	(2)		
RP	REVISIONS.		
RA	Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;		
RT	"Complete nucleotide sequences of functional clones of the AIDS virus."		
CC	AIDS Res. Hum. Retroviruses 3:57-69(1987).		
CC	(2)		
CC	Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.		
CC	-----		
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CC	-----		
DR	EMBL; AF03455; AAB50262.1; -		
DR	EMBL; AF038399; AAB99976.1; -		
DR	EMBL; AF038319; AAC82596.1; -		
DR	HIV; K03455; ENV5HXB2.		
DR	InterPro: IPR000328; Env_GP41.		
DR	InterPro: IPR000777; GP120.		
DR	Pfam; PF00516; GP120; 1.		
DR	Pfam; PF00517; GP41; 1.		
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.		
KW	Signal.		
FT	CHAIN	1	30
FT	CHAIN	512	856
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FT	DISULFID	228	239
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FT	DISULFID	385	418
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FT	DISULFID	385	418
FT	CARBOHYD	88	
FT	CARBOHYD	136	136
FT	CARBOHYD	141	141
FT	CARBOHYD	156	156
FT	CARBOHYD	160	160

FT	CARBOHYD	397	397	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	624	624	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	674	674	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC . .)	(POTENTIAL).
SQ	SEQUENCE	856 AA;	97212 MM;	6FABI6AF85107FFED CRC64;	
 Query Match                    100.0%; Score 179; DB 1; Length 856; Best Local Similarity         100.0%; Pred. No. 1.9e-14; Matches      33; Conservative   0; Mismatches    0; Indels        0; Gaps          0;					
Oy	1 LIHSLIESONQOEKNEQELLELDKWSIMWNF 33       641 LIHSLIESONQOEKNEQELLELDKWSIMWNF 673				
 RESULT 4					
ENV_HV1H3	STANDARD:	PRT:	856 AA.		
ID	ENV_HV1H3				
AC	P04624;				
DT	13-AUG-1987 (Rel. 05, Created)				
DI	01-FEB-1996 (Rel. 33, Last sequence update)				
DI	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (Hx83 isolate) (HIV-1).				
CC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.				
CO	NCBI_TaxID=11707;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=85226248; PubMed=2988795;				
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;				
RT	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";				
RL	Cell 41:979-986(1985).				
CC	-----				
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CC	-----				
DR	EMBL; M14100; AAA44679.1; -				
DR	HIV; M14100; ENVSHXB3.				
DR	InterPro; IPR000328; Env_GP41.				
DR	InterPro; IPR007777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.				
FT	SIGNAL	1	30		
FT	CHAIN	31	511	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFD	119	205	BY SIMILARITY.	
FT	DISULFD	126	196	BY SIMILARITY.	
FT	DISULFD	131	157	BY SIMILARITY.	
FT	DISULFD	218	247	BY SIMILARITY.	
FT	DISULFD	228	239	BY SIMILARITY.	
FT	DISULFD	296	331	BY SIMILARITY.	
FT	DISULFD	378	445	BY SIMILARITY.	
FT	DISULFD	385	418	BY SIMILARITY.	
FT	CARBOHYD	88	88	N-LINKED (GLCNAC . .) (POTENTIAL).	
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . .) (POTENTIAL).	

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FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373688B84C1AFC CRC64;

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Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LHSLSIESONOEKNEDELLDKWASLMMNF 33
DB 641 LHSLSIESONOEKNEDELLDKWASLMMNF 673

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RESULT 5
ENV_HVILM STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.

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OC Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OX Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=82834;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)".
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U12055; AAA76690.1; -
DR GLYCSuiteDB: Q70626;
DR InterPro: IPR000328; Env_GP41.

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DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7E6687 CRC64;

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Query Match 100.0%; Score 179; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LHSLSIESONOEKNEDELLDKWASLMMNF 33
DB 641 LHSLSIESONOEKNEDELLDKWASLMMNF 673

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RESULT 6
ENV_HVILM STANDARD; PRT; 861 AA.
AC P03377;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
ENV.
OC Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OX Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11686;
RN [1]

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FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA: 96912 MW: 3377B93B6F22ABA CRC64:

Query Match
Best Local Similarity 98.3%: Score 176: DB 1: Length 853:
Matches 32: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

1 LHSLSIESQNOQEKNEDELLEDKWASLWNMF 33
639 LHSLSIESQNOQEKNEDELLEDKWASLWNMF 671

RESULT 8
ENV_HV1SV1 STANDARD: PRT; 847 AA.
ID ENV_HV1SV1
AC P19550:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11691;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=90347635; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
RL J. Virol. 64:4390-4398(1990).
CC
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CC -----
DR EMBL: M65024; AAA5072.1; -
DR HIV: M38428; ENV5SF162.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR AIDS: PF00517; GP41; 1.
KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
KM
FT SIGNAL 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 338 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 381 408 BY SIMILARITY.

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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA: 96135 MW: 0A901317FD7FE2AB CRC64:

Query Match
Best Local Similarity 95.0%: Score 170: DB 1: Length 847:
Matches 31: Conservative 2: Mismatches 0: Indels 0: Gaps 0:

1 LHSLSIESQNOQEKNEDELLEDKWASLWNMF 33
632 LHSLSIESQNOQEKNEDELLEDKWASLWNMF 664

RESULT 9
ENV_HV1PV STANDARD: PRT; 856 AA.
ID ENV_HV1PV
AC P03376:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;
RT "Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC
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CC -----
DR EMBL: K02083; AAB59873.1; -
DR EMBL: X01762; CAA25903.1; ALT_SEQ.
DR PIR: A03974; VCLIVL.
DR HIV: K02083; ENV5PV22.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.

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DR Pfam: PF00517; GP41; 1.  
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 511  
 FT CHAIN 512 856  
 FT DISULFID 54 74  
 FT DISULFID 119 205  
 FT DISULFID 126 196  
 FT DISULFID 131 157  
 FT DISULFID 218 247  
 FT DISULFID 228 239  
 FT DISULFID 296 331  
 FT DISULFID 378 445  
 FT DISULFID 385 418  
 FT CARBOHYD 88 88  
 FT CARBOHYD 136 136  
 FT CARBOHYD 141 141  
 FT CARBOHYD 156 156  
 FT CARBOHYD 160 160  
 FT CARBOHYD 186 186  
 FT CARBOHYD 197 197  
 FT CARBOHYD 230 230  
 FT CARBOHYD 234 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
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 FT CARBOHYD 289 289  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 332 332  
 FT CARBOHYD 339 339  
 FT CARBOHYD 356 356  
 FT CARBOHYD 386 386  
 FT CARBOHYD 392 392  
 FT CARBOHYD 397 397  
 FT CARBOHYD 406 406  
 FT CARBOHYD 448 448  
 FT CARBOHYD 463 463  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 750 750  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97339 MM; 5FCD81DC3C1209B3 CRC64;  
 Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 96.9%; Pred. No. 2.5e-13;  
 Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LHSLSIESQNOOEKNEDELLEDKWASLWMN 32  
 Db 641 LHSLSIESQNOOEKNEDELLEDKWASLWMN 672  
 RESULT 10  
 ENV\_HV1SC STANDARD; PRT; 856 AA.  
 AC P05878; 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN ENV.  
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88219542; PubMed=3369091;

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,  
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;  
 RT "Envelope sequences of two new United States HIV-1 isolates."  
 RL Virology 164:531-536(1988).  
 CC -i- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
 CC 1984 IN SOUTHERN CALIFORNIA.  
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 CC -----  
 CC EMBL: M17450; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: B28922; VCLJSC.  
 DR HIV: M17450; ENVSSC.  
 DR InterPro: IPR000328; Env-GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KM Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;  
 KW Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 510  
 FT CHAIN 511 856  
 FT SITE 760 760  
 FT DISULFID 53 73  
 FT DISULFID 118 206  
 FT DISULFID 125 197  
 FT DISULFID 130 160  
 FT DISULFID 219 247  
 FT DISULFID 228 239  
 FT DISULFID 266 330  
 FT DISULFID 376 439  
 FT DISULFID 383 412  
 FT CARBOHYD 87 87  
 FT CARBOHYD 129 129  
 FT CARBOHYD 135 135  
 FT CARBOHYD 140 140  
 FT CARBOHYD 143 143  
 FT CARBOHYD 159 159  
 FT CARBOHYD 163 163  
 FT CARBOHYD 189 189  
 FT CARBOHYD 198 198  
 FT CARBOHYD 224 234  
 FT CARBOHYD 241 241  
 FT CARBOHYD 262 262  
 FT CARBOHYD 276 276  
 FT CARBOHYD 295 295  
 FT CARBOHYD 301 301  
 FT CARBOHYD 302 302  
 FT CARBOHYD 331 331  
 FT CARBOHYD 338 338  
 FT CARBOHYD 354 354  
 FT CARBOHYD 360 360  
 FT CARBOHYD 384 384  
 FT CARBOHYD 394 394  
 FT CARBOHYD 400 400  
 FT CARBOHYD 405 405  
 FT CARBOHYD 442 442  
 FT CARBOHYD 457 457  
 FT CARBOHYD 611 611  
 FT CARBOHYD 616 616  
 FT CARBOHYD 625 625  
 FT CARBOHYD 637 637  
 FT CARBOHYD 674 674  
 FT CARBOHYD 816 816  
 SO SEQUENCE 856 AA; 97055 MM; DAF4DA600EBA7A08 CRC64;  
 Query Match 95.0%; Score 170; DB 1; Length 856;  
 Best Local Similarity 93.9%; Pred. No. 2.5e-13;



FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CXC64;

Query Match 93.9%; Score 168; DB 1; Length 852;  
Best Local Similarity 90.9%; Pred. No. 4.3e-13;  
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LHSLSIESQNOEKNEQELLELDKWSLWVNF 33  
Db 637 LITSLIESQNOEKNEQELLELDKWSLWVNF 669

ENV\_HV1A2 STANDARD; PRT; 847 AA.  
AC P05380;  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.

OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
OX NCBI\_TaxID=11705;

RP MEDLINE=86235450; PubMed=3012778;  
Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,  
Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;  
"Genetic variation in HTLV-III/LAV over time in patients with AIDS or  
at risk for AIDS."  
Science 232:1548-1553(1986).  
-I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM  
BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO  
WAS PERINATALLY INFECTED BY HER MOTHER.

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DR EMBL: M12507; AAB12990.1; -  
DR HIV: M12507; ENV5WMJ2.  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;  
Signal.

FT SIGNAL 1 29  
FT CHAIN 30 501  
FT CHAIN 502 847  
FT DISULFID 53 73  
FT DISULFID 118 202  
FT DISULFID 125 193  
FT DISULFID 130 154  
FT DISULFID 130 242  
FT DISULFID 225 236  
FT DISULFID 293 326  
FT DISULFID 372 435  
FT DISULFID 379 408  
FT CARBOHYD 87 87  
FT CARBOHYD 134 134  
FT CARBOHYD 140 140  
FT CARBOHYD 151 151  
FT CARBOHYD 155 155  
FT CARBOHYD 183 183  
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FT CARBOHYD 238 238  
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FT CARBOHYD 327 327  
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FT CARBOHYD 350 350  
FT CARBOHYD 356 356  
FT CARBOHYD 380 380  
FT CARBOHYD 386 386  
FT CARBOHYD 390 390  
FT CARBOHYD 400 400  
FT CARBOHYD 438 438  
FT CARBOHYD 450 450  
FT CARBOHYD 602 602  
FT CARBOHYD 607 607  
FT CARBOHYD 616 616  
FT CARBOHYD 628 628  
SEQUENCE 847 AA; 96466 MW; CDE33D73AAB3CAE CXC64;

Query Match 91.6%; Score 164; DB 1; Length 847;  
Best Local Similarity 90.9%; Pred. No. 1.3e-12;  
Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LHSLSIESQNOEKNEQELLELDKWSLWVNF 33  
Db 632 IYSLIESQNOEKNEQELLELDKWSLWVNF 664

ENV\_HV1A2 STANDARD; PRT; 855 AA.  
AC P03378;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN ENV.

OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).  
OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.  
OX NCBI\_TaxID=11685;

RP MEDLINE=85090453; PubMed=2578227;  
Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,  
Levy J.A., Dina D., Lucif P.A.;  
"Nucleotide sequence and expression of an AIDS-associated retrovirus  
(ARV-2)."  
Science 227:484-492(1985).

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CC -----
DR EMBL: K02007; AAB59882.1; -
DR PIR: A03976; VCLJAZ.
DR HIV: K02007; ENV5SF2.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT DISULFID 53 73
FT DISULFID 118 208
FT DISULFID 125 199
FT DISULFID 130 155
FT DISULFID 221 250
FT DISULFID 231 242
FT DISULFID 299 333
FT DISULFID 380 442
FT DISULFID 387 415
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 140 140
FT CARBOHYD 154 154
FT CARBOHYD 158 158
FT CARBOHYD 184 184
FT CARBOHYD 190 190
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FT CARBOHYD 458 458
FT CARBOHYD 461 461
FT CARBOHYD 610 610
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FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC1A2 CRC64;

Query Match 91.6%; Score 164; DB 1; Length 855;
Best Local Similarity 90.6%; Pred. No. 1,3e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 2 HSLLEESQNOOEKNEQLLELDKQWASLWNF 33
DB 641 IYLLLEESQNOOEKNEQLLELDKQWASLWNF 672
RESULT 15

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ENV_HV1EL STANDARD: PRT: 853 AA.
AC P04581;
DR 13-AUG-1987 (Rel. 05, Created)
DR 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OC NCBI_TaxID=11689;
RX MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients."
RL Cell 46:63-74(1986).
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: K03454; AAA44329.1; -
DR EMBL: A07108; CA00616.1; -
DR HIV: K03454; ENVSELI.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 31
FT CHAIN 32 508
FT DISULFID 53 73
FT DISULFID 118 206
FT DISULFID 125 197
FT DISULFID 130 154
FT DISULFID 219 248
FT DISULFID 229 240
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FT CARBOHYD 406 406
FT CARBOHYD 411 411
FT CARBOHYD 445 445

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FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 853 AA; 96721 MW; F9CD864DAA0D07A5 CRC64;

Query Match 91.1%; Score 163; DB 1; Length 853;  
 Best Local Similarity 90.9%; Pred. No. 1.8e-12;  
 Matches 30; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LHSLSIESONOEKNEOELELDKKNASLWNP 33  
 ||:||||| ||||:|||||  
 Db 638 LHSLSIESOTOEKNEKELELDKKNASLWNP 670

Search completed: May 16, 2003, 11:13:34  
 time : 6.56626 secs

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GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:01:44 ; Search time 24.0542 Seconds  
(without alignments)  
282.676 Million cell updates/sec

Title: US-09-623-533a-119  
Perfect score: 179  
Sequence: 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_21:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.phage:\*  
11: sp.plant:\*  
12: sp.podent:\*  
13: sp.virus:\*  
14: sp.unclassified:\*  
15: sp.rviro:\*  
16: sp.bacteriaph:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	179	100.0	645 15 099336	099336 human immun
2	179	100.0	747 15 070607	070607 human immun
3	179	100.0	748 15 070606	070606 human immun
4	179	100.0	752 15 070604	070604 human immun
5	179	100.0	752 15 070605	070605 human immun
6	179	100.0	752 15 070608	070608 human immun
7	179	100.0	851 15 078243	078243 human immun
8	179	100.0	852 15 089797	089797 human immun
9	179	100.0	854 15 085582	085582 human immun
10	179	100.0	854 15 072502	072502 human immun
11	179	100.0	856 15 092877	092877 simian-huma
12	179	100.0	856 15 074599	074599 human immun
13	179	100.0	856 15 074090	074090 human immun
14	175	97.8	854 15 090178	090178 human immun
15	175	97.8	854 15 078705	078705 human immun
16	174	97.2	856 15 0905M7	0905M7 human immun

17	173	96.6	616 15 0993B0	0993B0 human immun
18	173	96.6	618 15 0993B2	0993B2 human immun
19	173	96.6	757 15 090722	090722 human immun
20	173	96.6	848 15 069990	069990 human immun
21	171	95.5	122 15 091XK6	091XK6 human immun
22	171	95.5	122 15 09Q1W0	09Q1W0 human immun
23	171	95.5	838 15 003806	003806 human immun
24	171	95.5	854 15 078225	078225 human immun
25	171	95.5	855 15 003805	003805 human immun
26	170	95.0	42 15 069910	069910 human immun
27	170	95.0	122 15 091XK2	091XK2 human immun
28	170	95.0	122 15 09YX08	09YX08 human immun
29	170	95.0	122 15 09YX00	09YX00 human immun
30	170	95.0	122 15 091J03	091J03 human immun
31	170	95.0	122 15 091J03	091J03 human immun
32	170	95.0	122 15 091J02	091J02 human immun
33	170	95.0	357 15 078118	078118 human immun
34	170	95.0	357 15 078119	078119 human immun
35	170	95.0	443 15 080023	080023 human immun
36	170	95.0	684 15 091K06	091K06 human immun
37	170	95.0	841 15 041556	041556 human immun
38	170	95.0	843 15 070008	070008 human immun
39	170	95.0	847 15 069996	069996 human immun
40	170	95.0	849 15 077368	077368 human immun
41	170	95.0	849 15 080851	080851 human immun
42	170	95.0	850 15 041591	041591 human immun
43	170	95.0	851 15 056110	056110 human immun
44	170	95.0	851 15 080852	080852 human immun
45	170	95.0	854 15 040222	040222 human immun

## ALIGNMENTS

RESULT 1  
099336 PRELIMINARY; PRT; 645 AA.  
ID 099336  
AC 099336;  
DT 01-JUN-2001 (TRENBLREL 17, Created)  
DT 01-JUN-2001 (TRENBLREL 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLREL 19, Last annotation update)  
DE Truncated envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1007;  
RX MEDLINE=21192672; PubMed=11287644;  
RA Surman S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,  
RA White S.W., Doherty P.C., Hurwitz J.L.,  
RT "Localization of CD4+ T cell epitope hotspots to exposed strands of  
RT HIV envelope glycoprotein suggests structural influences on antigen  
RT processing".  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).  
DR EMBL: AF321563; AAK18810.1;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR AIDS: Coat protein; Envelope protein; Glycoprotein; Polyprotein;  
KW Transmembrane.  
FT NON\_TER  
SO SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;  
Query Match 100.0%; Score 179; DB 15; Length 645;  
Best Local Similarity 100.0%; Pred. No. 8.5e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33  
DB 610 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 642

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RESULT 2
O70607 ID 070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
R Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
P "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA: 84250 MW: 732E836A52245F14 CRC64:

Query Match 100.0%; Score 179; DB 15; Length 747;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 636 LIHSLIESQNOEKNEQELLELDKWSLWNF 668

RESULT 3
O70606 ID 070606 PRELIMINARY: PRT: 748 AA.
AC 070606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
R Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
P "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA: 84224 MW: 56BEFF186C67694B CRC64:

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DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 748
SQ SEQUENCE 748 AA: 84224 MW: 56BEFF186C67694B CRC64:

Query Match 100.0%; Score 179; DB 15; Length 748;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 637 LIHSLIESQNOEKNEQELLELDKWSLWNF 669

RESULT 4
O70604 ID 070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
R Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
P "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12030; AAA7666.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
RA AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA: 84894 MW: 8B30AE894013B45A CRC64:

Query Match 100.0%; Score 179; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 9.9e-14;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LIHSLIESQNOEKNEQELLELDKWSLWNF 33
Db 641 LIHSLIESQNOEKNEQELLELDKWSLWNF 673

RESULT 5
O70605 ID 070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;

```

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW852;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW852;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12031; AAAT76667.1;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SQ SEQUENCE 752 AA; 84894 MW; 8B30AB994013B45A CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9.9e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEQELLELDKASLWNMF 33  
Db 641 LHSLSIESONQOEKNEQELLELDKASLWNMF 673

## RESULT 6

ID 070608 PRELIMINARY; PRT; 752 AA.  
AC 070608;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW87-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker  
infected with HIV type 1 (HIV type IIB).";  
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW87-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12035; AAAT76670.1;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
NON\_TER 752  
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 752;  
Best Local Similarity 100.0%; Pred. No. 9.9e-14;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEQELLELDKASLWNMF 33  
Db 641 LHSLSIESONQOEKNEQELLELDKASLWNMF 673

Db 641 LHSLSIESONQOEKNEQELLELDKASLWNMF 673

## RESULT 7

ID 078243 PRELIMINARY; PRT; 851 AA.  
AC 078243;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Env polyprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carlini F., Federic M., Equestre M., Ricci S., Ratli G., Zibai Q.,  
Verani P., Rossi G.B.;  
RT "Sequence analysis of HIV-1 proviral DNA from a non producer  
chronically infected HUT-78 cellular clone.";  
RN J. Viral Diseases 1:40-55(1992).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-89352106; PubMed-2765297;  
RA Federic M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Macci B., Mangiano N., Verani P., Rossi G.;  
RT "Biological and molecular characterization of producer and non  
producer clones from HUT-78 infected with a patient HIV isolate.";  
RN AIDS Res. Hum. Retroviruses 5:385-396(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Titti F., Federic M., Butto S., Orecchia A., Carlini F., Taddeo B.,  
Boretti A., Saggio I., Verani P., Rossi G.;  
RT "Variability of HIV-1 virus: characteristics of an infected but not  
productive clone.";  
RN Int. J. Immunopharmacol. 3:17-23(1990).  
DR EMBL: Z11530; CAA77628.1;  
DR InterPro: IPR000328; Env\_Gp41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 851;  
Best Local Similarity 100.0%; Pred. No. 1.1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEQELLELDKASLWNMF 33  
Db 636 LHSLSIESONQOEKNEQELLELDKASLWNMF 668

## RESULT 8

ID 089797 PRELIMINARY; PRT; 852 AA.  
AC 089797;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE Envelope glycoprotein.  
GN ENV.  
OS Human immunodeficiency virus type 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-LW90-2;  
RX MEDLINE-95127297; PubMed-7826699;  
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,  
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;  
RT "Viral variability and serum antibody response in a laboratory worker

RT Infected with HIV type 1 (HTLV type IIIB)."  
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).  
[12]  
RP SEQUENCE FROM N.A.  
RC STRAIN-1W90-2;  
RA Mulder K.E.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U12053; AAA76685.1; -;  
DR EMBL: U12036; AAA76671.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Envelope protein; Glycoprotein; Polypotein;  
KW Transmembrane.  
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4EB33CF CRC64;  
  
Query Match 100.0%; Score 179; DB 15; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 33  
Db 637 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 669  
|||||  
  
RESULT 9  
ID 085582 PRELIMINARY; PRT; 854 AA.  
AC 085582;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope polypeptide.  
CN ENV.  
RT Human immunodeficiency virus type 1.  
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OC NCBI\_TaxID=11676;  
OX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
FT J. Virol. 59:284-291(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RL Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.,  
[13]  
RP SEQUENCE FROM N.A.  
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.  
[4]  
RX MEDLINE=92219406; PubMed=1373204;  
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes."  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=119921; AAA44992.1; -;  
DR EMBL: M19921; AAA44992.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
KW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;  
  
Query Match 100.0%; Score 179; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1,1e-13;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 33  
Db 639 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 671  
|||||  
  
RESULT 10  
ID 072502 PRELIMINARY; PRT; 854 AA.  
AC 072502;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ENV polypeptide.  
CN ENV.  
RT Human immunodeficiency virus type 1.  
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OC NCBI\_TaxID=11676;  
OX [1]  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN-NLA-3;  
MEDLINE=96036482; PubMed=7483282;  
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,  
Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;  
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes  
from primary virus cultures using the polymerase chain reaction."  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN-NLA-3;  
MEDLINE=86281827; PubMed=3016298;  
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,  
Martin M.A.;  
RT "Production of acquired immunodeficiency syndrome-associated  
retrovirus in human and nonhuman cells transfected with an infectious  
molecular clone."  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92219406; PubMed=1373204;  
RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;  
RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on  
gp1 results in loss of killing by CD8+ A24-restricted cytotoxic T  
lymphocytes."  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=119921; AAA44992.1; -;  
DR EMBL: M19921; AAA44992.1; -;  
DR InterPro: IPR000328; Env\_GP41.  
DR InterPro: IPR000777; GP120.  
DR Pfam: PF00516; GP120; 1.  
DR Pfam: PF00517; GP41; 1.  
DR AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
KW AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.  
FT CONFLICT 214 214 H -> L (IN REF. 2).  
FT CONFLICT 530 530 A -> S (IN REF. 2).  
FT CONFLICT 739 739 G -> D (IN REF. 2).  
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;  
  
Query Match 100.0%; Score 179; DB 15; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 33  
Db 639 L1HSLIEESQNOOEKNEDELLELDKWSLWNP 671  
|||||  
  
RESULT 11  
ID 092877 PRELIMINARY; PRT; 856 AA.  
AC 092877;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Envelope glycoprotein.  
CN ENV.  
OS Simian-Human immunodeficiency virus.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=57667;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99098984; PubMed=9882298;

CAyabgab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,  
 Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,  
 Sodroski J.G.;  
 "Changes in human immunodeficiency virus type 1 envelope glycoproteins  
 responsible for the pathogenicity of a multiply passaged simian-human  
 immunodeficiency virus (SHV-HXBc2).";  
 J. Virol. 73:976-984(1999).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Cayabgab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,  
 Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;  
 Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 RL EMBL: AF041850; AAD12142.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97151 MW; C50BE038FB73659 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNF 673

## RESULT 12

ID 074599 PRELIMINARY; PRT; 856 AA.  
 AC 074599;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 VIROLOGY 174:103-116(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MCK1;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86068; BAA12995.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNF 673

## RESULT 13

074090

ID 074090 PRELIMINARY; PRT; 856 AA.  
 AC 074090;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Env.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RX MEDLINE-90101366; PubMed-1688473;  
 RA Cloyd M.W., Moore B.E.;  
 RT "Spectrum of Biological Properties of Human Immunodeficiency Virus  
 (HIV-1) Isolates.";  
 VIROLOGY 174:103-116(1990).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PM213;  
 RA Iwatani Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: D86069; BAA13003.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 100.0%; Score 179; DB 15; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 1,1e-13;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLIEESQNOQEKNEDELLELDKWSLWNF 33  
 DB 641 LHSLIEESQNOQEKNEDELLELDKWSLWNF 673

## RESULT 14

ID 090178 PRELIMINARY; PRT; 854 AA.  
 AC 090178;  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID-11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95074930; PubMed-7983770;  
 RA Fang H., Pincus S.H.;  
 RT "Unique insertion sequence and pattern of CD4 expression in variants  
 infected T cells.";  
 J. Virol. 69:75-81(1995).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Fang H., Pincus S.H.;  
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an  
 immunotoxin-resistant variant T cell line.";  
 Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF070521; AAC28452.1; -  
 DR InterPro: IPR000328; Env.GP41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 97.8%; Score 175; DB 15; Length 854;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-13;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWNF 33  
 ||||||||||||||||||||||||||||||||  
 Db 639 LIHSLIEESONQOEKNEQELLELDKWSLWNF 671

## RESULT 15

Q78705 PRELIMINARY; PRT; 854 AA.  
 AC Q78705;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Envelope glycoprotein gp120.  
 GN ENV.  
 OS Human immunodeficiency virus type 1.  
 VS Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 NCBI\_TaxID=11676;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96013815; PubMed-7474132;  
 RA Duensing T.D., Fang H., Dorward D.W., Pincus S.H.;  
 RT "Processing of the envelope glycoprotein gp160 in immunotoxin-  
 RT resistant cell lines chronically infected with human immunodeficiency  
 RT virus type 1.";  
 RL J. VIROL. 69:7122-7131(1995).  
 DR EMBL: I42371; AAA96326.1; -;  
 DR InterPro: IPR000328; Env\_Gp41.  
 DR InterPro: IPR000777; GP120.  
 DR Pfam: PF00516; GP120; 1.  
 DR Pfam: PF00517; GP41; 1.  
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.  
 SQ SEQUENCE 854 AA; 97199 MW; 5B9512216533E256 CRC64;

Query Match 97.8%; Score 175; DB 15; Length 854;  
 Best Local Similarity 97.0%; Pred. No. 3.5e-13;  
 Matches 32; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWNF 33  
 ||||||||||||||||||||||||||||||||  
 Db 639 LIHSLIEESONQOEKNEQELLELDKWSLWNF 671

Search completed: May 16, 2003, 11:19:46  
 time : 25.1256 secs

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:03:40 ; Search time 9.34337 Seconds  
(without alignments)  
103.919 Million cell updates/sec

Title: US-09-623-533a-119

Perfect score: 179

Sequence: 1 LHSLSIESONQOEKNEQELLELDKWSILMNWF 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCRTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	179	100.0	33	1 US-08-073-028-72	Sequence 72, Appl
2	179	100.0	33	3 US-08-484-223B-235	Sequence 235, App
3	179	100.0	33	4 US-08-554-616-72	Sequence 72, Appl
4	179	100.0	33	4 US-09-082-279B-61	Sequence 61, Appl
5	179	100.0	33	4 US-09-082-279B-639	Sequence 639, App
6	179	100.0	33	4 US-09-082-279B-801	Sequence 801, App
7	179	100.0	33	4 US-08-474-349A-417	Sequence 417, App
8	179	100.0	33	4 US-09-315-304B-61	Sequence 61, Appl
9	179	100.0	33	4 US-09-315-304B-639	Sequence 639, App
10	179	100.0	33	4 US-09-315-304B-801	Sequence 801, App
11	179	100.0	34	1 US-08-073-028-73	Sequence 73, Appl
12	179	100.0	34	4 US-08-554-616-73	Sequence 73, Appl
13	179	100.0	34	4 US-09-082-279B-800	Sequence 800, App
14	179	100.0	34	4 US-09-315-304B-800	Sequence 800, App
15	179	100.0	35	1 US-08-073-028-74	Sequence 74, Appl
16	179	100.0	35	4 US-08-484-223B-234	Sequence 234, App
17	179	100.0	35	4 US-08-554-616-74	Sequence 74, Appl
18	179	100.0	35	4 US-09-082-279B-638	Sequence 638, App
19	179	100.0	35	4 US-09-082-279B-799	Sequence 799, App
20	179	100.0	35	4 US-08-474-349A-416	Sequence 416, App
21	179	100.0	35	4 US-09-315-304B-638	Sequence 638, App
22	179	100.0	35	4 US-09-315-304B-799	Sequence 799, App
23	179	100.0	36	1 US-08-073-028-1	Sequence 1, Appl
24	179	100.0	36	3 US-08-486-099-1	Sequence 1, Appl
25	179	100.0	36	3 US-09-071-877-1	Sequence 1, Appl
26	179	100.0	36	3 US-08-360-107A-1	Sequence 1, Appl
27	179	100.0	36	3 US-08-484-223B-1	Sequence 1, Appl

28	179	100.0	36	3 US-08-484-223B-231	Sequence 231, App
29	179	100.0	36	3 US-08-484-223B-232	Sequence 232, App
30	179	100.0	36	3 US-08-484-223B-233	Sequence 233, App
31	179	100.0	36	3 US-08-919-597-1	Sequence 1, Appl
32	179	100.0	36	3 US-08-475-668A-1	Sequence 1, Appl
33	179	100.0	36	3 US-08-485-551A-1	Sequence 1, Appl
34	179	100.0	36	3 US-08-471-913A-1	Sequence 1, Appl
35	179	100.0	36	4 US-08-554-616-1	Sequence 1, Appl
36	179	100.0	36	4 US-08-485-264A-1	Sequence 15, Appl
37	179	100.0	36	4 US-09-082-279B-15	Sequence 497, App
38	179	100.0	36	4 US-09-082-279B-497	Sequence 498, App
39	179	100.0	36	4 US-09-082-279B-498	Sequence 559, App
40	179	100.0	36	4 US-09-082-279B-559	Sequence 560, App
41	179	100.0	36	4 US-09-082-279B-560	Sequence 561, App
42	179	100.0	36	4 US-09-082-279B-561	Sequence 603, App
43	179	100.0	36	4 US-09-082-279B-603	Sequence 630, App
44	179	100.0	36	4 US-09-082-279B-630	Sequence 631, App
45	179	100.0	36	4 US-09-082-279B-631	Sequence 631, App

## ALIGNMENTS

RESULT 1  
US-08-073-028-72  
; Sequence 72, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Danl P.  
; APPLICANT: Mathews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; NUMBER OF INVENTIONS: TRANSMISSION  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 33 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-073-028-72  
Query Match 100.0%; Score 179; DB 1; Length 33;  
Best local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 1 LHSLSIESONQOEKNEQELLELDKWSILMNWF 33  
1 LHSLSIESONQOEKNEQELLELDKWSILMNWF 33

RESULT 2  
US-08-484-223B-235  
Sequence 235, Application US/08484223B  
Patent No. 6020459  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 245  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 235:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-235

Query Match 100.0%; Score 179; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQLELLELDKWSLWNMF 33  
|||||  
Db 1 LHSLSIESONQOEKNEQLELLELDKWSLWNMF 33

RESULT 3  
US-08-554-616-72  
Sequence 72, Application US/08554616  
Patent No. 6133418  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Petleway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/554,616  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,028  
FILING DATE: 07-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-72

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQLELLELDKWSLWNMF 33  
|||||  
Db 1 LHSLSIESONQOEKNEQLELLELDKWSLWNMF 33

RESULT 4  
US-09-082-279B-61  
Sequence 61, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohamed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 61  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-61

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQLELLELDKWSLWNMF 33  
|||||

DB 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 5

US-09-082-279B-639

Sequence 639, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 639

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-639

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

DB 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 6

US-09-082-279B-801

Sequence 801, Application US/09082279B

Patent No. 6258782

GENERAL INFORMATION:

APPLICANT: Barney, Shawn

APPLICANT: Guthrie, Kelly

APPLICANT: Merutka, Gene

APPLICANT: Anwer, Mohamed

APPLICANT: Lambert, Dennis

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES

FILE REFERENCE: 7872-043

CURRENT APPLICATION NUMBER: US/09/082,279B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1515

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 801

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-082-279B-801

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

DB 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 7

US-08-474-349A-417

Sequence 417, Application US/08474349A

Patent No. 6333395

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Pelleway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA

TITLE OF INVENTION: VIRUS TRANSMISSION

NUMBER OF SEQUENCES: 517

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penite & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,349A

FILING DATE: 07-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-024

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 417:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-474-349A-417

Query Match

Best Local Similarity 100.0%; Score 179; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 7.7e-16;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

DB 1 LHSLSIESONQOEKNEDELLELDKWSLWNMF 33

RESULT 8

US-09-315-304B-61

Sequence 61, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

TITLE OF INVENTION: PROPERTIES

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 61  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-61

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33  
DB 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33

RESULT 9  
US-09-315-304B-639

Sequence 639, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 639

LENGTH: 33

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Core polypeptide

US-09-315-304B-639

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33  
DB 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33

RESULT 10  
US-09-315-304B-801

Sequence 801, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 801  
LENGTH: 33  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-801

Query Match 100.0%; Score 179; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 7.7e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33  
DB 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33

RESULT 11

US-08-073-028-73

Sequence 73, Application US/08073028

Patent No. 5464933

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSER: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,028

FILING DATE: 07-JUN-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-004-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8664/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-073-028-73

Query Match 100.0%; Score 179; DB 1; Length 34;  
Best Local Similarity 100.0%; Pred. No. 7.9e-16;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONOEKNEDELLELDKWSLWNWF 33  
DB 2 LHSLSIESONOEKNEDELLELDKWSLWNWF 34

RESULT 12

US-08-554-616-73

Sequence 73, Application US/08554616



APPLICATION NUMBER: US/08/073.028  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: COIUZZI, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 7872-004-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEFAX: (212) 869-8864/9741  
 TELEX: 66141 PENNITE  
 INFORMATION FOR SEQ ID NO: 74:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 35 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 US-08-073-028-74

Query Match 100.0%; Score 179; DB 1; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-16;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LIHSLIESQNOQEKNEQELLELDKWSLWNP 33  
 ||||||||||||||||||||||||||||  
 DB 3 LIHSLIESQNOQEKNEQELLELDKWSLWNP 35

Search completed: May 16, 2003, 11:22:12  
 Job time: 10.3434 secs

GenCore version 5.1.4-p5.4578  
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OM protein - protein search, using sw model

Run on: May 16, 2003, 11:20:00 ; Search time 14.4458 Seconds  
(Without alignments)  
220.333 Million cell updates/sec

Title: US-09-623-533a-119  
Perfect score: 179  
Sequence: 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues  
Number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: Published\_Applications\_AA:\*
  - 2: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
  - 3: /cgn2\_6/ptodata/1/pubppaa/PC7\_NEW\_PUB.pep:\*
  - 4: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
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  - 9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
  - 10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*
  - 11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*
  - 12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*
  - 13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
  - 14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	179	100.0	36	9 US-09-874-475-16	Sequence 16, Appl
2	179	100.0	36	9 US-10-116-797-1	Sequence 1, Appl
3	179	100.0	36	9 US-09-493-346-1	Sequence 10, Appl
4	179	100.0	36	10 US-09-796-202-10	Sequence 5, Appl
5	179	100.0	36	10 US-09-779-451-5	Sequence 1, Appl
6	179	100.0	36	10 US-09-834-628-1	Sequence 108, App
7	179	100.0	36	10 US-09-854-816-1	Sequence 41, Appl
8	179	100.0	36	9 US-09-848-616-176	Sequence 4, Appl
9	179	100.0	37	9 US-09-779-451-41	Sequence 84, Appl
10	179	100.0	46	10 US-09-779-451-4	Sequence 82, Appl
11	179	100.0	56	10 US-10-040-349B-2	Sequence 97, Appl
12	179	100.0	177	9 US-10-059-271-81	Sequence 16, Appl
13	179	100.0	221	9 US-10-059-271-84	Sequence 17, Appl
14	179	100.0	232	9 US-10-059-271-81	Sequence 18, Appl
15	179	100.0	254	9 US-10-059-271-82	
16	179	100.0	256	9 US-09-854-816-15	
17	179	100.0	268	10 US-09-854-816-17	
18	179	100.0	268	10 US-09-854-816-18	
19	179	100.0	268	10 US-09-854-816-18	

20	179	100.0	344	9 US-10-040-349B-1	Sequence 1, Appl
21	179	100.0	345	9 US-10-026-741-49	Sequence 49, Appl
22	179	100.0	345	10 US-09-779-451-8	Sequence 8, Appl
23	179	100.0	391	9 US-10-059-271-93	Sequence 93, Appl
24	179	100.0	519	10 US-09-756-351A-8	Sequence 8, Appl
25	179	100.0	853	9 US-10-003-035-33	Sequence 33, Appl
26	179	100.0	856	10 US-09-476-242-1	Sequence 1, Appl
27	179	100.0	861	9 US-10-026-741-103	Sequence 103, App
28	179	100.0	1101	9 US-10-003-035-53	Sequence 53, Appl
29	179	100.0	1186	9 US-10-003-035-55	Sequence 55, Appl
30	176	98.3	36	10 US-09-912-824-1	Sequence 1, Appl
31	176	98.3	268	10 US-09-854-816-19	Sequence 19, Appl
32	173	96.6	1231	9 US-10-059-271-94	Sequence 94, Appl
33	171	95.5	268	10 US-09-854-816-13	Sequence 13, Appl
34	170	95.0	46	10 US-09-854-816-109	Sequence 109, App
35	170	95.0	233	10 US-09-854-816-50	Sequence 50, Appl
36	170	95.0	267	10 US-09-854-816-38	Sequence 38, Appl
37	170	95.0	268	10 US-09-854-816-9	Sequence 9, Appl
38	170	95.0	268	10 US-09-854-816-26	Sequence 26, Appl
39	170	95.0	268	10 US-09-854-816-41	Sequence 41, Appl
40	170	95.0	269	10 US-09-854-816-6	Sequence 6, Appl
41	170	95.0	269	10 US-09-854-816-12	Sequence 12, Appl
42	170	95.0	269	10 US-09-854-816-43	Sequence 43, Appl
43	170	95.0	619	10 US-09-891-609-4	Sequence 4, Appl
44	170	95.0	646	10 US-09-891-609-2	Sequence 2, Appl
45	170	95.0	847	10 US-09-476-242-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-874-475-16  
Sequence 16, Application US/09874475  
Publication No. US20020182592A1  
GENERAL INFORMATION:  
APPLICANT: Petropoulos, Christos J.  
APPLICANT: Parkin, Neil T.  
APPLICANT: Whitcomb, Jeanette  
APPLICANT: Huang, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE  
TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS  
FILE REFERENCE: 2793/6516  
CURRENT APPLICATION NUMBER: US/09/874, 475  
CURRENT FILING DATE: 2001-06-04  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Fusion Inhibitor Peptide  
US-09-874-475-16

Query Match 100.0%; Score 179; DB 9; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 33  
Db 4 LIHSLIEESONQOEKNEQELLELDKWSLWVWF 36

RESULT 2  
US-10-116-797-1  
Sequence 1, Application US/10116797  
Publication No. US2003004411A1  
GENERAL INFORMATION:  
APPLICANT: Olsen, William C.  
APPLICANT: Maddon, Paul J.  
TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION  
FILE REFERENCE: 64672-A  
CURRENT APPLICATION NUMBER: US/10/116, 797  
CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-797-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 9; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
|||||  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 3

US-09-493-346-1  
Sequence 1, Application US/09493346  
Publication No. US20030082185A1  
GENERAL INFORMATION:

APPLICANT: Olson, William C  
APPLICANT: Maddon, Paul J  
TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1  
TITLE OF INVENTION: Infection  
FILE REFERENCE: 61009  
CURRENT APPLICATION NUMBER: US/09/493,346  
CURRENT FILING DATE: 2000-01-28  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: T20 peptide  
US-09-493-346-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 9; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
|||||  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

## ULT 4

US-09-796-202-10  
Sequence 10, Application US/09796202  
Patent No. US2002006813A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 10  
LENGTH: 36  
TYPE: PRT  
ORGANISM: unknown  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(36)  
OTHER INFORMATION: T-20  
US-09-796-202-10

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
|||||  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 5

US-09-779-451-5  
Sequence 5, Application US/09779451  
Patent No. US2002009452A1  
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.  
APPLICANT: Allaway, Graham P.  
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors  
FILE REFERENCE: 1900.030003  
CURRENT APPLICATION NUMBER: US/09/779,451  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: US 60/235,901  
PRIOR FILING DATE: 2000-09-28  
PRIOR APPLICATION NUMBER: US 60/181,543  
PRIOR FILING DATE: 2000-02-10  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 5  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-09-779-451-5

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
|||||  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

## RESULT 6

US-09-834-628-1  
Sequence 1, Application US/09834628  
Patent No. US2002011922A1  
GENERAL INFORMATION:

APPLICANT: YU, YEON GYU  
APPLICANT: KIM, BONG-SUK  
APPLICANT: JIN, BONG-SUK  
TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION  
FILE REFERENCE: 05823.0198-00000  
CURRENT APPLICATION NUMBER: US/09/834,628  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: KR 00-65664  
PRIOR FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 1  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
OTHER INFORMATION: DP178  
US-09-834-628-1

Query Match  
Best Local Similarity 100.0%; Score 179; DB 10; Length 36;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 33  
|||||  
DB 4 LHSLSIESQNOQEKNEQELLELDKWSLWNMF 36

RESULT 7  
US-09-854-816-1  
; Sequence 1, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Pheasant  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/854,816  
; FILING DATE: 15-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, Ph.D., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P1005R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: DP178  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
09-854-816-1  
Query Match 100.0%; Score 179; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5,8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESONOQEKNEQELLELDKWSLWMP 33  
|||||  
DB 4 LHSLSIESONOQEKNEQELLELDKWSLWMP 36  
|||||  
RESULT 8  
US-09-854-816-108  
; Sequence 108, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Pheasant  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same  
; NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Winpatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, Ph.D., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 108:  
US-09-854-816-108  
Query Match 100.0%; Score 179; DB 10; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5,8e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESONOQEKNEQELLELDKWSLWMP 33  
|||||  
DB 4 LHSLSIESONOQEKNEQELLELDKWSLWMP 36  
|||||  
RESULT 9  
US-09-848-616-176  
; Sequence 176, Application US/09848616  
; Publication No. US20030054010A1  
; GENERAL INFORMATION:  
; APPLICANT: Sebbel, Peter  
; APPLICANT: Dunant, Nicolas  
; APPLICANT: Bachmann, Martin  
; APPLICANT: Tissot, Alain  
; APPLICANT: Lechner, Franziska  
; TITLE OF INVENTION: Molecular Antigen Array  
; FILE REFERENCE: 1700.0180002  
; CURRENT APPLICATION NUMBER: US/09/848,616  
; CURRENT FILING DATE: 2001-05-05  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 176  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: DP178c peptide  
US-09-848-616-176  
Query Match 100.0%; Score 179; DB 9; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5,9e-15;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LHSLSIESONOQEKNEQELLELDKWSLWMP 33  
|||||

Db 5 LHSLSIESONQOEKNEQELLELDKWSLWNWF 37

RESULT 10

US-09-779-451-41

; Sequence 41, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 41

LENGTH: 46

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-41

Query Match 100.0%; Score 179; DB 10; Length 46;

Best Local Similarity 100.0%; Pred. No. 7.4e-15;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWNWF 33

Db 14 LHSLSIESONQOEKNEQELLELDKWSLWNWF 46

RESULT 11

US-09-779-451-4

; Sequence 4, Application US/09779451

; Patent No. US20020094521A1

; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.

; APPLICANT: Allaway, Graham P.

; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors

; FILE REFERENCE: 1900.0300003

; CURRENT APPLICATION NUMBER: US/09/779,451

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: US 60/235,901

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/181,543

; PRIOR FILING DATE: 2000-02-10

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 56

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

US-09-779-451-4

Query Match 100.0%; Score 179; DB 10; Length 56;

Best Local Similarity 100.0%; Pred. No. 9.1e-15;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWNWF 33

Db 19 LHSLSIESONQOEKNEQELLELDKWSLWNWF 51

RESULT 12

US-10-040-349B-2

; Sequence 2, Application US/10040349B

; Publication No. US20030082521A1

; GENERAL INFORMATION:

; APPLICANT: Brassecr, Robert

; APPLICANT: Charlotiaux, Benoit

; APPLICANT: Chevalier, Michel

; APPLICANT: El Habib, Raphaelle

; APPLICANT: Krell, Tino

; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV

; FILE REFERENCE: 01-078-A

; CURRENT APPLICATION NUMBER: US/10/040,349B

; CURRENT FILING DATE: 2002-07-09

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 177

TYPE: PRT

; ORGANISM: Human immunodeficiency virus type 1

FEATURE:

NAME/KEY: Peptide

LOCATION: (1)..(177)

; OTHER INFORMATION: polypeptide derived from gp41 LAT

US-10-040-349B-2

Query Match 100.0%; Score 179; DB 9; Length 177;

Best Local Similarity 100.0%; Pred. No. 2.9e-14;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWNWF 33

Db 107 LHSLSIESONQOEKNEQELLELDKWSLWNWF 139

RESULT 13

US-10-059-271-84

; Sequence 84, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDD, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

; FILE REFERENCE: ALBRE-22

; CURRENT APPLICATION NUMBER: US/10/059,271

; CURRENT FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: DE 101 06 295

; PRIOR FILING DATE: 2001-02-02

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 84

LENGTH: 221

TYPE: PRT

; ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-059-271-84

Query Match 100.0%; Score 179; DB 9; Length 221;

Best Local Similarity 100.0%; Pred. No. 3.6e-14;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LHSLSIESONQOEKNEQELLELDKWSLWNWF 33

Db 134 LHSLSIESONQOEKNEQELLELDKWSLWNWF 166

RESULT 14

US-10-059-271-81

; Sequence 81, Application US/10059271

; Publication No. US20030082208A1

; GENERAL INFORMATION:

; APPLICANT: REPKE, HEINRICH

; APPLICANT: BUDD, ECKHARD

; APPLICANT: NICOLAUS, STEFAN

; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND